Title

A Model-based Evaluation of the Impacts of Human Mobility and Prevention Behavior on Vector-borne Disease Transmissions: Implications for Disease Prevention and Control

Author

Luo, Nana

Publication Date

2020

SAN DIEGO STATE UNIVERSITY AND

UNIVERSITY OF CALIFORNIA

Santa Barbara

A Model-based Evaluation of the Impacts of Human Mobility and Behavior on Vector-borne Disease Transmissions: Implications for Disease Prevention and Control

A Dissertation submitted in partial satisfaction of the

requirements for the degree Doctor of Philosophy

in Geography

by

Nana Luo

Committee in charge:

Professor Atsushi Nara, Chair, San Diego State University

Professor Susan Cassels, Co-Chair

Professor Ming-Hsiang Tsou, San Diego State University

Professor Konstadinos (Kostas) Goulias

December 2020

The dissertation of Nana Luo is approved.

Ming-Hsiang Tsou

Konstadinos (Kostas) Goulias

Susan Cassels, Committee Co-Chair

Atsushi Nara, Committee Chair

September 2020

A Model-based Evaluation of the Impacts of Human Mobility and Prevention Behavior

on Vector-borne Disease Transmissions: Implications for Disease Prevention and Control

by

Nana Luo

ACKNOWLEDGEMENTS

In looking back on the past five years as a doctoral student, I was taught to be “inherently interdisciplinary” – to incorporate all that I have, to communicate and collaborate with a myriad of other disciplines, and to explore the peripheral realms where geographic perspectives interact with those from other fields. From my research to teaching experiences, I have noticed that communication and collaboration has been the one common element. I am very fortune to have received a Ph.D. in Geography from University of California Santa Barbara (UCSB) and San Diego State University (SDSU) in 2020 with the supports from my advisors, family, and colleagues. I would like to start by thanking my parents who not only raised and encouraged me but also helped me take care of my kids; my daughters for motivating me to overcome any difficulty in both career and life; and my husband for being my long-time mentor.

I also would like to express the deepest appreciation to my committee chair, Dr. Atsushi Nara, who gave me considerable supports: he convincingly and continually conveyed an enquiring mind in regard to research and teaching. Without his persistence and guidance, this dissertation would be impossible. The second year in UCSB built my academic career and rejuvenated my passion for science. Working with Drs. Susan Cassels and Konstadinos (Kostas) Goulias promoted my research to higher standards. I would like to sincerely appreciate Dr. Susan Cassels and Dr. Konstadinos Goulias’ advising and being experts on the fields of infectious disease modeling and transportation simulation. I also want to address gratitude to Dr. Ming-Hsiang Tsou for providing valuable projects and resources. Working in his Center for Human Dynamics in the Mobile Age (HDMA) benefits me from experiencing a variety of promising projects and techniques, and understanding the future trends and hot issues in GIS. Beyond my committee members, I would like to thank Dr. An Li, Dr. Fernando Bosco, Dr. Piotr Jankowski, Dr. André Skupin, and Dr. Kate Swanson, who made themselves available to me and provided valuable suggestions and ideas in their domain areas. In addition, a thank you to the support staff at SDSU and UCSB, specifically Patti O'Leary, Candra Young, Marcus Chiu, Harry Johnson, Mo Lovegreen, Patty Murray, and Consuelo Rivera.

I would not survived the Joint PhD program at UCSB and SDSU without the supports and accompanying from these people. Thank you all for making my past five years a fun journey.

VITA OF NANA LUO

EDUCATION

Bachelor of Geomatics Engineering, Jilin University, September 2007
Master of Geographic Information System, Capital Normal University, September 2011
Doctor of Geography, University of California, Santa Barbara and San Diego State University, August 2015

PROFESSIONAL EMPLOYMENT

2015-20: Teaching Assistant, Department of Geography, San Diego State University
2014–15: Research Assistant, Department of Land Surveying and Geo-Informatics (LSGI), The Hong Kong Polytechnic University

PUBLICATIONS AND CONFERENCES

1. Luo, N. & Nara, A. (2020). A spatially and temporally explicit framework for simulating daily travel dynamics using an integrated Bayesian Network and Activity-Based Model. The John Odland Award SAM Student Paper Competition, Association of American Geographers Annual Meeting.

2. Yan, X., Luo, N., Liang, C., Zang Z., Zhao W., Shi W. (2020). Simplified and Fast Atmospheric Radiative Transfer model for satellite-based aerosol optical depth retrieval. Atmospheric Environment, 224, 117362.

3. Yan, X., Liang, C., Jiang, Y., Luo, N., Zang, Z., Li, Z. (2020). A deep learning approach to improve the retrieval of temperature and humidity profiles from a ground-based microwave radiometer. IEEE Transactions on Geoscience and Remote Sensing, doi: 10.1109/TGRS.2020.2987896.

4. Luo, N., Shi, W., Liang, C., Li, Z., Wang, H., Zhao, W., Zhang, Y., Wang Y., Li, Z. & Yan, X. (2019). Characteristics of atmospheric fungi in particle growth events along with new particle formation in the central North China Plain. Science of The Total Environment, 683, 389-398.

5. Yan, X., Li, Z., Luo, N., Shi, W., Zhao, W., Yang, X., Liang, C., Zhang, F. and Cribb, M. (2019). An improved algorithm for retrieving the fine-mode fraction of aerosol optical thickness. Part 2: Application and validation in Asia. Remote Sensing of Environment, 222, 90-103.

6. Nara, A., Luo, N., Ghanipoor Machiani, S., Ahmadi, A., Tominaga, K., & Tsou, M-H. (2019). Examining human decision making factors toward wildfire evacuation using Twitter. Social Media & Society 2019, Toronto, Canada, July 20-21.

7. Luo, N. & Nara, A. (2019). An Activity-based Method to Simulate Finer-scale Human Daily Movement. Association of American Geographers 2019 Annual Meeting, Washington D.C., April 3-7.

8. Kinoshita, A., Nara, A., & Luo, N. (2018). Exploring spatial and temporal trends between wildfires, climate, and human development in the contiguous United States. American Geophysical Union (AGU) 2018 Fall Meeting, Washington, D.C., December 10-14.

9. Yan, X., Li, Z., Luo, N., Shi, W., Zhao, W., Yang, X., & Jin, J. (2018). A minimum albedo aerosol retrieval method for the new generation geostationary meteorological satellite Himawari-8. Atmospheric Research, 207, 14-27.

10. Yan, X., Shi, W., Li, Z., Li, Z., Luo, N., Zhao, W., Wang, H. and Yu, X. (2017). Satellite-based PM2.5 estimation using fine-mode aerosol optical thickness over China. Atmospheric environment, 170, 290-302.

11. Yan, X., Li, Z., Shi, W., Luo, N., Wu, T., & Zhao, W. (2017). An improved algorithm for retrieving the fine mode fraction of aerosol optical thickness, part 1: Algorithm development. Remote sensing of environment, 192, 87-97.

12. Luo, N., An, L., Nara, A., Yan, X., & Zhao, W. (2016). GIS-based multielement source analysis of dustfall in Beijing: A study of 40 major and trace elements. Chemosphere, 152, 123-131.

13. Luo, N., Nara, A., & Huang, C-C. (2016). Modeling friendship and interaction in social networks using Bayesian inference. Symposium on Human Dynamics Research: Social Media and Big Data, Association of American Geographers 2016 Annual Meeting, San Francisco, CA, March 29 - April 2.

14. Wang, Y., Zhen, S., Luo, N., Han, C., Lu, X., Li, X., Xia, X., He, Z. and Yan, Y. (2016). Low molecular weight glutenin subunit gene Glu-B3h confers superior dough strength and breadmaking quality in wheat (Triticum aestivum L.). Scientific reports, 6, 27182.

15. Huang, C-C., Nara, A., Gibbons, J., & Luo, N. (2016). Using Instagram data for measuring gentrification dynamics: Alternative way to identify gentrification typology. Symposium on Human Dynamics Research: Social Media and Big Data, Association of American Geographers 2016 Annual Meeting, San Francisco, CA, March 29 - April 2.

16. Subburaj, S., Luo, N., Lu, X., Li, X., Cao, H., Hu, Y., Li, J. and Yan, Y. (2016). Molecular characterization and evolutionary origins of farinin genes in Brachypodium distachyon L. Journal of applied genetics, 57(3), 287-303.

17. Luo, N., Wong, M. S., Zhao, W., Yan, X., & Xiao, F. (2015). Improved aerosol retrieval algorithm using Landsat images and its application for PM10 monitoring over urban areas. Atmospheric Research, 153, 264-275.

18. Yan, X., Shi, W., Zhao, W., & Luo, N. (2015). Mapping dustfall distribution in urban areas using remote sensing and ground spectral data. Science of the Total Environment, 506, 604-612.

19. Luo, N., Zhao, W., & Yan, X. (2014). Integrated aerosol optical thickness, gaseous pollutants and meteorological parameters to estimate ground PM2.5 concentration. Fresenius Environmental Bulletin, 23(10 A), 2567-2577.

20. Zhu, C., Luo, N., He, M., Chen, G., Zhu, J., Yin, G., Li, X., Hu, Y., Li, J. and Yan, Y. (2014). Molecular characterization and expression profiling of the protein disulfide isomerase gene family in Brachypodium distachyon L. PLoS One, 9(4), e94704.

21. Yan, X., Shi, W. Z., Zhao, W. J., & Luo, N. (2014). Impact of aerosols and atmospheric particles on plant leaf proteins. Atmospheric Environment, 88, 115-122.

22. Luo, N., Zhao, W., & Yan, X. (2013). Impact of dust-fall on spectral features of plant leaves. Spectroscopy and Spectral Analysis, 33(10), 2715-2720.

