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Toolbox for Visual Explorative Analysis of Complex Temporal Multiscale Contact Networks Dynamics in Healthcare

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Abstract

Public healthcare can be cast as a complex systems and network analysis is one of the methodological approaches that are commonly used to study these types of systems. In this paper we describe a multi-scale and multi-level interpretation of complex networks in public healthcare. Our contribution is to provide a toolbox for visualization and visual data-driven analysis of complex multiscale temporal contact networks that allows to simulate various dynamic processes using user-defined models. An example of explorative analysis of a dataset from real clinical data obtained from the Federal Almazov North-West Medical Research Centre in Saint Petersburg is described.

Keywords: Multiscale networks, Graph and network visualization, Interactive simulation, EMR

1 Introduction

Public healthcare can be cast as a complex system because of its interdisciplinary nature, heterogeneous elements that interact with each other, non-linearity, persistence over time and adaption to changing circumstances. System dynamics and network analysis are two of the methodological approaches that are commonly used to study these types of systems [1]. The structure and processes of complex systems networks display a rich variety of temporal, multiscale and multidimensional configurations depending on specific aspects of the system under consideration. A convenient and compelling way to analyze structure and processes in complex networks is visualization [2], [3].

Due to the complexity and multiscale nature of processes occurring throughout the healthcare system, network structures will be present on a many different scales and levels [4]. One commonly studied process is infection spreading. This multiscale problem requires data from macroscale mobility networks and spatial spreading [5] to microscale spreading in individual contact networks [6]. An important and urgent task is better understanding and controlling of spreading of infectious diseases within hospitals and other large health care centers [7], [8].

The use of visual analytics of complex data and processes in multiscale networks within medical decision support systems (DSS), especially at the scale of hospitals and larger [9] can improve the usability of such DSS for the applied end-user as well as for the efficiency of the whole system. In addition, with the ability to use visualization in conjunction with interactive simulation of network processes, a medical DSS can be used in emergency situations to quickly identify sources of threats or forecast potential threats. Our main contribution is to provide a toolbox for visualization and visual data-driven analysis of complex multiscale temporal contact networks that allows to simulate various dynamic processes using user-defined models.

2 Related works

Visual representation could help in understanding the nature of specific network features. The main goal of visual analysis is to study the processes occurring in networks and to explore new features, which is usually hard to detect directly from data analysis [10]. Nowadays, the representation of networks as graph had become widely spread: this way of visualization proved successful in several projects [11], [12] for the last two decades. Taking into account features of networks software designed specifically for visualization of graph structures was developed. The results obtained with the help of this kind of applications should satisfy certain criteria [13]. The most important are minimization of edge intersections, total edge length, and size of network area.

Matching visualization of the aforementioned criteria could be achieved by different ways of graph representation [14]. Various graph layouts in two and three-dimensional space could enhance the understanding of graph structure and simplify its analysis; the most preferable graph layout is force directed [15] and its extensions [16].

With evolving technologies allowing to process huge amount of data, the visualization of large networks occupies a special place. It is important to correctly display the network structure and to avoid the overabundance of final visualization with unnecessary data [17]. A significant role is taken by scalability of graphs [2], where on the different visualization levels different number of nodes are displayed while preserving the overall structure. One of the most popular framework for large graph visualization is Gephi [18] developed in 2008. This platform allows to visualize large and dynamic networks, which are changing their structure over time. However, a user cannot run the processes on the network in real-time because of the need for pre-calculations and despite the presence of a high quality vector rendering engine, three-dimensional layouts are not supported.

Visualization of dynamic processes [19] in temporal networks could be displayed by nodes appearing and disappearing with time, as well as by changing node-to-node interaction and by managing some visual characteristics such as shape and size of nodes [20]. Moreover, color encoding could also be used in exploring processes in dynamic graph. For example, Collberg et al. [21] used a color palette to indicate node activity. To distinguish current data from outdated information, color intensity could be varied depending on elapsed time: earlier events should be displayed with less intensity value than occurring events [22].

