Faculty of Computer Science and Information Technology

Identifying COVID-19 Hotspots using Bipartite Network Approach

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Master of Science
2023

Identifying COVID-19 Hotspots using Bipartite Network Approach

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A thesis submitted

In fulfillment of the requirements for the degree of Master of Science

(Computational Science)

Faculty of Computer Science and Information Technology
UNIVERSITI MALAYSIA SARAWAK
2023

DECLARATION

I declare that the work in this thesis was carried out in accordance with the regulations of Universiti Malaysia Sarawak. Except where due acknowledgements have been made, the work is that of the author alone. The thesis has not been accepted for any degree and is not concurrently submitted in candidature of any other degree.

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ACKNOWLEDGEMENT

I would like to thank my supervisor, Professor Dr Jane Labadin for her constructive advices, guidance and encouragements throughout my years of study. Also, I am indebted to her supportive and excellent supervision. She is there for me every time I need advices. Our countless sessions of discussion have always been enlightening, motivating, assuring, and fruitful in provoking new thoughts and evaluations to existing ideas. I am thankful for the invaluable experiences I gained from her through conducting the research writing of scientific papers, coordinates the projects, preparing presentations and attending conferences. Thanks for accepting me as who I am, helping me to accomplish my Master endeavour and provided me precious opportunities in this journey.

Special thanks to Universiti Malaysia Sarawak for the Zamalah Graduate Scholarship which has provided me with monthly allowance. Besides, special thanks are also extended to Ministry of Higher Education Malaysia as appointed me as research assistant for PGRS/1/2020/ICT05/UNIMAS/0201 and GL/F08/KPT/02/2020. This made my dream to pursue a Master's degree a reality. My heartfelt thanks go to the Faculty of Computer Science and Information Technology for providing me with a conducive environment. Thanks to Dean and Deputy Deans for the wholehearted support. Thanks to all lecturers especially lecturers from Computational Science programs for your insightful advices. I also acknowledge the administrative staff members of the faculty and the Centre for Graduate Studies for their constant help. I would also like to also deliver my sincere appreciation to the Bintulu Division Health Office and Dr Melvin for the help and support in providing the research data generously. Thank you.

Thanks to my thoughtful friends for spending their precious time proofreading the draft of this thesis. Kian Soon, thank you for your generosity in proofreading my literature reviews, advises and comments on my writing. Yun Ta and Hwee Jia, thank you for your help in proofreading my draft and for providing me with constructive suggestions. Thanks for your friendship, warm advice and great support. Vei Ling, my best roommate, thank you for always giving me support during my research journey. Yong Xian, Ting Sun, Mei Wen, Chee Xian and many others, thank you for your time, understanding and motivation. I am blessed to have all of you along with me throughout my research journey. Thanks to all my friends who greet me happy and give me support and encouragement. I am unable to list everyone but you are always on my mind.

Last but not least, I am deeply grateful to my dearest family members. Thanks to my parents for raising me with a love of knowledge and lovingly encouraging me to strive for my master's dream. Also, thanks to both my sisters for their endless support in motivating me. My family contributed significantly to the accomplishment of my master's degree. Thank you. Dedicated to the memory of my grandmother, who always believed in my ability to be successful in the academic arena. You are gone but your belief in me has made this journey possible.

ABSTRACT

The COVID-19 pandemic has affected countries worldwide, causing major disruptions in both health and economic systems. While lockdowns have been effective in controlling the spread of the virus, their negative impact on the economy has prompted the need for alternative, cost-balanced control measures. Contact tracing has emerged as a promising solution in identifying community outbreaks of COVID-19. To improve the efficacy of contact tracing, this study aimed to formulate a contact network model for COVID-19 transmission. Conventional approaches were found to be inadequate in modelling the transmission of COVID-19, particularly in identifying the source of infection. To address this, the study utilized a bipartite network modelling approach to account for the heterogeneity of transmission routes, human hosts, and visited locations. The human host and visited location were identified as the two discrete entities in the research scenario. Using data from the Bintulu Health Office's contact tracing investigation forms, six network models were formulated. The link weight between the human host and location nodes was quantified using the summation rule, taking into consideration various factors such as environmental properties, building characteristics, human and pathogen characteristics, and transmission modes. The location and human nodes were then ranked using a web-based search algorithm based on their respective ranking values. The results of the study showed that the bipartite network modelling approach was successful in formulating the contact network model. Verification analysis revealed a root mean square error of 0.0002244 and 0.001419 for the location and human nodes, respectively, which were well within the threshold value of 0.05. The ranking between the target and validated models was found to have strong similarity with a good Spearman’s rank correlation coefficient of above 0.70 ($p < 0.001$), indicating a high degree of relevance in improving contact tracing for COVID-19. The study also found

that all parameters used in the model were relatively significant, and that the model had the ability to predict potential hotspots with 90% accuracy within a 600m radius for the subsequent week. These findings highlight the potential of the bipartite network modeling approach in improving contact tracing for COVID-19 and reducing the spread of the virus in high-risk areas.