AWARDS

The second place of the John Odland Award SAM Student Paper Competition, The Spatial Analysis and Modeling Specialty Group (SAM) at the American Association of Geographers (AAG), 2020

The Cotton-Bridges Award for GIS Emphasizing Techniques, San Diego State University, 2019

The National Scholarship, Capital Normal University, 2013

Department of Geo-exploration Science and Technology scholarship, Jilin University, 2010

Department of Geo-exploration Science and Technology scholarship, Jilin University, 2009

Department of Geo-exploration Science and Technology scholarship, Jilin University, 2008

ABSTRACT

A Model-based Evaluation of the Impacts of Human Mobility and Prevention Behavior on Vector-borne Disease Transmissions: Implications for Disease Prevention and Control

by

Nana Luo

For vector-borne diseases dynamics in human-vector contact play an importance role, and human behavior including mobility and prevention behavior has been studied as a key contributor to drive the variations in host-vector contact. Human mobility can increase the human risk of exposure to vector-borne pathogens, while human prevention strategies effectively introduced to communities can reduce the risk of disease transmission and outbreak. Various modeling approaches from mathematical to simulation have been applied to examine the impacts of human mobility and prevention behavior on disease transmissions; however, conventional models are often limited by their coarser and aggregated representations in space, time, and human behavior. This study proposes a novel modeling framework (Activity-ABM) that integrate the Activity-Based Model and the Agent-Based Model. The proposed model incorporates individual-scale human mobility and prevention behavior at the level of both individuals and population into an epidemiology simulation, and is capable of representing complex virus transmission dynamics emerged from bottom-up human-vector interactions across space over time. Such individual-scale investigation also allows artificial laboratory experiments to explore scenarios with the intervention strategies associated with human mobility and prevention behavior and to examine the effectiveness of the interventions in the local context. The activity-based model embedded in the Activity-ABM creates heterogeneous daily movement of all individuals in a population from travel surveys and demographic data. The Activity-ABM then generates prevention behavior of all individuals in the population, including the host-based controls, the vector-based controls, and the host-vector contact-based controls, and examines the disease transmissions engaged in the generated movement and prevention behavior. As a case study, this research takes the 2016 Zika outbreak event in Miami-Dade County, Florida. Our modeling results suggest that the vector-based controls are the most effective, as the 2016 Zika outbreak in Miami-Dade County ended after an outdoor spraying to control mosquitoes. With the emphasis on the role of human mobility and prevention behavior to disease transmissions, this dissertation research makes theoretical contributions to the literature on behavioral geography, complex systems, and spatial epidemiology. The proposed Activity-ABM is applicable to simulate other infectious disease transmission dynamics, and can be extended to a general disease.

TABLE OF CONTENTS

1. Introduction

1.1 Research Background

Vector-borne disease outbreaks are a major threat to global health, economy, and society. In the United States, the Zika virus epidemic in 2015-16 resulted in 5,102 cases and the short-term economic impact of US$3.5 billion. For vector-borne diseases such as Dengue and Zika dynamics in host-vector contact are crucial because exposure to vectors to various extents in space and time often reduces or amplifies transmission rates (Galvani & May, 2005; Perkins et al., 2013; Reiner et al., 2014; Smith et al., 2007; Steven T. Stoddard et al., 2009). Therefore, exploring the factors that drive the dynamics in host-vector contacts is important to disease prevention and control as well as associated public health policy-makings(Eubank et al., 2004; Steven T. Stoddard et al., 2009; Woolhouse et al., 1997). Within the existing literature, human behavior as a key factor has been intricately linked to the spread of many vector-borne diseases, and has been broadly investigated in two aspects: (1) human mobility and (2) human prevention behavior. Human mobility often leads to high host-vector contact and ultimately increases transmission rates (S. T. Stoddard et al., 2013). Massad et al. (Massad et al., 2016) predicted 508 and 1,778 Zika infections to import into Europe in 2016 using a previously developed mathematical model for the importation of dengue virus. This model recognizes the casual relationship between the extent of infection and mobility-related factors such as travel volume and travel time. On the other hand, human prevention behavior such as vaccinating behavior (Griffin et al., 2010; Perisic

& Bauch, 2009b, 2009a; Chen, 2006), bed-net usage behavior (Barnes et al., 2009; Kleinschmidt et al., 2007; O’Meara et al., 2008) and spraying behavior (Griffin et al., 2010; Shanks et al., 2005), often causes expected declines in diseases. During the outbreak of Severe Acute Respiratory Syndrome (SARS) in 2003, the whole south China experienced empty streets, school closures, and wearing face masks. In the coronavirus disease 2019 (COVID-19) outbreak event, China prohibited all transport in and out of Wuhan city (Tian et al., 2020). These behavior responses have been found to be noticeably and clearly linked to the decline of the disease (Steven T. Stoddard et al., 2009; Tian et al., 2020). In 2016, the United States, especially the State of Florida, experienced a Zika outbreak. Miami-Dade County, Florida previously reported as the most Zika-active area experienced a dramatic decrease in Zika infection after an outdoor spraying to control mosquitoes. The Center for Disease Control and Prevention (CDC) also promulgated a variety of control behaviors including mosquito repellent, regular bed-nets, wearing long clothing, using screens on windows and doors via newspaper, social media and TV station. In contrast to human mobility, these prevention behaviors reduce Zika infection by blocking human-mosquito contact, decreasing peoples’ susceptibility to virus, or minimizing vector population.

Despite the increasing interest among researchers in examining the role of human behavior underlying the transmission cycles of vector-borne diseases (Cooley et al., 2016; Mao, 2011; Tian et al., 2020), little is known about the interrelated influences of human mobility and prevention behavior on epidemic dynamics. Conventional methodologies such as compartmental modeling and regression analysis have been used to account for the effects of crucial variables on diseases (Bingenheimer & Raudenbush, 2004; Hernán et al., 2000; Kim & Kim, 2019; Vanwambeke et al., 2006); however, they are ill equipped to investigate complicated host-vector, human-environment and vector-environment interactions embedded in the transmission cycles of diseases (Auchincloss & Diez Roux, 2008a).

Today, one approach is to regard epidemic dynamics as a complex system. In such a system, the dynamics emerge from bottom-up interactions of disaggregated, heterogeneous, and autonomous entities within an environment. The bottom-up interactions can lead to emergent behavior, which are more than a summing of independent activities (Holland 1998). Agent-based modeling (ABM) is a method to simulate such complex systems. In the past two decades, ABM has been employed to simulate vector-borne disease transmission dynamic (Alderton et al., 2016; Dommar et al., 2014; Jacintho et al., 2010; Jindal & Rao, 2017; Manore et al., 2015; Mniszewski et al., 2014; Mulyani et al., 2017). The approach takes into account individual heterogeneity and stochasticity among pathogens, vectors and hosts as well as interactions among them in respect to biological, geographical, behavioral, social, economic and environmental variables at a local scale. The population-level transmission dynamics then emerge from bottom-up interactions between autonomous individuals and environments, feedback effects, and adaptive behaviors in the non-linear transmission system of an epidemic.

1.2 Research Questions and Solutions

This research aims at exploring the impact of human mobility and prevention behavior on epidemic dynamics, in particular, finer-scale transmission dynamics of a vector-borne disease. In a broader sense, this research facilitates evaluating the locally efficient and effective public health intervention strategies. The specific research question to be answered in this dissertation is as follows: ***How does human-vector interaction dynamics engaged in human mobility and prevention behavior influence the transmission of a vector-borne epidemic in the local context?*** To answer this question, this study proposes a model-based investigation that consists of three primary modeling components: 1) individual-scale human daily mobility and travel behavior, 2) human (vector-borne diseases) prevention behavior, and 3) coupling of human mobility, human prevention behavior and dynamic human-mosquito interaction with an epidemic at a local scale. With the proposed model, three simulation scenarios are built to examine the effectiveness of the prevention strategies regarding human mobility and prevention behavior. The rest of this thesis intends to fill this overarching goal by answering the questions posted in each modeling component.

Chapter 2 focuses on generating the daily mobility and travel behavior of all individuals of the population in a study area, and investigates the following question: *Individual travels vary between weekdays and weekends and even across days of a week, which plays an important role in the transmission of vector-borne diseases as a crucial contributor to dynamic host-vector contacts. How can we model such day-varying human mobility and travel behavior?* ***This section presents a novel activity-based***

modeling framework that integrates Time Geography, activity-based models, and Bayesian network (BN) to simulate daily travels and activities of a population at the level of individual travelers. To generate daily activity scheduling of an individual, the proposed model formulates Time Geography by retrieving their alternating time budgets on weekdays and weekends. To take into account dynamics in an individual's daily travels and activities, the model introduces Bayesian networks into an activity-based model to compute probabilities of all travel-activity values, and interprets the alternating predictive results derived from random sampling as indicating their daily travel changes. The intellectual merit of Chapter 2 is the expected contribution to the methodology for modeling day-varying human mobility and travel behavior as well as creating a richer behavioral modelling component.

Chapter 3 addresses defining the nature of various human (vector-borne diseases) prevention behaviors on disease prevention and control. This component intends to answer the following two questions: *What prevention behavior have been applied to control vector-borne diseases? How should these controls become effective in the transmission cycles of vector-borne diseases?* **This study reviews and categorizes current human prevention behaviors for vector-borne diseases, formulates the transmission cycles of the diseases based on an earlier compartment model, and extends the transmissions to take into account the impacts of the categorized human prevention behaviors.** ***The intellectual merit of Chapter 3 is the expected contribution to the behavior-based epidemiological theory by integrating human disease prevention behavior and virus transmission cycles. Another expected contribution of***

this section is to aid disease prevention and control.