A number of applications have been developed for bioinformatics [23], biology and medicine that could be easily applied to other domains. In 2003, Breitkreutz, Stark and Tyers [24] presented a system for static visualization of biological processes where different kind of processes were encoded by different colors. For analysis of patient network in a hospital there was developed the tool Ayasdi Care

was developed [25], which allows to evaluate the effectiveness of treatment for different type of diseases. Nevertheless, this application operates only with static graphs and does not support dynamic visualization. Heer and Perer [3] presented a system for modelling and visualization of multidimensional heterogeneous networks. This system allows to explore dynamic processes in a network, for example, the symptom evolution during the diseases. In spite of the fact that system allows to represent network as graphs, the dynamic processes are displayed as matrix [26].

Despite the ongoing evolution in technique and software for graph visualization and visual analysis, there is a lack of applications enabling exploration of dynamic processes in complex networks with real-time interaction abilities.

3 Conceptual background

3.1 Multi-scale multi-layered dynamic contact networks

General dynamic contact networks can be considered within a context of temporal networks [27] as a graph with dynamically changing edges. Core contact network is usually built around personal contacts defined explicitly or implicitly (e.g. through some proximity measure). Within our work, we propose extension of the network structure with additional classes of objects that enable reflection of the following aspects: a) mobility of agents on various temporal and spatial scales (local mobility within the particular rooms and places, moving between different locations in the city, etc.); b) indirect contacts (e.g. by the collective use of specific objects, location in the same place but in different time). As a result, temporal network contains the following vertices (see fig. 1a):

1. Agents (people) who are the main actors within the analyzed contact network. There can be several roles for the agents, and different behavioral scenarios. Temporal contacts (i.e. edges of the graph) can be identified by proximity measures or explicit mentioning in data.
2. Objects which can be used by agents to interact by collective access. They can be either mobile (as personal belongings of the agent) or located in particular place. The passive objects are introduced in the network as in some cases it should be considered within a context of connectivity (e.g. for infection spreading process).
3. Local (usually indoor) places with floor plans and furniture which can be used to precise identification of positions, mobility, interaction and proximity. The agents and local objects are situated at particular position within the location (which can change over time).
4. Global location which refer to certain geographical position and include hierarchically local places with its plans. Global locations exist in the environment (e.g. city) and are used to describe global mobility of agents: moving through the city, transferring from one location to another etc.

To extend the temporal network and enhance its exploration process in addition to temporal edges several aggregated edges can be introduced to describe connectivity of the vertices (see dashed lines in fig. 1a). Selected aggregated edges are identified between vertices of the same class by analysis of historical contacts (for agents and objects) or mobility of agents (for locations and places).

As the important part of the temporal network analysis is time-propagation of contacts, our approach to analysis includes several techniques to analyze temporal structure of contacts. First, indirect contacts are introduced as paths between vertices which are contacted by any mediator on previous step(s) (see fig. 1b). Mediator can be either an object of another agent. Additionally, the mediator can be from a specific subclass of the agents or objects. E.g. an indirect contact network of physicians can be reconstructed using patients as mediators.

Second, a tree of possible influence propagated back in time (see fig. 1c) is introduced a concept used to analyze a sub-graph of possible contacts build from particular vertex (here p_0) starting from

particular time and going back in the past. A declining influencing function which decreases with increasing time delay is selected empirically. Contacts detected in the past initialize the value for corresponding vertices (here $p_1 \dots p_6$) according to the current value of the influencing function of transmitter and length of the contact. Such tree allows to analyze the possible coverage of the network and paths of transmitting within a context of spreading process with visual representation on the static graph.

