Prediction System-Based Community Partition for Tuberculosis Outbreak Spread

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ABSTRACT

In this work, the goal is to design and investigate a new simulation system based on detection communities for control and prediction of TB outbreak. The latter is mainly based on four subsystems, namely susceptible-infected-removed (SIR) system, detection community system, visualization system, and prediction system. The SIR including reservoir within small world (SW) network system is applied to take better advantage of its modeling property and understanding epidemic spread. In order to characterize the influence of communities' structure, they use Louvain method to identify communities in human complex network. Then, they propose a predictive approach for identifying the hottest outbreak communities based on communities' detection as well as mapping areas at risk. Current results show the performance of the proposed system and the important role of detection communities in the process of epidemic spreading and prediction.

KEYWORDS

1. INTRODUCTION

Every year, infectious diseases are the leading cause of major morbidity and mortality. Despite the sanitation devices built, programs applied in the field and the implementation of preventive measures, there are very few infectious diseases that have been eradicated.

Decision support systems dedicated to epidemiology are developed for various purposes, such as: monitoring, surveillance, prevention, control, alert, etc. (Quah, 2016). Indeed, some problems related to the spread of infectious diseases are of a complex nature and involve many factors. Among these later, the social structure of individuals. The epidemic spreads across a population in both time and space. In order to control and monitor its dynamics of infection as well as its capacity to evolve and "emerge" in its form, it is necessary to analyze it in a spatiotemporal dimension. Moreover, it is impossible to predict firmly and in advance the spread of the disease in the future.

In this context, prevention aims at limiting or slowing the progression of the epidemic. It is noted that the epidemic can never be stopped in a definitive way because it is multifactorial.

The problem discussed in this paper lies at the confines of various disciplines, the main one is epidemiology. Outbreaks of infectious diseases can pose a serious threat to the health of individuals. Indeed, several research teams have invested in the study of the epidemic propagation mechanism in order to propose a reliable and robust monitoring system.

Mathematical and simulation systems are increasingly used in order to:

- Study the transmission of infectious diseases to predict how they might spread in a human population in the event of an epidemic (pandemic).
- Evaluate different intervention strategies.
- Help public health decision makers to bring the outbreak under control more quickly (Younsi et al., 2019).

Mathematical epidemic models can be used to represent the different state of patients in the course of the illness (S: susceptible, E: exposed, I: infective, R: removed, etc.). In the current study, we used the SIR model within SW to explore the dynamics of an epidemic including a reservoir. The transmission of epidemic occurs through reservoir to person and/or person-to-person contact, and contact between susceptible and/or infected individuals takes the form of a network. Because simple SIR epidemic model including a reservoir cannot model the dynamic of transmission, it must be integrated with a social network model, to understand the spread of the epidemic. Moreover, the structural properties (e.g., density, diameter, clustering coefficient, etc.) of networks play an important role in affecting diffusion behavior.

Recent research found that community structure plays an important role in epidemic spreading on networks, in which existing studies focused on networks with non-overlapping communities. They found, also, that community structure affected the epidemic threshold, epidemic prevalence, and information lifetime in complex networks (Shang et al., 2015). In the literature, there exist several community detection algorithms, namely: BigClam (Yang & Leskovec,2012), greedy hierarchical method based on modularity maximization, Louvain (Blondel et al., 2008), label propagation based approach, COPRA (Gregory, 2010), etc. The most appropriate method for community detection in static graph is the Louvain Method, because it is the fastest and the most accurate method (it achieves better modularity). Furthermore, when society is faced with the threat of serious health crisis, decision makers are in need of simple and powerful mapping tools to explore, synthesize and analyze spatial and temporal data such as identification of risk areas. Indeed, displaying outbreak areas on a map is managed by a GIS (Geographic Information System).

1.1 Our Contribution

The main objective of the current research is to develop and discuss a new extension of Spatio-Temporal Decision Support System (SIDSYS+) for epidemic monitoring and prediction. The proposed system is based on simulation system using the SIR including reservoir model, detection community using the Louvain Method, GIS and prediction system. It allows, in one hand, to simulate the phenomenon of the epidemic spread in a human population in order to control and monitor the evolution of the disease in time and space. On the other hand, it enables to detect the communities in order to understand the social structure of individuals' network. Moreover, it allows the prediction of the area (s) susceptible to being infected in the future and visualizes a risk map on GIS. The prediction system relies on the communities' detection approach that allows predicting the behavior of outbreaks and visualizing risk maps. The model is managed by the decision maker (public health officials).

Our major contribution in the paper can be summarized as follow:

- Detect communities in a network of individuals using the Louvain method (Younsi & Hamdadou, 2017);

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