Chapter 4 focuses on developing an integrated activity-based model and agent-based model and apply it to a case study of the 2016 Zika virus epidemic in Miami-Dade County, Florida. Three simulation scenarios are built to investigate the role of human mobility and prevention behavior in the local context. This study answers the following research question: *How does human-vector interaction dynamics engaged in human mobility and prevention behavior influence the transmission of vector-borne diseases in the local context? What localized prevention should be the most effective?* ***This study develops a novel agent-based modeling framework that embeds activity-based behavioral modeling component to include heterogeneous individual travel behaviors. In this study, the role of human mobility and prevention behavior in the transmission cycle of an epidemic is investigated. According to the interaction between individuals and vectors, the model computes individuals' risk of infection and updates their health state in a spatially and temporally explicit manner. Such individual-scale investigation will facilitate evaluating the effectiveness of a localized public health intervention. Another intellectual merit of this study is the expected contribution to the behavior-based spatial epidemiological theory by introducing a richer human activity-based mobility modeling component and a human disease prevention behavior modeling component into the transmission cycles of an epidemic.***

1.3 Zika

As a case study, this research takes the 2016 Zika virus epidemic Miami-Dade County, Florida. The rest of this section presents an overview of Zika virus as well as the past and recent outbreaks all over the world.

1.3.1 Zika Overview

Zika virus (ZIKV) is a mosquito-borne flavivirus, in the family Flaviviridae, and related to dengue (DENV), yellow fever, chikungunya and West Nile (WNV) viruses (Pierson & Diamond, 2018). Although Zika virus can be transmitted from the mother to the fetus, via sexual intercourse, and through a blood transfusion, this dissertation research is interested in the human-mosquito-human transmission cycle, including transmission from mosquitoes to people through the bite of an infectious mosquito and transmission from people to mosquitoes by biting an infectious person, which is the primary transmission cycle of Zika virus in suburban and urban environments (Petersen et al., 2016).

On April 18, 1947, a rhesus monkey in the Zika Forest of Uganda was first discovered to get infected with Zika virus, and human infections were then found across Africa and Asia from the 1960s to 1980s (Kindhauser et al., 2016). In April 2007, the first known Zika virus outbreak occurred on Yap Island in Federated States of Micronesia, followed by a major epidemic in the French Polynesia in 2013–2014, and recent outbreaks in Camaçari, Bahia, Brazil, U.S. states and the District of Columbia in 2015 (Campos et al., 2015; Hayes, 2009; Kama et al., 2019; Armstrong et al., 2016).

The emergence of ZIKV in the continental United States has rapidly become a major public health concern across the country due to not only economic impacts but also the severe symptoms developed by newborn babies (Ferraris et al., 2019). In the United States, the Zika virus epidemic in 2015-16 resulted in 5,102 cases and the short term economic impact of US$3.5 billion. And in the regions affected by ZIKV the apparent increased number of babies born with microcephaly and structural brain abnormalities have been reported (Mlakar et al., 2016; Pierson & Diamond, 2018; Vianna et al., 2018). Currently, no antiviral treatment or vaccine have been approved to cure Zika virus infection (Ferraris et al., 2019), although multiple vaccine candidates such as DNA vaccines, purified inactivated virus vaccines and mRNA vaccines have been developed (Abbink et al., 2018).

1.3.2 Zika all over the World

The CDC has conducted a number of works with respect to the geographical distribution of Zika in various scales including a global scale, a country scale and a state scale:

1). In a global level, the 2016 Zika outbreak that excludes the areas only travel-related infection have been reported in the South America such as Brazil, Peru, Argentina and Colombia, Mexico and the United States.

2). In the United States the 2016 Zika outbreak is reported by state. These Zika cases are the laboratory-confirmed symptomatic Zika cases. Florida and New York have been reported to have the most serious Zika infection (1,083 and 1,004, respectively), while Wyoming, South Dakota, North Dakota, Idaho and Montana have less than 10 reports.

3). In South Florida the 2016 Zika outbreak includes the areas where Zika is popular and pregnant women should consider postponing their travels, the areas where Zika is deadly serious and pregnant women should not travel, and the areas changing from a red serious area to a yellow cautionary area. In August and October, 2016, three areas including a 1.5-square-mile area of Miami Beach, a 1-square-mile area of Little River, and a 1-square-mile area of the Wynwood neighborhood have reported Zika cases.

4). In Brownsville, Texas the 2016 Zika outbreak reported the first case of local mosquito-borne Zika infection on November 8th, 2016, and additional cases have been identified later in this region.

1.3.3 Case study

Miami-Dade County, Florida is situated in the southeastern part of the United States (Figure 1). According to the CDC, the first outbreak of local transmission of Zika virus in the continental United States was observed in Miami-Dade County, Florida in August, 2016. To investigate new cases of locally-acquired Zika infection, the CDC worked with Florida health officials. Infected individuals are generally characterized by fever, rash, arthralgia and conjunctivitis (Ferraris et al., 2019; Petersen et al., 2016). On August 1, 2016, a total 14 locally-transmitted cases have been reported in Miami-Dade County, and the local transmission ended after an outdoor spraying to control mosquitoes.

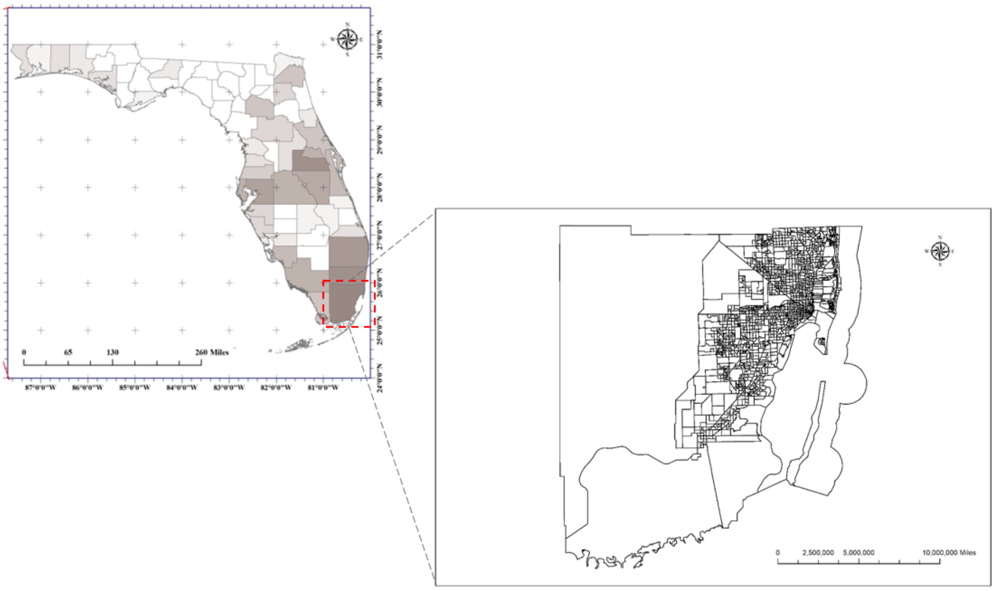


Figure 1. Study Area.

2. Human Daily Travel Modeling

2.1 Introduction

Human mobility and daily travel play a critical role in the diffusion of infectious diseases. Conventional travel demand modeling in urban transportation planning provides a useful tool to estimate travel behavior and travel demand based on a number of independent variables at various scales from population- to individual- levels. Four-step models, known as one of the first-generation travel demand models developed in the late 1950's, forecast traffic flows between traffic zones. This population-level model has been used to assess the impact of transport investments (e.g., new road construction) on travel demand typically applied at a regional or sub-regional scale (McNally, 2000). Later, the second-generation travel demand models, such as activity-based models (ABM[*1]), have been developed to model human activity and travel behavior at a household or an individual scale. This disaggregated approach estimates detailed daily trips and activities of individuals based on travel/activity dairies as well as their demographic and socioeconomic characteristics (Vovsha et al., 2005). Including such individual-scale human travel behavior in the transmission cycles of an epidemic will facilitate taking into account heterogeneity and stochasticity in individual decision-makings concerned with preferred disease control measures in an epidemic outbreak event. Further, it is capable of examining epidemic transmission dynamics originating from complicated interactions of hosts, vectors and surrounding environments engaged in their behavior.

A traditional activity-based model is often integrated with population synthesis to simulate travel decision/behavior of individuals. Operated at the level of individual travelers, an activity-based model requires household- and personal- level attribute information for a population to forecast travel demand; however, no such detailed individual-scale data at a population level exist. Traditional travel diary surveys have disaggregated household and personal attribute information for a sample of households from a population. Therefore, the first step of an activity-based model is to generate a synthetic population with detailed comprehensive data on person and household attributes to represent the actual population. Advanced approaches have been developed such as Iterative Proportional Fitting (IPF), Iterative Proportional Updating (IPU), Entropy Optimization (EO) and Enhanced IPU to generate a synthetic population (Konduri et al., 2016; Ye et al., 2009; Bar-Gera et al., 2009). To evaluate an estimated population, Ye et al. proposed that a traditional method i.e. the absolute relative error may not be a good measure for comparing the desired and estimated joint distributions because it masks the differences in magnitude between the estimated and desired distributions (Ye et al., 2009). Some studies proposed an alternative measure of fit, the chi-square ($\chi 2$) statistic, to compare the desired and estimated distributions statistically (Ye et al., 2009; Bar-Gera et al., 2009).

Within the existing literature, a conventional activity-based model that uses regression models to simulate travel/activity records often ignores the uncertainty from individual decision-makings in preferred activities. Human mobility and travel behavior are shaped by many factors such as location of interest, personal demographics and socioeconomic status, individual social tie, available transportation system and environmental constraints. These factors increase the complexity of modeling human mobility and travel behavior (Kang et al., 2010; Laurila et al., 2012; Tatem et al., 2014). Individuals sharing same attributes would have different daily activity schedules. Individuals may have different travels and activities between weekdays and weekends, and even across days of a week (Lee and Goulias 2018). Earlier activity-based models are typically designed for weekdays, and ignores such dynamics, and fails to investigate epidemic transmission dynamics emerged from complicated interaction of individuals and their surroundings due to their behavior. Therefore, a key technique that models such dynamics in human daily mobility and travel behavior is needed, and will be studied in this section.