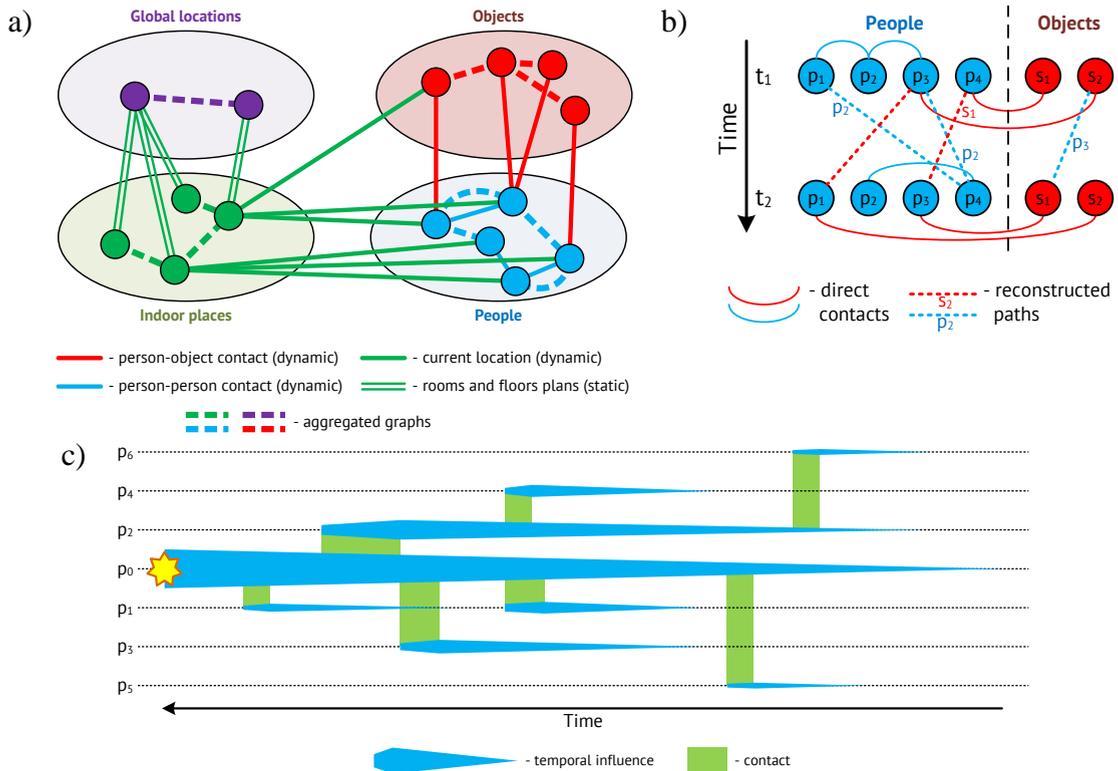


Figure 1: Analysis of temporal contact networks a) multi-scale dynamic network; b) temporal contact paths tracing; c) temporal influence propagation

3.2 Multiscale modeling and simulation

Within the proposed approach a contact network can include different scales with related patterns of mobility, proximity measures and information sources. For healthcare, a network can be initially built using basic information about mobility, locations and activity of agents of different roles (physicians, patients, visitors in hospital etc.). This information can be obtained from medical information systems or collected using a range of sensors (camera records, electronic passes, health-tracking wristbands etc.). Moreover, the network can be refined and extended using simulation-based techniques with incorporation of different models. This section describes our multiscale approach to develop a complex system of models which enable support of temporal contact network reconstruction in the healthcare context.

We distinguish three scales of agents' mobility (see fig. 2):

1. City scale depicts mobility of agents between different hospitals and departments as well as transferring of patients from/to home or recreation centers. This includes a set of hospitals and other locations in the city and suburban with certain geospatial location.

Patient mobility data include information on patients' entry and departure for hospitals. To extent the information on this layer a traffic model can be used to estimate transfer time and routes using regular or ambulance cars [28].

2. Hospital scale includes information on transfers between departments in hospital with respect to the structure of the building(s) and high-level floor plans. Beside the department-level transferring mobility this scale can include scheduled access to medical facilities, surgeries and hospital-scale personal mobility (e.g. canteen visiting, going out for personal needs etc.).
3. Personal scale includes personal behavioral models based on scheduled activity of agents according to their roles. Interaction with doctors, other patients and visitors in a ward, observation rooms and corridors are included as well. Higher-level context of these interactions and mobility is based on the scheduled activity planned or stored in medical records, while lower-level contact network and proximity measuring is performed using agent-based modeling (ABM).