Keywords: Bipartite network modelling, COVID-19, hotspot, ranking

Mengenal pasti Titik Panas COVID-19 menggunakan Pendekatan Rangkaian Dwipartit

ABSTRAK

Pandemik COVID-19 telah menjejaskan negara di seluruh dunia, menyebabkan gangguan besar dalam kedua-dua sistem kesihatan dan ekonomi. Walaupun penguncian telah berkesan dalam mengawal penyebaran virus, kesan negatifnya terhadap ekonomi telah mendorong keperluan untuk langkah kawalan alternatif yang seimbang kos. Pengesanan kenalan telah muncul sebagai penyelesaian yang menjanjikan dalam mengenal pasti wabak komuniti COVID-19. Untuk meningkatkan keberkesanan pengesanan kenalan, kajian ini bertujuan untuk merumuskan model rangkaian hubungan untuk penularan COVID-19. Pendekatan konvensional didapati tidak mencukupi dalam memodelkan penularan COVID-19, terutamanya dalam mengenal pasti punca jangkitan. Untuk menangani perkara ini, kajian itu menggunakan pendekatan pemodelan rangkaian dwipartit untuk mengambil kira kepelbagaian laluan penghantaran, hos manusia dan lokasi yang dilawati. Hos manusia dan lokasi yang dilawati dikenal pasti sebagai dua entiti diskret dalam senario penyelidikan. Menggunakan data daripada borang siasatan pengesanan kenalan Pejabat Kesihatan Bintulu, enam model rangkaian telah dirumuskan. Berat pautan antara hos manusia dan nod lokasi dikira menggunakan peraturan penjumlahan, dengan mengambil kira pelbagai faktor seperti sifat persekitaran, ciri bangunan, ciri manusia dan patogen, dan mod penghantaran. Lokasi dan nod manusia kemudiannya ditarafkan menggunakan algoritma carian berasaskan web berdasarkan nilai kedudukan masing-masing. Hasil kajian menunjukkan pendekatan pemodelan rangkaian dwipartit berjaya merumuskan model rangkaian kenalan. Analisis pengesahan mendedahkan ralat purata kuasa dua akar 0.0002244 dan 0.001419 masing-masing untuk lokasi dan nod manusia, yang berada dalam nilai ambang 0.05. Kedudukan antara sasaran dan model yang disahkan didapati

mempunyai persamaan yang kukuh dengan pekali korelasi kedudukan Spearman yang baik melebihi 0.70 (p <0.001), menunjukkan tahap perkaitan yang tinggi dalam meningkatkan pengesanan kenalan untuk COVID-19. Kajian juga mendapati bahawa semua parameter yang digunakan dalam model adalah agak ketara, dan model itu mempunyai keupayaan untuk meramalkan potensi titik panas dengan ketepatan 90% dalam radius 600m untuk minggu berikutnya. Penemuan ini menyerlahkan potensi pendekatan pemodelan rangkaian dwipartit dalam meningkatkan pengesanan kenalan untuk COVID-19 dan mengurangkan penyebaran virus di kawasan berisiko tinggi.

Kata kunci: *Permodelan rangkaian bipartite, COVID-19, hotspot, kedudukan*

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LIST OF ABBREVIATIONS

ABM	Agent-based modelling
ASHRAE	American Society of Heating, Refrigerating and Air-Conditioning Engineers
API	Application programming interface
ANN	Artificial neural network
BCC	Bipartite COVID-19 Contact
BNM	Bipartite Network Model
BNM-RMF	Bipartite network-based research methodology framework
CCS	COVID-19 contact strength
CHR	COVID-19 hotspot ranking
CRR	COVID-19 risk infection ranking
ET	Epidemiology Triangle
GPS	Global Positioning System
HCW	Health-care workers
HITS	Hypertext Indexed Topic Selection
ID	Identification
MCO	Movement control order
PDE	Partial differential equation
RMSE	Root-Mean-Square-Error
STDs	Sexual transmission diseases
SRCC	Spearman's Rank Correlation Coefficient
SI	Susceptible-infectious
SIR	Susceptible-infectious-removal

WHO	World Health Organization

CHAPTER 1

INTRODUCTION

1.1 Introduction

Contact tracing is one of the pillars of control measures to contain the outbreak of infectious diseases (Eames & Keeling, 2003). Herein, identifying high-risk areas is crucial to the effectiveness of contact tracing. This study focused on high-risk areas of COVID-19 transmission which can be denoted as hotspots or source of infection (Lessler et al., 2017). Many traditional approaches for contact tracing focused on the interaction between humans; however, the locations visited by the infected individuals are not factored. Moreover, conventional modelling, for instance, compartmental modelling, may not be suitable when integrating the spatial components because it is non-linear; hence, incorporating location or environmental properties becomes more complicated (Garnett, 2002; Nelson & Perelson, 2002). Accordingly, there is a need to identify and use an appropriate approach to detect hotspots of COVID-19 transmission.