*1: ABM in Chapter 2 refers to Activity-Based Model.

2.2 Literature Review

The activity-based approach to travel demand modeling and analysis was originally developed in response to demands for testing and analyzing a wide variety of transportation policies (Beckx et al., 2009; Goulias et al., 2011; Malayath & Verma, 2013). The activity-based method can specify complete travel-activity patterns at a disaggregate level for a population and embed a rich behavioral modelling component. Earlier examples of activity-based model include PCATS (Kitamura & Fujii, 1998), RAMBLAS (Veldhuisen et al., 2000), TASHA (Miller and Roorda 2003), CEMDAP (Bhat et al., 2004), FAMOS (Pendyala et al., 2005), CT-RAMP (W. Davidson et al., 2010), ALBATROSS (Shiftan & Ben-Akiva, 2011), SANDAG, and SIMBA MOBi (Scherr et al., 2019). These ABMs are designed to model activities and travels on weekdays. Today, researchers have empirically observed different spatiotemporal patterns in traffic flows and peaks between weekends and weekdays (Soulakellis et al., 2019), and even day-varying activities and travels of an individual (Clark & Doherty, 2008; Nurul Habib et al., 2012; Ruiz & Roorda, 2008). Ignoring such travel variations could result in the simulation result that is not representative of the underlying population, and weekend travels play a crucial role in the spread of an epidemic as well as disease prevention and control (Cooley et al., 2016; Mao, 2011).

Despite an increasing interest among researchers in understanding and modeling an individual's daily travel dynamics, extending an activity-based model to generate complete daily-varying activity scheduling for a population has limited progress (Arentze et al., 2011). Some new activity-based models have been developed to account for certain dynamic aspects in individual travels. Cirillo and Axhausen (2010) have developed an activity-based model that considers dynamics in individual travel purpose and timing from a six-week multiple-day travel diary survey, part of Mobidrive Survey. Habib and Miller (2008) presented a comprehensive econometric modeling framework that takes into account day-to-day and within-day dynamics in individual travel purpose and frequency using random utility maximization approach. This utility-based framework models day-to-day dynamics by incorporating previous day's total executed activities as variables and builds non-skeletal activity time-budgets for capturing within-day dynamics. Bhat (2005) proposed a similar modeling framework, the Multiple Discrete Continuous Extreme Value (MDCEV). These activity-based frameworks demonstrate successful applications in travel purpose, travel frequency and travel timing. Recent activity-based models have been extended to generate complete intra-day and inter-day travel dynamics of a population; howbeit, they often require additional datasets. Bellemans et al. developed a multi-stage FEATHERS framework that formulates activity dynamics including transport mode, travel purpose and other travel-activity attributes as function of time pressure (Baqueri et al., 2019). In addition to a traditional travel diary survey, their FEATHERS framework requires data on individual-level activity rescheduling choices and household-level multi-day activity scheduling choices, which are not easily accessible.

Today developing an activity-based model to generate complete, multi-day activity scheduling for a population is receiving growing interest (Arentze et al., 2011), and the activity-based models cited above provide a solid and suitable basis for this end. Against this background, the purpose of this section is to develop an activity-based model that is capable of generating multi-day activities and travels from a traditional one-day travel diary survey. To achieve this aim, here a novel activity-based modeling framework, BN-ABM that integrates Bayesian Network (BN), Activity-Based Model, and Time Geography is proposed. This proposed framework generates and forecasts complete dynamic activity scheduling for a population by taking into account individual fixed and mandatory activities as well as semi-dynamic time-budgets varying between weekdays and weekends. The rest of this section is organized as follows. Section 2.2 describes the proposed methodology in detail, in particular, an overview of the BN-ABM framework. Section 2.4 focuses on the results of the application of the BN-ABM to Miami-Dade County, Florida. Section 2.5 concludes with a summary of findings and discusses problems as well as future works.

2.3 Methodologies

2.3.1 Overview of the BN-ABM Modeling Framework

Figure 2 illustrates the overview of the BN-ABM that consists of two sub-models, the synthetic population generator and the activity attribute simulator. The BN-ABM model recognizes the relationship between travel-activity attributes, including travel frequency, travel purpose, travel mode, activity duration, travel destination location, and travel duration, and household- and person- level demographic and socio-economic attributes, including personal age, personal income, employment, household size, the number of children in the household, and if the individual uses a vehicle. A traditional ABM is utilized at the level of individual travelers, and requires household- and person-level attributes for an entire population, which is never available (Ye et al., 2009). Therefore, the BN-ABM begins with the synthetic population generator. This sub-model generates a simplified microscopic synthetic population that represents the actual population, which serves as input to the activity attribute simulator to generate individual activity scheduling of the population and forecast travel demand at the population level. The input of the synthetic population generator is a traditional one-day travel diary survey and the American Community Survey data (ACS). To generate a synthetic population, this sub-model samples households from the travel diary survey such that the joint distributions for the attributes of interest, including household size, household income, and personal age, in the sampled population match the known distributions for these attributes derived from the American Community Survey data. The output of this sub-model is a microscopic synthetic population in which all synthetic individuals feature three types of attributes. They are person-level attributes such as age, income, employment, if the individual uses a vehicle, household-level attributes such as household size, the number of children in the household, and weekday time-budgets.

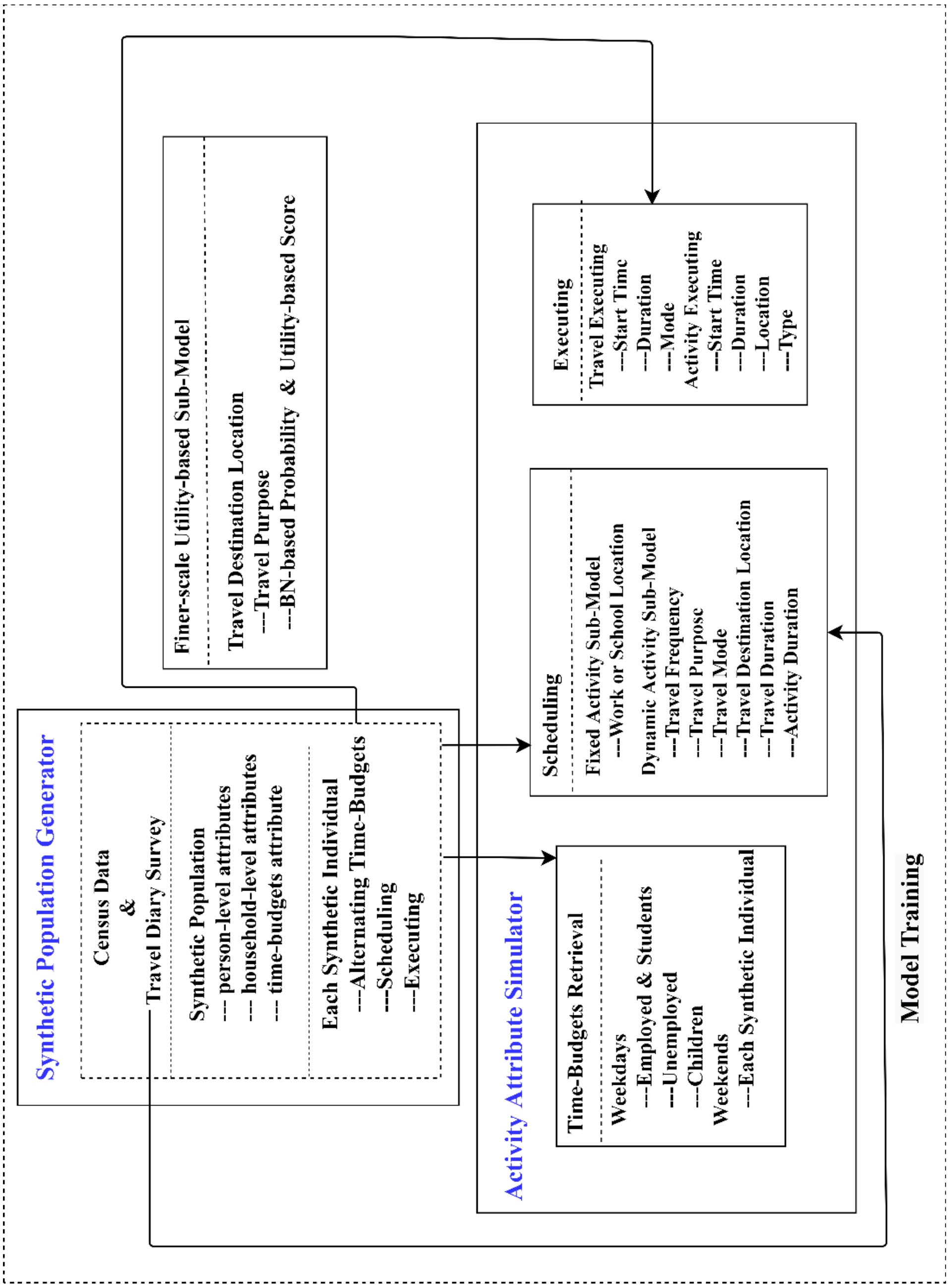


Figure 2. Overview of the BN-ABM framework and conceptual illustration of this model for daily travels of a population, and the sub-models underlying this proposed framework.