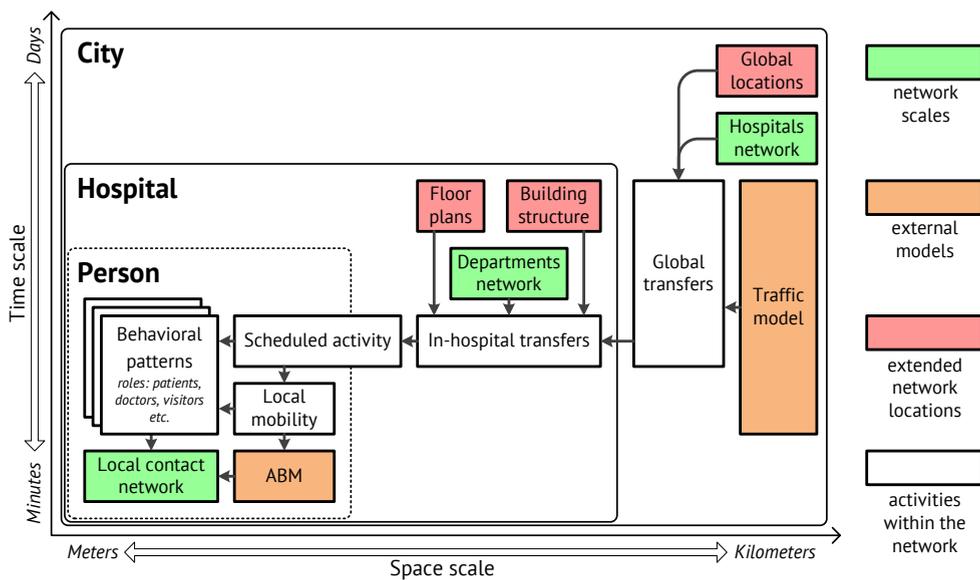


Figure 2: Multiscale modeling of temporal networks

As a result of interconnection of the mentioned models a multi-scale temporal network reconstruction can be considered twofold: a) data-driven approach on the basis of medical records, sensors data and traffic information to estimate original or planned mobility and contacts of agents; b) simulation-based estimation of local mobility of agents using ABM and global transfers according to the traffic information using traffic models.

3.3 Visual interactive analysis of spreading process

Visualization is an effective tool for understanding and communication with data than the use of common numerical tools alone. Visualization of networks as a spatial graph allows quickly determine and clearly understand structure of this network. Using three-dimensional graph layouts is not the most common approach for displaying networks in static way. However, in cases of explorative analysis of large networks third spatial dimension (other than sampling, clustering and other techniques) bring more freedom and flexibility in the course of the study. The ability to navigate in three-dimensional space in this case is an integral functional satellite. Spatial layout of networks also very suitable for exploring and analysis of spreading processes in virtue of intuitively clear displaying of the process. As toolbox

we propose to use an interactive environment with graphic user interface that complements processes displayed on the spatial visualization of contact networks.

4 Experimental study

4.1 Visualization toolbox implementation description

A visualization toolbox was developed as a standalone DirectX11 application using the Fusion Framework [29], C# and HLSL. As input data, the system can import a set of descriptive data – a simple list of vertices and links (Trivial Graph Format). Extended information about nodes and edges such as time and duration of an event, link weight, semantic description, affiliation to a group, network of another level or scale can be imported. Furthermore, it is possible to add information about additional entities, for instance, patients could be represented either as node in a contact network or as a set of edges that links the physicians over time. All extra data could be used during the simulation to achieve the most accurate playback of visualizing process.

As a basis for graph drawing we used an improved force-directed layout algorithm [30], where the major part of spatial layout computations was moved to a GPU. It is possible to draw the graph in two modes: static and dynamic. In the static mode, a node position depends on forces for all nodes and links assuming they all are constant and the graph topology is not evolving through time. For dynamic graphs, the forces of mutual repulsion are permanent for all vertices, in contrast, the attractive forces are computed upon appearance of an edge between two nodes and during contact time. These computations perform within the GPU considering all supplementary parameters, which could be modified for each particular case individually.

