Smart monitoring and controlling of Pandemic Influenza A (H1N1) using Social Network Analysis and cloud computing

Rajinder Sandhu*, Harsuminder K. Gill, Sandeep K. Sood

Department of Computer Science and Engineering, Guru Nanak Dev University, Regional Campus, Gurdaspur, Punjab, India

ABSTRACT

H1N1 is an infectious virus which, when spread affects a large volume of the population. It is an airborne disease that spreads easily and has a high death rate. Development of healthcare support systems using cloud computing is emerging as an effective solution with the benefits of better quality of service, reduced costs and flexibility. In this paper, an effective cloud computing architecture is proposed which predicts H1N1 infected patients and provides preventions to control infection rate. It consists of four processing components along with secure cloud storage medical database. The random decision tree is used to initially assess the infection in any patient depending on his/her symptoms. Social Network Analysis (SNA) is used to present the state of the outbreak. The proposed architecture is tested on synthetic data generated for two million users. The system provided 94% accuracy for the classification and around 81% of the resource utilization on Amazon EC2 cloud. The key point of the paper is the use of SNA graphs to calculate role of an infected user in spreading the outbreak known as Outbreak Role Index (ORI). It will help government agencies and healthcare departments to present, analyze and prevent outbreak effectively.

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1. Introduction

According to the World Health Organization (WHO), United States (US) spends world's highest percentage of gross domestic budget for health related issues on their citizens [1]. Healthy citizens contribute to nation's development in large extent. Every government has dedicated big amount of budgets for Information Technology (IT) based healthcare support services. IT can provide efficient methods to store and convey information related to the health of every citizen. So, sincere efforts are required to provide ubiquitous healthcare support services using IT infrastructure. Major challenge in any nationwide healthcare support services is the requirement of huge amounts of storage and fast computational power along with its day-to-day maintenance issues. However, with the involvement of distributed technologies such as cloud computing, it is very easy to deploy and use IT systems with varying computational demands. Cloud computing is a highly cost effective IT paradigm which provides on-demand IT resources on a pay-as-use pricing model. Successful adoption of cloud computing by the reputed organizations has inspired researchers to provide healthcare support services over the cloud computing infrastructure [2].

Leveraging cloud computing for healthcare support services facilitates many additional benefits such as ease in swapping records between hospitals and local clinics as well as in effective management of centralized medical records. It not only relives user from storage and processing infrastructure capital investment, but also prevents maintenance and licensing issues [3]. Accessibility, scalability, availability, storage capability, cost effectiveness and agility are some of the major benefits that can encourage any nation's healthcare departments or private hospitals to shift towards e-health clouds.

The most crucial part of any healthcare support service is the continuous monitoring of an outbreak for any deadly disease. H1N1 is an infectious virus which on spreading affects a large volume of the population. This infectious disease had affected global population in the past due to which approximately 5% of the total world's population had died and hence it had proved to be the deadliest outbreak ever. Alone in the 20th century, the H1N1 virus outbreak has occurred thrice which had affected 500 million people all over the world [1]. WHO states non-existence of primary H1N1 immunity in humans is the root cause of its epidemic. People need to get educated about precautions and handling of this deadly disease. There is a need of using both pharmaceutical as well as non-pharmaceutical strategies to decrease its harmful effects. Cloud computing technologies can be efficiently employed to prevent and keep track of this virus strain. Cloud computing provides virtually

* Corresponding author.
   E-mail address: rajsandhu1989@gmail.com (R. Sandhu).

unlimited storage, web services and processing capabilities so, huge amount of virus related data can be linked through social networking and other health aided cloud web services. Moreover, using cloud computing for healthcare support services enables an individual to manage their own health status more effectively. Vital statics of whole country regarding the epidemic at different level of abstraction can be accessed with high accuracy. Thus, cloud computing can effectively improvised the detection of H1N1 virus at its initial stages. The objectives of the study conducted in this paper is to provide feedback about the individual health condition, design effective information sharing mechanism and real-time representation of the current status of the epidemic. The designed system keeps track of the current status of this pandemic and stores all the records for later use as well. The main contribution of this work is the categorization of patients into different categories, continuous monitoring of infected patients and identifying the probability of each user in spreading or receiving the infection by analyzing his/her relationship with infected patients.

To achieve above said objectives in this paper, a real-time H1N1 monitoring and diagnosis system with large scale data processing and analysis capabilities is proposed using cloud computing. It initially screens H1N1 virus infected patients using random decision tree into five categories based on their respective symptoms. Based on these categories, various control measures are suggested and patients are monitored regularly using a personalized monitoring routine. For every user, Outbreak Role Index (ORI) is calculated which represents his/her future probability in spreading or receiving the infection. Apart from ORI, several other outbreak metrics such as centrality, cluster coefficient, edge embeddeness are also computed using Social Network Analysis. Continuous alerts in case of health threatening conditions are generated and are sent to respective patients. Information and suggestions based upon the respective H1N1 category of user are also provided. The querying capability of this system allows users to intuitively retrieve personalized information. The aim of this paper is to provide a blueprint of the plan to be exercised during this deadly pandemic.