The following sub-model is the activity attribute simulator that learns a BN predictive model for a travel-activity attribute and constructs activity scheduling of all individuals in the population. The inputs of this sub-model are the travel diary survey and all synthetic individuals generated in the synthetic population generator, and the output is their minute-level activity scheduling at the census tract level. The activity attribute simulator defines an individual in the BN-ABM as “featuring alternating time-budgets from weekday to weekend”, “scheduling”, “executing”, and “traveling regularly and day-varyingly”:

1). **Alternating time-budgets from weekdays to weekends.** To model individual dynamic travels, the activity attribute simulator retrieves weekday and weekend time-budgets of all individuals in the population. This time-budget retrieval is motivated by the recognition that various constraints in space and time are imposed on an individual’s daily travels and activities. A few fixed activities arise to govern their mobility. Fixed activities refer to long-term activities such as work activities or school activities, and limits the scheduling of non-fixed activities in respect to location, duration, travel mode, and type. Here we assume that an individual’s daily time-budgets vary from weekday to weekend, but not daily. We retrieve such “semi-dynamic” time-budgets as follows: (1) an individual’s weekday time-budgets are directly derived from the survey, and (2) their weekend time-budgets resemble the unemployed peoples’ time-budgets in the survey, and are derived using random sampling.

2). **Scheduling.** The activity attribute simulator develops a BN-based scheduling generation algorithm, which learns predictive BNs for travel-activity attributes from the travel diary survey (model training) and generates individual activity scheduling from the learned BNs (model prediction). In the training step, the dependent variable is a travel-activity attribute, and the independent variables are the household-level and person-level demographic and socio-economic attributes from the travel dairy survey. The subjective of this step is to learn the conditional probabilities of a travel-activity attribute over these independent variables. In the prediction, the first stage of implementing the BN-based scheduling simulation is to generate long-term, fixed activity scheduling for all employed and student individuals, including work or school location choices. Next, the BN-based scheduling generates their non-fixed activity scheduling by predicting the travel frequency for each time-budget, and the travel purpose, the travel mode, the travel destination location, the activity duration, and the travel duration for each travel. One distinguishing feature of the BN-based scheduling is that it integrates BNs into an ABM by building BN predictive models for travel-activity attributes. Although the BN-based scheduling approach is fundamentally different from traditional methods such as decision tree, logit regression and utility maximizing theory (W. Davidson et al., 2010; Auld & Mohammadian, 2012; Yasmin et al., 2015), , our ABM has flexibility in using these scheduling methods.

3). **Executing.** The following stage of the activity attribute simulator requires an executing function to construct an individual’s activity records from the BN-based scheduling generation result and update their location based on current time. An activity record contains current activity type, travel purpose (next activity type), departure time, arrival time, travel mode, current location and travel destination location. If an individual is determined to execute the “travel” action based on current time, the model will update their travel mode, and travel duration. If an individual executes the “activity” action, their location, activity duration, and activity type will be updated.

4). **Regular and day-varying travel.** The BN-based activity attribute simulator takes into account regularity and irregularity in an individual’s daily travels and activities by implementing probability-based scheduling generation algorithm based on the learnt BNs. A BN determines what variables are related to retrieve a travel-activity attribute and compute the conditional probability distributions over the travel-activity attribute and the selected variables from the travel survey. Next, the activity simulator predicts and constructs activity records of an individual by random samples based on the leant BN probabilities of travel-activity attributes. Such random sampling could ensure that both the most likely scheduling and the less likely scheduling be selected, especially for a large population.

2.3.2 Synthetic Population Generator Sub-Model Overview and Statistical Test

The BN-ABM starts with a population synthesis that generates a synthetic population at both the person-level and household-level using the Iterative Proportional Updating (IPU) algorithm proposed by Ye et al. (Ye et al., 2014). This approach can efficiently match both person-level and household-level attributes by iteratively adjusting and reallocating weights for the households in a sample until the joint distributions of critical attributes in the weighted sampled population match the known distributions of the attributes available through the American Community Survey. As the goodness-of-fit between the sampled population and the Census population, the synthetic population generator based on the updated household weights random draws households from the survey to generate a synthetic population.

The population synthesis is intrinsically a mathematical optimization problem as follows:

$$Minimize \sum_{j} \left[\frac{\sum_i d_{i,j} w_i - c_j}{c_j} \right]^2$$

where j is an attribute of interest, i is a household in the survey, $d_{i,j}$ is the frequency of the attribute j in household i, w_i is the weight attributed to household i, and c_j is the value for the attribute j. Minimizing this function represents measuring the inconsistency between the weighted frequency of the attributes of interest in the synthetic population and the known frequency available through the American Community Survey. The IPU, inherently a heuristic iterative procedure, monitors the goodness-of-fit to determine the point where the procedure should be terminated (Ye et al., 2014). And the steps are as follows (Ye et al., 2014):

```
Generate a frequency matrix D where a row is a household from the travel diary survey, a column is a value of an attribute $j$, and an element is the frequency of a specific attribute value in the household or the number of individuals for a specific attribute value in the household.

Obtain joint distributions of the attributes of interest using the standard IPF procedure and store them into a column vector C where $c_j$ represents the value of the attribute $j$ and $j = 1, 2 ... m$.

Initialize the weight vector W, such that $w_i = 1$, where $i = 1, 2... N$, initialize a scalar $\delta = \frac{\left(\sum_j \left[\frac{\sum_i d_{i,j} w_i - c_j}{c_j}\right]^2\right)}{m}$, and set $\delta_{min} = \delta$.

For each iteration
    Go through matrix D:
        For each column $j_k$
            For each row $i$
                Calculate $s_{i,j_k} = d_{i,j_k} * w_i$
            End Loop
            Sum $s_{i,j_k}$, $where\ i = 1, 2... N$, to $s_{j_k}$, and calculate the adjustment for $j_k$,
            $\rho_{j_k} = \frac{c_{j_k}}{s_{j_k}}$
        End Loop
    Update W, $w_{j_k} = \rho_{j_k} * w_{j_k}$
    Set $\delta_{Pre} = \delta$
    Update $\delta = \frac{\left(\sum_j \left[\frac{\sum_i d_{i,j} w_i - c_j}{c_j}\right]^2\right)}{m}$
    Calculate the improvement in goodness-of-fit, $\Delta = |\delta - \delta_{Pre}|$
    If $\delta < \delta_{min}$
        Then $\delta_{min} = \delta$
    If $\Delta < \varepsilon$, which is a small positive number i.e. $1 * 10^{-5}$
        Break
```

Subsequently, it is necessary to evaluate the representativeness of the generated synthetic population as well as the performance of the synthetic population generator. The Pearson's Chi-square Test (χ^2) is a statistical test to evaluate the difference between two frequency distributions. Integration of the χ^2 test into the BN-ABM facilitates testing the null hypothesis stating that the distribution of the synthetic population is consistent with the Census distribution. The p-value serves as an appropriate measure of fit in respect to the matching of person-level distributions.

2.3.3 Activity Attribute Simulator Sub-Model Overview and Validation

Conceptual considerations. The aim of the activity attribute simulator is to uncover the relationship between an individual's daily travels and their person-level and household-level attributes as well as environmental impacts. Here we take into account two types of environmental impacts that governs peoples' daily activities and travels. They are environmental attractions such as local business, recreational sites, school enrollment and land use types, and environmental restrictions such as environmental endangered sites, contamination areas and dump sites.

Model specification. Bayesian Networks as a probabilistic graphical model learn and estimate conditional dependencies among a large set of variables based on Bayesian statistical inference, and use graph-based representation to express conditional structure between these critical variables. A BN typically consists of a directed acyclic graph and a joint probability distribution of the variables that is computed by $\mathrm{P}(\mathrm{X}_1, \mathrm{X}_2, \ldots \mathrm{X}_\mathrm{n})$ at a specific value, for example $\mathrm{X}_1 = \mathrm{a}_1, \mathrm{X}_2 = \mathrm{a}_2, \ldots, \mathrm{X}_\mathrm{n} = \mathrm{a}_\mathrm{n}$:

$$P(X_1, X_2, \ldots X_n) = \prod_i p(X_i | Parents(X_i))$$

where $\mathrm{X}_1, \mathrm{X}_2, \ldots \mathrm{X}_\mathrm{n}$ denotes the variables of interest, or called nodes in the graph, and $\mathrm{Parents}(\mathrm{X}_\mathrm{i})$ denotes all parent variables of variable X_i. Here the variables are the person-, household- and travel- level attributes from the travel diary survey. The aim of this section is to learn a travel-activity attribute BN. To achieve this goal, we identify the crucial variables that are related to predict the travel-activity attribute, find all parent nodes for each selected variable, and compute conditional probabilities among them. Incorporation of BNs into activity-based models (the activity attribute simulator) is to build and learn a predictive BN for a travel-activity attribute. A travel-activity attribute BN is defined as BN (A, A_), where A is the activity attribute and A_ are the variables considered to be conditionally related to A:

$$BN\ (A, A_{-}) = P(A, A_1, \dots, A_n)$$

Model Learn. Learning BN from observations generally consists of two steps: structure learning and parameter estimating. Structure learning is to identify the BN graphical structure that best describes the data, and parameter learning is to compute conditional probability distributions of all variables in the leant structure. Given the data, learning BN structure is to explore conditional dependencies between variables and represent these relationships using directed arrows. For example, an arrow A->B denotes that variable B is conditionally related to variable A, and the probability of B at a specific value given A at a specific value is computed by parameter learning. Several methods have been developed to learn BN structure and broadly classified into two categories: score-based structural learning and constraint-based structural learning (Daly et al., 2011; Gámez et al., 2011; Larrañaga et al., 2013; Yuan, n.d.). Behjati and

Beigy summarized the pros and cons of these two methods and proposed the hybrid method that integrates their advantages (Behjati & Beigy, 2018). The score-based approach due to well-defined scoring functions, regardless of data, is theoretically well-suited in every situation. In practice, it is known to generate better structures than the constraint-based approach. Its major drawback is time consuming as variables increase. The constraint-based approach is known to be unstable and sensitive to a small change. The hybrid method has been proposed to integrate the advantages of constraint-based methods and score-based methods to solve the structure learning problem. Here we use the Min–Max Hill Climbing (MMHC) algorithm, one of the widely-used hybrid learning methods, to learn travel-activity attributes' BNs. This method starts with an initial structure learned from the constraint-based method and identifies higher-scoring structures using greedy search technique. Using MMHC, we identify the best travel-activity attribute BNs given a set of household-level and person-level attributes from the travel diary survey. To learn a travel-activity attribute BN, we compare all possible BNs derived from adding and/or deleting variable nodes and selects the BN wherein all variables are effectively directed and conditionally dependent on each other. Next, we estimate conditional probability distributions of all variables in the learnt structure using the maximum likelihood estimation method (MLE), and the principle of this method is to find the parameters that maximize the likelihood function:

$$Maximize\ \ L(\theta : D) = P(D|\theta) = \prod_{k=1}^{K} \theta_k^{N_k}$$

where L is the likelihood function, D is the data for an attribute variable, θ is the probability distribution for the attribute variable, K is the number of the values in D, $k = 1, \dots, K$, N_k is the frequency of the value k occurring in D, and $P(D|\theta)$ is to measure how likely θ represents the observed data D.