Our graph visualization system in the toolbox makes possible to define desired visual encodings for each aspect of the graph in advance or set the rule for dynamic changes during the visualization of network processes. Edges could be colored by gradients (using node-dependent coloring) as well as by a solid color. For dynamic visualization this approach allows to demonstrate the direction of the edge between nodes.

4.2 Multiscale contact network

To analyze the capabilities of the toolbox a sample multiscale contact network was reconstructed using electronic medical records (EMR) for 3980 episodes with resuscitation related to heart diseases obtained from the Federal Almazov North-West Medical Research Centre (further, FANWMRC) in Saint Petersburg*. Several networks were reconstructed within the multi-scale structure presented in Section 3.2.

City-scale network includes a set of locations (hospitals, home addresses) where the patients were situated and transfer between those locations. As an example, fig. 3a shows transfers from different hospitals in Saint-Petersburg area to FANWMRC (size of nodes represents number of transfers from particular hospital, numbers represent the id of hospitals).

Hospital-scale network includes transfers between departments in hospital as well as hospital-scale scheduled activity. The network can be extended with specific meta-nodes which depicts classes of in and out flow of patients. For example, fig. 3b shows main departments of FANWMRC involved into treatment within the considered cases. Two classes of departments (different by color) depict two subdivisions of FANWMRC (central office and branch office, situated at different locations in the city). To show possible incomes the following meta-nodes are included into graph: urgent (ambulance), transfer from other hospital, planned admission and free-run (fig. 3b, pink nodes). Another class of meta-

* <http://www.almazovcentre.ru/?lang=en>

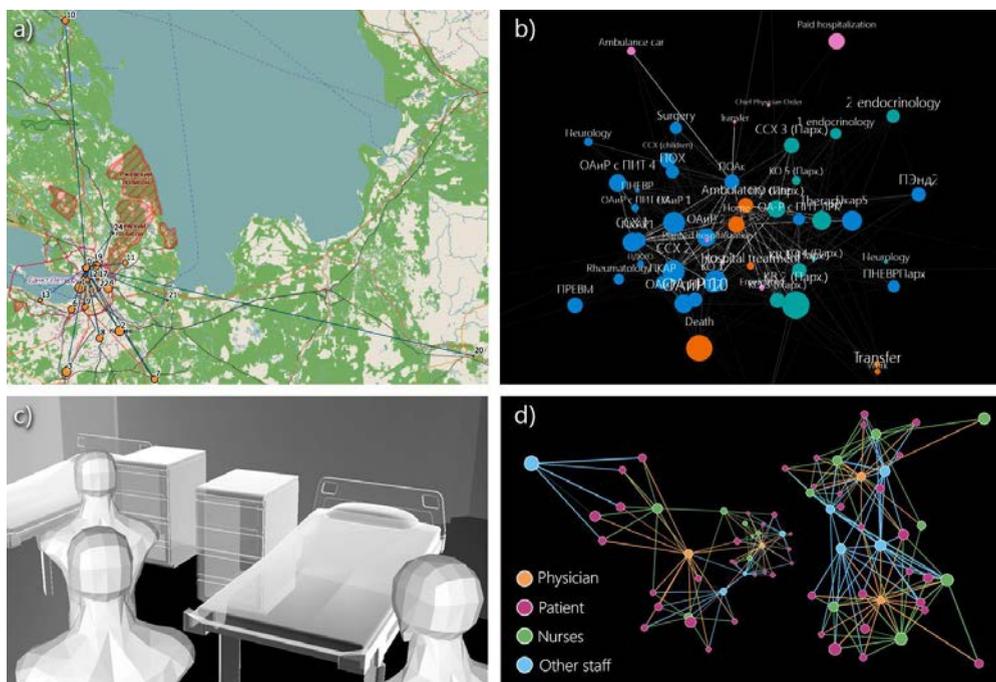


Figure 3: Multiscale modeling of temporal networks - a) city-scale network; b) departments of hospital; c) visualization of agent-based modeling of in-hospital contacts; d) reconstructed local contact network

nodes are dismissal (fig. 3b, orange nodes): home, ambulatory medical care, rehabilitation treatment, transfer to another health facility, hospital care and death. The nodes are connected within temporal network while the depicted graph presents integrated weighted edges with weight proportional to the transfer rate. To connect the network to higher scale meta-nodes of several classes can be expanded to reach distant locations on the city-scale.