The rest of the paper is organized as follows. Section 2 discuss the related work about H1N1 virus infection and cloud computing in the field of Bioinformatics. Section 3 proposes architecture to monitor, investigate and detect H1N1 virus infection in detail. Section 4 provides experimental results and its discussion. Section 5 concludes the paper.

2. Related work

Related work is divided into three sections which are Pandemic Influenza A (H1N1) virus infection, ICT and mathematical models in H1N1 outbreak and use of cloud computing in the field of Bioinformatics. First section discusses characteristics, causes, and results of H1N1 outbreaks. Second section provides the use of communication and mathematical models in H1N1 infections. Lastly, use of cloud computing in the field of Bioinformatics has been provided.

2.1. Pandemic Influenza A (H1N1) virus infection

H1N1 outbreak in 2009 effected very large number of population across the world. Many authors studied the cause, effect and precaution measures of the 2009 attack. Dawood et al. [4] firstly identified H1N1 influenza virus with about 642 confirmed cases on 15th April 2009. They provided its initial symptoms and effects on the human body. Garten et al. [5] studied antigenic and genetic characteristics of H1N1 virus. Jain et al. [6] examined the clinical characteristics of patients admitted in April to June 2009 affected with H1N1. Neumann et al. [7] reviewed the H1N1 emergence in 2009 and its potential to spread again if not properly controlled.

CDC's Advisory Committee on Immunization Practices (ACIP) [8] also submitted their recommendations on vaccination for H1N1 influenza virus in 2009. As the vaccination of H1N1 is highly recommended for pregnant ladies to prevent infants from infection, McMillan et al. [9] reviewed its need and safety concerns for both mother and infant. Takeda et al. [10] in 2015 studied the effect of latest H1N1 vaccination during pregnancy on both mother and infant. In 2014, WHO [1] piled up health related data for all of its 194 member countries. Progress made in health related targets and associated goals were included. Annual life expectancy and mortality rates due to improper health were estimated by WHO. Data collected by WHO indicated that there is high neonatal mortality rates in low income countries due to improper health guidance. In 2009, Ministry of Health and Family Welfare Pandemic Influenza A (H1N1) [11] also published guidelines on categorization of Influenza A (H1N1) virus infection. Based on various physiological signals, patients were screened and categorized into various categories of infection. According to these categories, relevant information and suggestions were also provided.

2.2. ICT and mathematical models in H1N1 epidemic

Information and Communication Technologies have been extensively used for prevention and early prediction of this deadly epidemic.

Computer science has been also extensively used for analyzing virus epidemiology and its changes. In 2015, Hu [12] examined the change in interdependence of Hemagglutinin and Neuraminidase in H1N1 virus using time series analysis from the data of 2009–2013. In 2014, Kim et al. [13] compared the H1N1, H5N1, H5N2 and H7N9 influenza virus using apriori algorithm. In 2013, Dimitrakopoulou et al. [14] proposed a clustering method known as OLYMPUS for calculating gene expressions. They used data of host response to H1N1 infection for validating the proposed method. In 2013, Bankhead et al. [15] developed a framework in which critical aspects of viral infection are simulated based on spatial temporal data.

Various decision support systems have been proposed by authors for preventing H1N1 outbreaks. In 2015, Lai et al. [16] developed a H1N1 pandemic forecasting system based on daily influenza cases and total population in Hong Kong. They used spatial–temporal and stochastic SEIR methods to predict number of cases for next two days. In 2015, Cruz et al. [17] studied the importance of effective communication system in case of any large scale pandemic. In 2014, Wang et al. [18] examined the spread of H1N1 in 2009 for the schools of China. They found that most of the infection transmission is within the same grade and cross grade infection transmissions are very few. In 2014, Dias and Arruda [19] proposed a mathematical based cost optimization model for controlling H1N1 pandemic based on mean of finite difference method. In 2014, Cui et al. [20] demonstrated the public attention model for epidemics like H1N1 using spatial–temporal patterns. In 2014, Bdeir et al. [21] discovered some of hidden social networks between different organizations during H1N1 epidemics. They also suggested that relevant and timely exchange of information between different organizations can result in better prevention of epidemics. In 2014, Farah et al. [22] developed a dynamic epidemic model for H1N1 using a Bayesian based emulator. Emulator took basic epidemic details and time series of all reported infections to design the model. In 2013, Zhong et al. [23] compared standard as well as modified compartment model of epidemic controlling using H1N1 2009 epidemic data of Arizona state. In 2013, Duan et al. [24] applied a triple approach known as artificial societies, computational experiments and parallel execution to study and control epidemics. They used the data of H1N1 2009 outbreak in China University and examined the social network, student behavior,