Model validation. The activity attribute simulator inputs synthetic individuals to the learnt BNs, and generates their activity scheduling. To validate the learnt BNs, we employ the k-fold cross-validation by dividing the travel diary survey into training and testing datasets (k=10). The training dataset (90% of the total survey) is to learn the BN structures and estimate the BN parameters, while the test dataset (10% of the survey) is to validate the learnt BNs. We use accuracy to measure the cross-validation results of discrete activity choices, including travel mode, travel purpose and travel destination location, and use residual to measure cross-validation results of continuous activity choices, including travel frequency, travel duration, and activity duration. The equations are as follows:

$$Accuracy = \frac{the\ number\ of\ the\ correct\ prediction\ reccords}{the\ total\ number\ of\ the\ testing\ reccords}$$

$$Residual = |the\ predicted\ value - the\ observed\ value|$$

2.3.4 Finer-scale utility-based location choices

Although the BN-ABM can operate at various spatial scales ranging from census block group to traffic analysis zone, this study utilizes the model at the census tract level. One disadvantage of the BN-ABM is its poor performance in predicting a great number of choices. Using a simple example, the destination location choices in the case study have 519 values, which makes training and learning the location choice BN difficult. To solve this issue, we propose a hieratical location choice model that integrates the coarse-scale BN-based location choice model and the finer-scale utility-based location choice model. In the utility-based location choice model, we use random forest to determine the first four "most important" variables to a specific travel propose or activity type, and compute utility-based scores of all census tracts in the study area based on the importance measure in random forest. This utility-based model is motivated by the utility-based choice theory that an individual has preference in the alternative maximizing their utility. Here we assume that the utility that an individual derives from one location to another location is a function of environmental attractions, environmental limitations, and travel purpose. The independent inputs of the sub-model are a set of GIS-based environmental variables, including the number of groceries, the number of restaurants, the number of dump sites, the number of parks, the number of major malls, the number of golf sites, the number of trips, area for a specific land use type, and school enrollment per tract, the tract to the nearest environmental-endangered site distance, and the tract to the nearest contamination area distance. The dependent input is the number of a specific activity type per tract derived from the travel survey. The outputs are the importance measures of each independent variable mentioned above for a specific activity type. Then the total utility-based score of a census tract i for a particular travel purpose a is computed as follows:

$$U_i(a) = im_{v1} * v_{1,i} + im_{v2} * v_{2,i} + \cdots + im_{vn} * v_{n,i}$$

where i denotes the census tract i, $\mathrm{U}_i(\mathrm{a})$ denotes the total utility-based score of the census tract i for travel purpose a, $\mathrm{v}_{1,\mathrm{i}}, \dots, \mathrm{v}_{\mathrm{n},\mathrm{i}}$ denotes the values of the independent variables $\mathrm{v}_1, \dots, \mathrm{v}_\mathrm{n}$ at the census tract i, and $\mathrm{im}_{V1}, \dots, \mathrm{im}_{Vn}$ denotes the importance measure for the variable $\mathrm{v}_1, \dots, \mathrm{v}_\mathrm{n}$. Finally, we combine the finer-scale utility-based scores and the coarse-scale BN-based probabilities to simulate individual location choices.

2.3.5 In-travel and out-travel ratios

The in-travel and out-travel ratios per tract at particular times based on a one-weekday simulation result are calculated as follows:

$$in\ ratio\ (z) = \frac{in\ travels\ (z)}{in\ travels(z) + out\ travels(z)}$$
$$out\ ratio\ (z) = \frac{out\ travels\ (z)}{in\ travels(z) + out\ travels(z)}$$

where z denotes a tract census zone, $\mathrm{out\ travels\ (z)}$ denotes the number of activities that departure from the zone z, and $\mathrm{in\ travels\ (z)}$ denotes the number of activities that origin from other zones and go to the zone z.

2.4 Data Sources

To test the efficacy of the proposed BN-ABM, we take Miami-Dade County, Florida as a case study. The required data are the American Community Survey, a traditional travel diary survey, and multiple GIS data. In the BN-ABM, the travel diary survey is combined with the ACS to generate a synthetic population in the population synthesis generator, and then is used to train and test the BNs for travel-activity attributes in the activity attribute simulator. The activity attribute simulator also requires multiple GIS data to model and predict location choices.

2.4.1 Travel Diary Survey Data

The 1999 Southeast Florida Household Travel Survey was collected by the Florida Department of Transportation (FDOT) Districts and metropolitan areas, and was intended to investigate how Southeast Florida residents use transportation services in the region. The respondents were asked for their activities and travels during a 24-hour period as well as detailed information regarding their travel mode, travel purpose, departure and arrival time, and pairs of origin-destination location. We extract the Miami-Dade travel survey data from the 1999 Southeast Florida Household Travel Survey that includes Broward, Miami-Dade and Palm Beach. Figure 3 visualizes the survey data for the Miami-Dade region. This survey also includes 18 sociodemographic variables at both the person- and household- level, and Table 1 depicts these variables as well as their values and types.

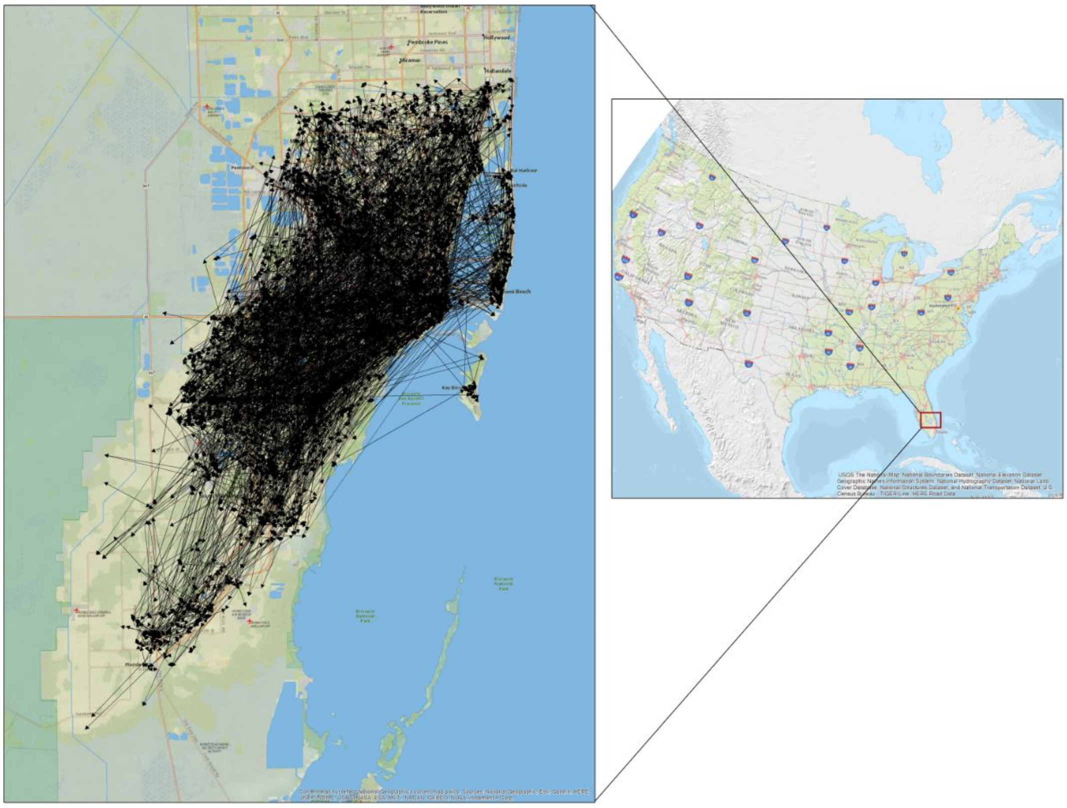


Figure 3. Visualization of the 1999 Southeast Florida Household Travel Survey for the Miami-Dade region. The black lines are the daily travel trajectories of the respondents in the survey.

Table 1. The sociodemographic variables in the 1999 Southeast Florida Household Travel Survey.

Description	Values	Type	Description	Values	Type
Annual income	21 levels from under 5k to over 100k	Person	Number of persons	Integer	Household
Personal Age	Integer	Person	Number of persons	Integer	Household
Residential status	Full time or Part time	Person	Number of Children	Integer	Household
Employed	Yes, no or child under 16	Person	Number of licensed drivers	Integer	Household
Employ Status	Full time or Part time	Person	Number of out of town	Integer	Household
Work Type	11 work types e.g. farming	Person	Number of vehicles	Integer	Household
Retired	Retired or Unemployed	Person	Dwelling unit type	13 housing types e.g. single family home	Household
Vehicle use	Yes or no	Person	Annual income	21 levels from under 5k to over 100k	Household
Telecommute	Yes or no	Person	County of residence	Broward, Miami-Dade and Palm Beach	Household

2.4.2 Census and Environmental Data

The American Community Survey data provides information about people, housing, business and industry, governments, and other topics at various spatial and temporal scales in the United States. Here we use the 2012-2016 ACS 5-year estimates data at the census tract level for Miami-Dade County regarding age, household income, household size, and the number of workers in a household.