Personal patient-doctor contact network can be reconstructed using EMR which stores information on types and timeline of contacts between selected patients and doctors within the treatment process. This level of network extends hospital-level mobility with direct personal contacts. It includes surgeries, scheduled visits of doctor, clinical tests and other procedures which can be considered within a scope of contacts. This network level is described and demonstrated with more details in Section 4.3.

Agent-based contact network extends personal contact network with simulation based contact network which is reconstructed using agent-based modeling to reflect local mobility of patients and doctors within selected department of hospital (see fig. 3c).

The environment and agents are required parts of agent-based model. The environment is represented as scheme of hospital with obstacles, rooms and points of interests (such as beds, toilets etc.), while agents are represented by behavioral and physical features. In order to represent the behavior of agents four roles of was defined: (1) patients, (2) doctors, (3) nurses, (4) ward maids. Mobility of agents is implemented as multilevel system: the first level is navigation in space and the second is collision avoidance. The model takes into account the duration of contact, the type (direct or droplet), and the roles of the contacting agents. The example of contact network obtained by agent-based simulation is represented on fig. 3d.

4.3 Interactive visualization

Personal patient-doctor contact network used to extract an indirect patients contacts. This network was reconstructed using EMRs of patients with acute coronary syndrome (ACS) treated in 2014. We decided to take all physicians as a nodes and transfers of patient between two nearest physicians in time according to the entries order in EMR as an edges. Thus the complete sequence of edges for each patient gives us the lifeline of the patient for all time of treatment. But, after obtaining the data from FANWMRC medical information system (MIS) it became clear that due to the negligence of making records in MIS there is a lot of noise in the data like random, synchronous or backdated timestamps of records. This led to the emergence of a large number of implausible transfer sequences between physicians in the path of patient's treatment and distortion in the overall system dynamics. The use of such noisy "as is" data gives a distortion of the topology of the entire contact network and, as a result, inaccuracy in final simulation results. Therefore, after filtering the dataset from excessively noisy data, we have allocated treatment cards of 122 patients that satisfied the requirements of data credibility. The filtered dataset contains records from 486 unique physicians. Fig. 4a shows non-temporal force-directed layout of the resulting network considering all of its connections. The final picture changes when dynamic temporal layout is applied (fig. 4b), however, the overall visual characteristics of the network (two explicit clusters of nodes) are still retained.

In addition, for interconnection of this scale and level of network with others (hospital- and city-scales described in previous subsection) we included two sets of meta-nodes for patients' admission (ambulance, transfer from other hospital, planned admission and free-run) and dismissal (home, ambulatory medical care, rehabilitation treatment, sanatorium-resort therapy, hospital care and death) – fig.4, green and red nodes accordingly. Thus, we also completed the sematic path of each patient – from admission node through the doctors been in contact to dismissal node.