The graph-theoretic network modelling approach that was recognised as a heuristic framework has the potential (Bunn, Urban & Keitt, 2000 in Liew, 2016, p. 1). Heuristics is a problem-solving technique that applies practical methods which do not promise an optimal solution but can generally produce solutions that are sufficient for practical use (Wahid & Hussin, 2016). This supports the present study to employ a bipartite network-based research methodology framework (BNM-RMF) (Liew, 2016) to address the research problem. To use that framework, the domain problem must be formulated into network models where the nodes and edges are well defined for location detection. The network structure is converted into a suitable format that can be used as input into the network model. Afterward, the model

is verified and validated, and analytical results were generated. It identifies the locations with high risks of COVID-19 transmission and rank those based on the estimated virus density. Such findings may serve an important cognizance for the authorities working on contact tracing and control measurements.

This chapter discusses the background of the problem and presents the problem statement; research questions, objectives, scope, methodology and significance; and the thesis outline.

1.2 Background of the Study

The first case of COVID-19 was reported in Wuhan, China, in December 2019. Accordingly, China notified the outbreak to the World Health Organization (WHO) as pneumonia of unknown aetiology. The virus had been identified as a novel coronavirus (2019-nCoV) and further named COVID-19 on 11 February 2020. Chinese government's attempts to contain the virus have failed, and it rapidly spread across the globe due to the high volume of air traffic and insufficiency of control measures. As many countries were already affected by the outbreak, WHO declared it as a pandemic on 11 March 2020, 3 months after the first case was reported. According to an investigation, the origin of the pathogen of COVID-19 was from a bat (Jiancheng Zhang et al., 2020) and escalate to the human population. COVID-19-infected individuals can transmit the virus directly and indirectly. Direct transmission involves, whereas indirect transmission includes airborne and fomite means (WHO, 2020). In addition, mass gathering, especially religious gathering events, is the main cause of outbreak in many countries (Ebrahim & Memish, 2020; Jeong et al., 2020; Mat et al., 2020). In Malaysia, the second wave of the outbreak originated from a Muslim Tablighi event in Sri Petaling, Selangor, on 27 February 2020. This event consists attendees from many countries, which amplifies the transmission (Mat et al., 2020; Dass et

al., 2021). Moreover, this event became the cause of infection in Malaysia and other countries in Southeast Asia. Consequently, a nationwide lockdown had been implemented in Malaysia on 18 March 2020, named Movement Control Order, and slowed down the outbreak at that time (Gill et al., 2020). This Movement Control Order caused a huge impact on Malaysia's economy. To curb the outbreak, control measures such as contact tracing, early detection of potential infection and quarantine are vital to limit the transmission (Xiao & Torok, 2020).

Contact tracing is a disease surveillance approach to obtain the possible transmission path by identifying the person who may have contact with an infected person. The main purpose of contact tracing is to break the current transmission chain (WHO, 2017). Contact tracing has been proven effective and widely used in several communicable diseases, i.e. droplet-transmitted diseases such as SARS, Middle East respiratory syndrome (MERS) and H1N1 (Shankar et al., 2014; Kwok et al., 2019); airborne-transmitted diseases such as tuberculosis and measles (Begun et al., 2013; Thole et al., 2019); and sexually transmitted diseases such as HIV/AIDS (Hyman et al., 2003). The common characteristic of the abovementioned diseases is that they transmit via close contact; thus, contact tracing can identify the index patient and the possible exposed individuals and avoid the disease from spreading further. Besides, some studies of vector-borne diseases such as dengue and malaria are using contact tracing (Kok, 2017; Vazquez-Prokopec et al., 2017). Those studies focused on the location the patient visited to identify the place of infection.