In addition to the Census sociodemographic data, the BN-ABM requires multiple GIS data, including groceries, restaurants, contamination areas, dump sites, parks, major malls, golf sites, land cover and land use, school enrollment, and environmental endangered sites. We collect the grocery and restaurant data for Miami-Dade County by using Yelp Search API to access their local businesses with the keywords “groceries” and “restaurants”. The searching returns the latitudes and longitudes of all groceries or restaurants in Miami-Dade County on the search day. Then we aggregate the data, originally collected at the point level, to the total of groceries or restaurants per census tract.

Miami-Dade County also provides many open GIS data in respect to boundaries, buildings, education, environment, infrastructure, location, parks, zoning property, and planning. We collect point-based dump site, park, major mall, golf site, and school enrollment data, and polygon-based contamination area, land cover and land use, and environmental endangered site data. Then, the point-based datasets are aggregated to the total per census tract. The polygon- based land cover and land use data is intersected with the Census tract shapefile, and aggregated to the total area per land type per census tract. The distance of a census tract to the nearest environmental endangered polygon, and the distance of the tract to the nearest contamination polygon are also calculated. Table 2 depicts the statistical summary of all datasets required in the BN-ABM as well as how they are utilized in the model.

Table 2. The statistical summary of all datasets required in the BN-ABM.

Dataset	Variable Description	Scale	Statistic Summary	Simulation
American Community Survey	Household size, household income, the number of workers in the household, and personal age	Census tract 2016	Total 2,680,607 Persons, and 860,380 Households	**Input** of the synthetic population generator
Southeast Florida Household Travel Survey	Household-, person-, and travel- level attributes (current activity type, next activity type, begin time, end time, travel duration, travel mode, latitude of the origin, longitude of the origin, latitude of the destination, and longitude of the destination)	Minute-level GPS 1999	Total 1,253 Households and 2,445 Persons	**Input** of the synthetic population generator; **Input** of the activity attribute simulator
Miami-Dade County Open GIS Data	Contamination areas, dump sites, parks, major malls, golf sites, land cover and land use, school enrollment, and environmental endangered sites	Point or polygon 2016	Total 394,470 enrollment and 1,163 schools	**Input** of the location BN in the activity attribute simulator
Yelp Local Business Data	Restaurants and groceries	Point 2016	Total 6,791 restaurants and groceries	**Input** of the location BN in the activity attribute simulator

2.5 Results

This section describes the results of the case study of Miami-Dade County. A synthetic population that represents the actual population in Miami-Dade County is generated, and the goodness-of-fit of the generated synthetic population is tested using the Pearson's Chi-square Test. A total 9 BNs are then built and validated using k-fold cross-validation. Finally, one-weekday individual activity scheduling for the population in the study area is created, and in-travel and out-travel ratios of the prediction results at 8:00 am and 18:00 pm are calculate.

2.5.1 Synthetic Population Generation

Four valuables including household size, household income, personal age, and the number of workers in the household are used to create the populations of all census tracts in Miami-Dade County. To assess the goodness-of-fit of the generated synthetic population and the ACS population, we use the Pearson's Chi-square Test (χ^2) and the computed p-value as a measure of fit. Here the hypothesis H_0 is that the distribution of a synthetic population is consistent with the ACS distribution, and the alternative hypothesis H_1 is that the distribution of a synthetic population is inconsistent with the ACS distribution. Of 505 synthetic populations (excluding 14 zero cells in the 519 tract-level populations in Miami-Dade County), 122 populations exhibit the χ^2 value greater than the critical value for 5 degrees of freedom at the significance level α=0.05. We reject the null hypothesis and conclude that the distributions of the 122 populations are significantly different from the ACS distributions. 388 synthetic populations are consistent with the ACS.

2.5.2 Predictive BNs in the Activity Attribute Simulator

We build a total of 9 BNs including travel purpose BN, travel mode BN, employed people and students' travel frequency BN, unemployed people and children's travel frequency BN, employed people and students' activity duration BN, employed people and students' travel duration BN, unemployed people and children's activity duration BN, and unemployed people and children's travel duration BN from the survey data. The BNs of travel frequency, employed people and students' activity duration, and employed people and students' travel duration are continuous Gaussian Bayesian networks, while the rest are discrete. Table 3 shows the detail description of the 9 BNs as well as the values of all trip-level variables in the model.

Table 3. The detailed description of the 9 BNs.

	BN Model	BN Type	Variable Description
1	Travel purpose	Discrete	6 discrete travel purpose choices including home activities, work activities, school activities, social activities, shopping activities or other activities; 3 discrete employment status (1: yes, 2: no, 3: children under 16)
2	Travel mode	Discrete	5 discrete travel mode choices including car, pool car, public transport, walk or bike
3	Travel frequency for employed individuals and students	Continuous	Integer travel frequency choices; 4 discrete age ranges including 0 under 20, 1 from 20 to 50, 2 from 50 to 70, or 3 over 70; continuous open-period duration choices
4	Travel frequency for unemployed individuals and children	Discrete	5 travel frequency choices ranging from under 2 to over 8; 6 discrete open-period duration choices ranging from under 100 to over 1000
5	Activity duration for employed individuals and students	Continuous	Integer activity duration choices; Integer open-period duration choices
6	Travel duration for employed individuals and students	Continuous	Integer travel duration choices
7	Activity duration for unemployed individuals and children	Discrete	8 activity duration choices ranging from under 40 to over 800
8	Travel duration for unemployed individuals and children	Discrete	6 travel duration choices ranging from under 10 to over 60
9	Coarse-level travel destination	Discrete	Coarse-level travel destination location choices including 6 administrative zones

Figure 4, 5, 6, and 7 show the conditional dependencies and the crucial conditional probability tables (CPT) of the 9 BNs. In particular, person-level, household-level and trip-level attributes including residential type, employment status, personal income, whether an individual use a vehicle, the number of children in the household, current location, current activity, and begin time, end time and duration of peoples' time-budget are closely associated with their travel-activity choices. The BNs exhibit the direct conditional relationship between a travel-activity attribute and these person-level, household-level and trip-level variables: (1) between travel mode and employment status, (2) among travel purpose, current activity and employment status, (3) among travel frequency, time-budget duration, age, and residential type, (4) among activity duration, time budget, and travel purpose, and (5) among travel duration, travel mode, current time, and current activity.

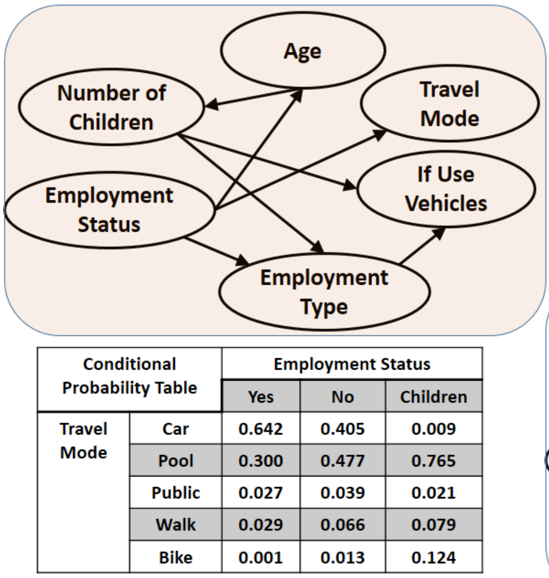
Next step is to compute a CPT for all variables in a BN. In the travel mode BN, the probability that an employed individual drives to conduct an activity is 0.642, the probability that a child is a passenger to conduct an activity is 0.765, and the probability that an unemployed individual drives to conduct an activity is 0.405. In the travel purpose BN, the probability that an employed individual goes to work from home is 0.550, the probability that a child goes to school from home is 0.573, and the probability that an unemployed individual goes shopping or conducts other activities from home is 0.235 and 0.452. In the employed and children's travel frequency BN, the conditional density of travel frequency over time-budget and personal age is estimated rather than a CPT, which instinctively is liner Gaussian regression between travel frequency and time-budget in a specific age group:

$$\begin{array}{lll} \textit{Travel Frequency} = & 1.001 + 0.0040 * \textit{time budget} & \textit{age} < 20 \\ & 1.107 + 0.0060 * \textit{time budget} & 20 \leq \textit{age} < 50 \\ & 1.157 + 0.0052 * \textit{time budget} & 50 \leq \textit{age} < 70 \\ & 1.038 + 0.0050 * \textit{time budget} & \textit{age} \geq 70 \end{array}$$

In the employed and children's activity duration BN, the conditional density of activity duration over time-budget is as follows:

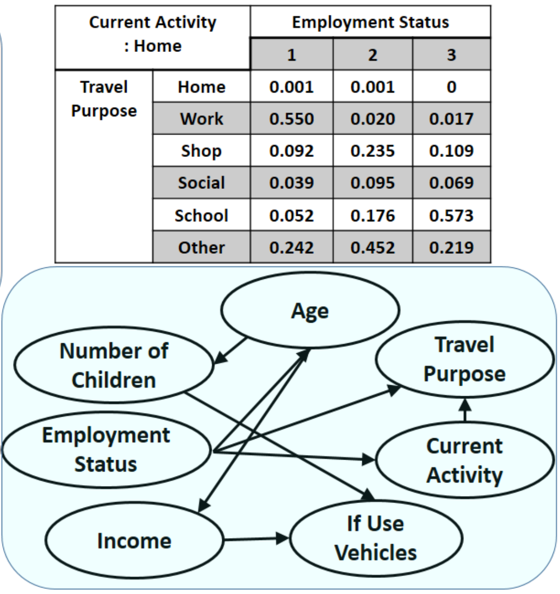
$$Activity\ Duration = 1.899 + 0.413 * time\ budget$$

In the location BN, the probability that an individual goes to Zone 1 from Zone 2 is 0.441, while the probability that they remain in Zone 1 for next activity is 0.440.