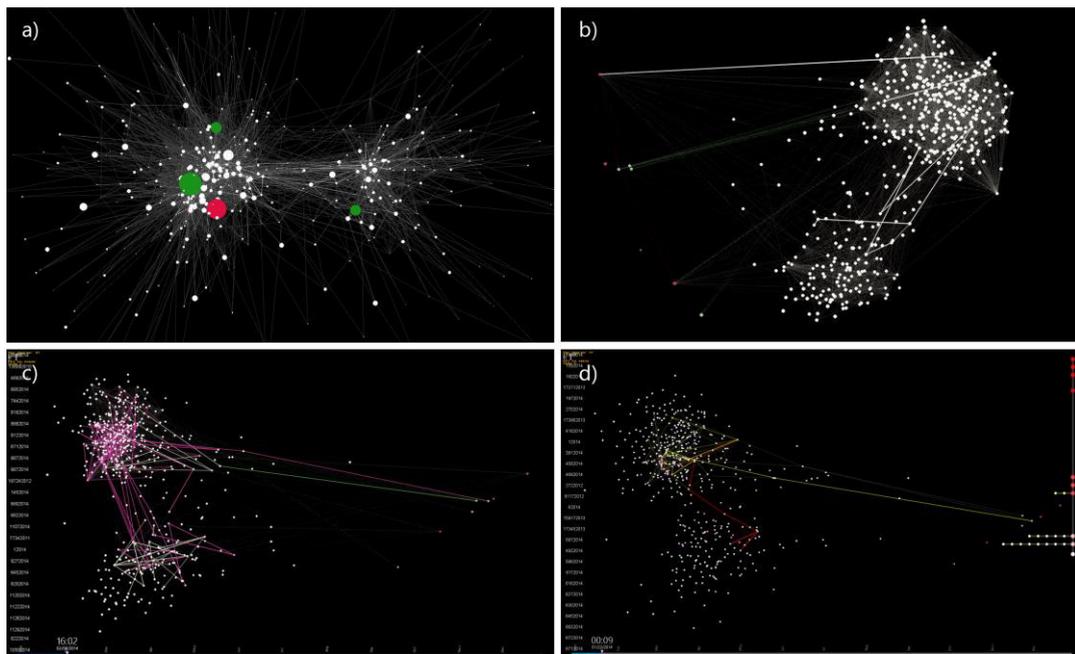


Figure 4: Visualization and interactive simulation of infection disease spreading in nosocomial contact network reconstructed from EMRs – a) temporal force-directed layout with dynamic of patients' movement; b) force-directed layout of entire time range of temporal network; c) simulation of infection disease spreading in network through indirect contacts – purple edges; d) search of possible ways of disease contamination for identified infected patient – red and yellow edges.

We have considered three types of temporal processes: the movement of patients through the network of physicians, infection spreading through indirect contacts of patients and search of possible ways of disease contraction for identified infected patient.

In order to demonstrate the movement of patients between physicians, we used node-dependent coloring of the edges. When the patient moves from one doctor to another appearing edge lights with maximum brightness on both sides, and eventually begins to fade from the side of previous node. Prior to the transfer of the patient to the next doctor brightness of the edge from the side of current doctor remains maximum and then begins to fade together with the end of edge from current to next physician. Thus when patients path displayed on a graph over time it will be seen as a bright tail with intensity fadeout which the brightest side is the current position of the patient in the network (fig. 4b). Also, for an additional demonstration of temporal dynamics we created an interactive timeline in user interface showing the current time and events (visits of doctors by patients) which occurred in network over time (at the bottom of screenshots at fig. 4 c, d).

Apart from patients' dynamic across network we made simulation of hypothetical infection spreading in this network on the basis of indirect patients' contacts through physicians' visits. A coarse SIR model was used for simulation of infection spreading. The model uses a hypothetical infection to test and demonstrate features of our interactive toolbox in the case of study of dynamic processes in temporal networks. In this case, physicians have been used as vectors with very small recovery period (about 4 hours, nodes became purple), and the patients have a long recovery period (randomly varied between 5 and 10 days). Color of the infected patients' paths edges became purple (fig. 4 c), while maintaining the visual effect of attenuation described for the regular dynamics of patients. To increase interactivity, we have also implement an ability to infect doctors by clicking on the node of graph.

The third step of the interactive visual analysis implemented in the toolbox is an explorative search of the disease source according to the temporal influence propagation described in Section 3. When we click on one of the patients from a list at the left side of the screen the toolbox computes the whole tree of possible ways of getting infected for selected patient. Visually time on a timeline starts to run backwards and retrospective ways of disease propagation highlights in red for selected patient and in yellow for all patients who could affect to the patient's infection (fig. 4, d). The color intensity of the edges depends on the probability of disease contamination for selected patient. Also, for more evident display of hypothetical ways to get patient infected on the right side of the screen displays flat diagram of the patient's path for the estimated time of disease progression (vertical branch with red nodes) and branches of primary indirect contacts of the patient with other patients through physicians (horizontal branches with yellow nodes).