Generally, the contact tracing will be initiated when a patient is admitted to a hospital or a public health officer received a notification. The public health officer will interview the patient to obtain the contact and activity history. After identifying the close contacts, they will be asked to be home quarantined if they are identified as low risk; otherwise, they will

be referred to isolate in a hospital if they are categorised as high risk (WHO, 2017). The procedure mentioned is a manual contact tracing because it requires human resources to interview patients and trace their activities. The cost of manual contact tracing is high in terms of manpower and human lead error. The needed activity and contact history of the patient is up to 14 days (MOH, 2020); thus, patients tend to forget their activity/contact history, which will affect the efficiency of the procedure. To address the issues of manual contact tracing, a digital approach has been introduced. Digital contact tracing will make use of a mobile application to capture the activity and contact history of every citizen. This approach has been used in many countries during the COVID-19 pandemic (Jalabneh et al., 2020). According to Jalabneh, 15 countries developed a mobile application to conduct contact tracing, which showed the importance of this approach in controlling the spread of COVID-19. The application will collect several personal information such as name, age and post-code, with some applications further recording global positioning system (GPS) and Bluetooth contact data.

However, early transmission studies did not well integrate the contact tracing data collected manually or digitally because they focused on the prediction of outbreaks and simulation of the epidemic curve (Gill et al., 2020; Kucharski et al., 2020; Shen et al., 2020; Wu et al., 2020). These studies used the conventional approach to formulate a mathematical model, assuming the population is well-mixed. Due to this assumption, the model is difficult to incorporate with the mobility data (contact tracing) heterogeneously. Some studies considered the contact rate among the population distinctive based on age group (Prem et al., 2020; Zaplotnik et al., 2020; Juanjuan Zhang et al., 2020). These studies are beneficial in implementing control measures, i.e. school closing, work from home, or public place closure. Nonetheless, these studies are focused on the macro-level of the population, that is,

the national level, wherein contact tracing data were not utilised. In addition, transmission of the disease became complex when it involves transmission route, physical properties of the sites, human behaviour and characteristics of the pathogen (Killingley & Nguyen‐Van‐Tam, 2013; Sze-To et al., 2014). These factors highly affect the stability of the pathogen of COVID-19. It is found viable for more than 1 day on the surface of an object (Bueckert et al., 2020; Chin et al., 2020) and in the air (Ahlawat et al., 2020; Anderson et al., 2020; van Doremalen et al., 2020), resulting in onerous tracing of COVID-19 transmission compared with other diseases and difficulties in employing conventional approaches. Although other approaches, i.e. partial differential equation, agent-based modelling, or deep-learning approaches, may solve this issue, these are non-linear and of high dimension and need more computational power (Cheng et al., 2003). Somehow, the outputs generated from deep-learning approaches lack sense, making it hard for decision-makers to interpret (Zohuri & Moghaddam, 2020).

Recent researchers utilised network modelling approaches to address the limitations of the abovementioned approaches for the epidemiology domain (Eubank et al., 2004; Eubank, 2005; Eze et al., 2011; Gao et al., 2016; Kok et al., 2017). The network modelling approach originated from graph theory, which is a study to identify the relationship between the vertices and edges (Pavlopoulos et al., 2011; Gao et al., 2018). Any problems that can be simplified into vertex and edge are suitable for graph theory use. In terms of contact tracing, researchers used network modelling approaches to identify the transmission clusters between individuals (Eames & Keeling, 2003; Kiss et al., 2008; Begun et al., 2013). Eames and Keeling (2003) highlighted the effectiveness of the network model utilised with real-life data to identify the disease clusters, promptly eliminate the outbreak and reduce the burden on health resources. Although Begun et al. (2013) claimed that data on the effect of individual

behaviours and location visited by the close contacts are required to improve the efficacy of contact tracing, however, most of the network modelling of COVID-19 studies focused on the transmission between humans rather than their locations (Benlloch et al., 2020; Karaivanov, 2020; Xue et al., 2020). This is because formulating a contact network for human-to-human transmission is more convenient (Danon et al., 2011).

The lack of a location component in the contact network makes the study of indirect transmission of diseases insufficient, especially for vector-borne and airborne diseases (Danon et al., 2011). As the host and location are discrete components, researchers employed a bipartite network model (BNM) to incorporate these into a contact network. Early studies of BNM focused on the interaction between the host and location in the network by examining the network properties such as node degree, centrality and connectivity (Ancel Meyers et al., 2003; Eubank et al., 2004). Although these studies only emphasise the network properties of BNM, they provided insights for other studies to use BNM in identifying the risk of infection for a host and the risk of transmission for a location. Eze et al. (2011) adopted BNM to create a contact network for malaria transmission and successfully replaced the mosquito node with a location node. The location node quantified by Eze et al. integrated the environmental properties of a location with the behaviour of mosquitoes such as life cycle, survival rate and biting rate. According to this study, a mosquito normally flies within a certain distance from a particular location; hence, the location node is more suitable in the network instead of the mosquito node. Similarly, Kok et al. (2017) used BNM to identify the hotspot of dengue in Malaysia by integrating the human mobility into the network. Both of these studies demonstrate the capability of BNM to address vector-borne diseases. One of their contributions is resolving the issue raised by Pellis et al. (2015), that is, to merge the