5 Results and Discussion

During visual analysis of the dataset through our toolbox, we have identified two distinct clusters. In fact, at FANWMRC two offices exist in distant locations in the city involved in the treatment of ACS, but patients' treatment cards that we used do not contains any information about physicians' department affiliation. Also, through dynamic of patients' transfers between doctors the pulsating rhythms of daily and weekly activities (activity at the weekends is much lower) of doctors were clearly distinguished, despite the fact that a large number of patients in the dataset was coming through the ambulance or emergency transfer from another hospital.

During the interactive study of infection spreading we identified specific time periods (mainly in spring) and places in the network (in the center of a large cluster) when contamination of a few doctors resulted in snowballing process of infection spreading in the network. In other cases, the infection of a large number of physicians leads to a small amount of infected patients and the epidemic quickly fades due to self-recovery of patients. We do not limit the simulation possibilities to the only one very simplified infection spreading SIR model described in Section 4. It was used only in order to show the

opportunities and ways to work with infection models in proposed toolbox, and instead any other model can be used.

Our research has shown that having a real hospital data much more interesting and plausible results can be acquired in the simulation of infection spreading. And, more importantly, it is possible to model traces and the causes of potential contamination based on real contacts, since in actual practice, it is very important to quickly and correctly react when unexpected threat arises.

We do not propose as a main contribution to our work an another stand-alone solution to work with graphs, especially as a competitor to such powerful products as Gephi or Cytoscape. Existing solutions will definitely surpass our toolbox in many features separately (layout, modeling capabilities, and so on). Nevertheless, we could not find a suitable flexible ready-to-use solution to implement and test our techniques in visualization, simulation and interactivity at the same time. Thus, we used our own technological developments as the basis for implementation. Main goal of our ongoing research is to investigate suitable techniques and their combinations for visual explorative analysis of multiscale temporal networks as a tools for stakeholders in public healthcare and medicine for further incorporation this tools to the medical DSS. This requires intuitive tools that will be suitable not only for complex networks specialist, and for user from applied domain who have to work with the final complex system (in our case - physicians).

Valuable interactivity with the system (with visualization as well as with simulations in network) allows to explore data derived from actual practice deeper and in more details. By combining interactive visual analysis with the ability to dynamically build scenarios (setting the initial conditions and characteristics of the processes, dynamic change of models' behavior according to the changing circumstances, etc.), connect models that simulates various processes in networks, use various sources of data and knowledge the proposed toolbox can be a very powerful and useful part of medical DSS.

On the other hand, the scope, designated in our work (public healthcare and infection spreading), is not a strict limitation on the applicability of proposed toolbox. It can be easily used for any subject area where exist necessity in study of dynamic, temporal and multiscale networks, processes in these networks, exploring scenarios and interactive visual analysis.

6 Conclusion and future works

Main contribution of this work is to propose a toolbox for visual explorative analysis of complex temporal multiscale contact networks dynamics in medicine and healthcare. We described a sufficiently broad multi-scale and multi-level background of complex networks in public healthcare. Although, implemented example only partially involves the multiscale nature by reducing it to the visualization and interconnectivity of studied scales between each other through border conditions, it demonstrate promising opportunities of the developing solution. As future work, we plan to study in more details technical abilities in visualization of multiscale dynamic processes, as well as applicability of the multiscale processes simulations (mobility, disease spreading, information spreading [31], etc.). Additionally, we plan to conduct experimental studies of various scenarios within dynamic multiscale contact network reconstructed using data obtained from FANWMRC to determine the effectiveness and applicability of our toolbox. For example, it will be valuable to analyze the potential vulnerabilities of such type of network for known nosocomial infections using FANWMRC's organizational structure as a working example.

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