Conditional Probability Table		Employment Status		
		Yes	No	Children
Travel Mode	Car	0.642	0.405	0.009
	Pool	0.300	0.477	0.765
	Public	0.027	0.039	0.021
	Walk	0.029	0.066	0.079
	Bike	0.001	0.013	0.124

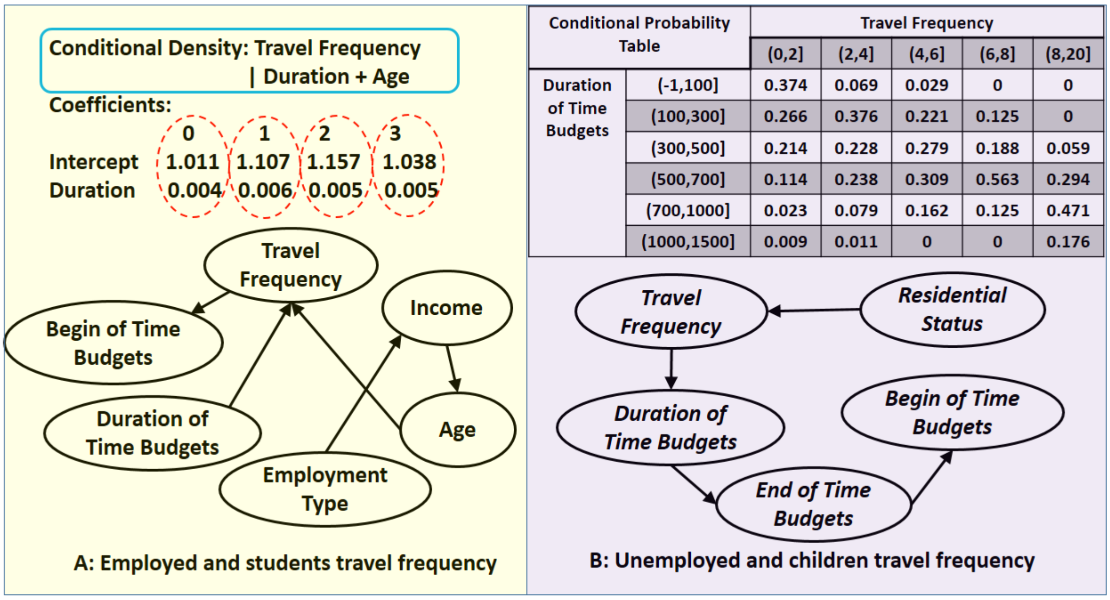
A: Travel Mode



Current Activity : Home		Employment Status		
		1	2	3
Travel Purpose	Home	0.001	0.001	0
	Work	0.550	0.020	0.017
	Shop	0.092	0.235	0.109
	Social	0.039	0.095	0.069
	School	0.052	0.176	0.573
	Other	0.242	0.452	0.219

B: Travel Purpose

Figure 4. The travel purpose and travel mode BNs. In A, the top is the travel mode BN, and the bottom is the conditional probability table of travel mode given employment status. In B, the bottom is the travel purpose BN, and the top is the conditional probability table of travel purpose given employment status. The values in the CPTs are the conditional probabilities of travel mode at a specified value over employment status at a specified value.



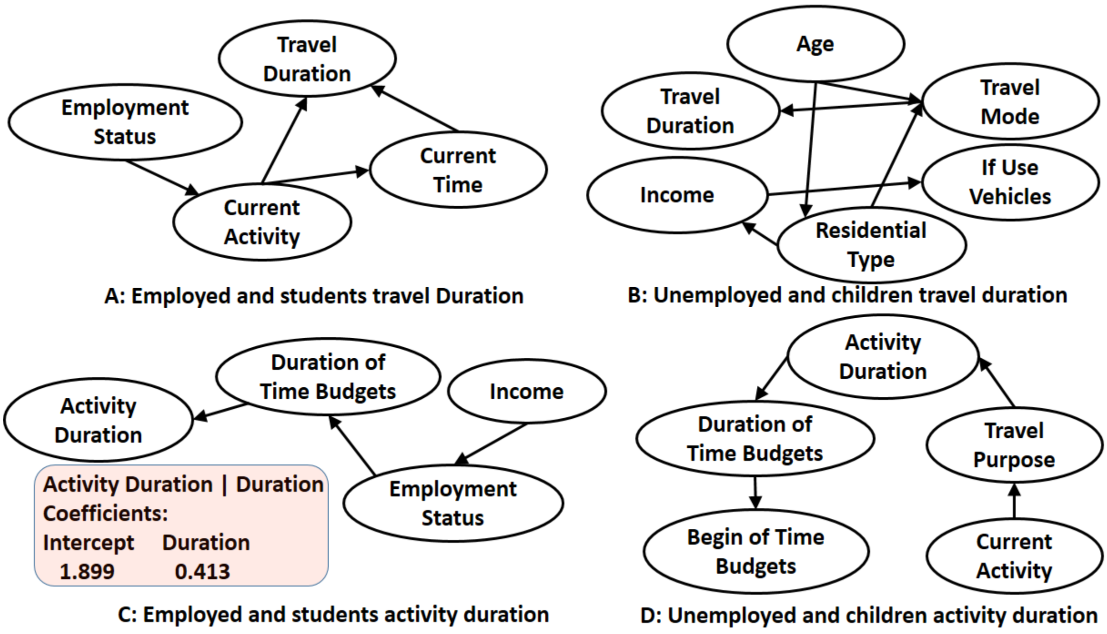
Conditional Density: Travel Frequency | Duration + Age

Coefficients:

	0	1	2	3
Intercept	1.011	1.107	1.157	1.038
Duration	0.004	0.006	0.005	0.005

Conditional Probability Table		Travel Frequency				
		(0,2]	(2,4]	(4,6]	(6,8]	(8,20]
Duration of Time Budgets	(-1,100]	0.374	0.069	0.029	0	0
	(100,300]	0.266	0.376	0.221	0.125	0
	(300,500]	0.214	0.228	0.279	0.188	0.059
	(500,700]	0.114	0.238	0.309	0.563	0.294
	(700,1000]	0.023	0.079	0.162	0.125	0.471
	(1000,1500]	0.009	0.011	0	0	0.176

Figure 5. The travel frequency BNs. In A, the bottom is the employed people and students' travel frequency BN, and the top is the conditional density of employed people and students' travel frequency choices given time budget and personal age. In B, the bottom is the unemployed people and children's travel frequency BN, and the top is the conditional probability table of unemployed people and children's travel frequency choices given time budgets and residential status. The values in the CPT are the conditional probabilities of travel frequency at a specified value over time budget at a specified value, and the conditional density is the Gaussian liner regression of travel frequency from age and time-budget.



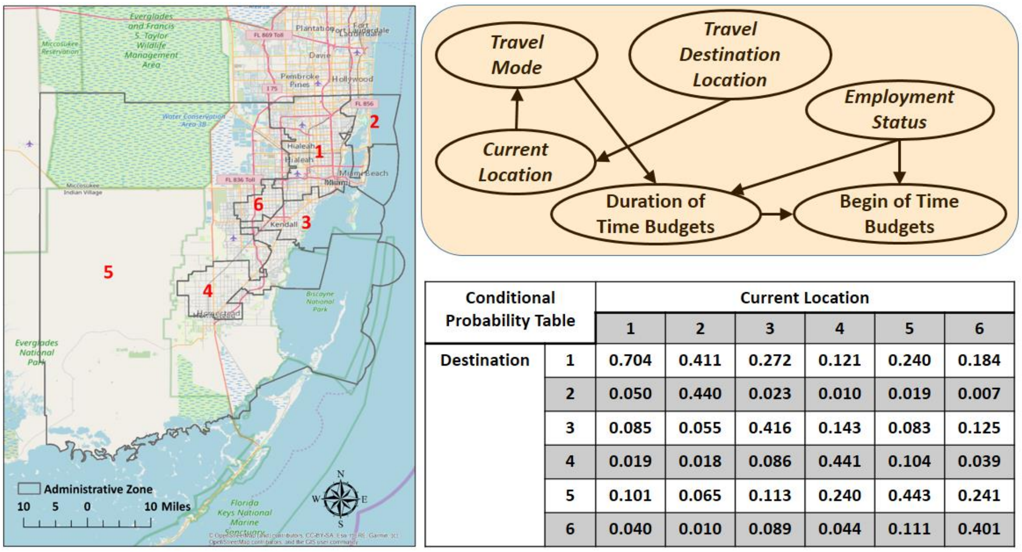
A: Employed and students travel Duration

B: Unemployed and children travel duration

C: Employed and students activity duration

D: Unemployed and children activity duration

Figure 6. The activity duration and travel duration BNs. A is the employed people and students' travel duration BN, B is unemployed people and children's travel duration BN, C is the employed people and students' activity duration BN, and D is the unemployed people and children's activity duration BN.



Conditional Probability Table		Current Location					
		1	2	3	4	5	6
Destination	1	0.704	0.411	0.272	0.121	0.240	0.184
	2	0.050	0.440	0.023	0.010	0.019	0.007
	3	0.085	0.055	0.416	0.143	0.083	0.125
	4	0.019	0.018	0.086	0.441	0.104	0.039
	5	0.101	0.065	0.113	0.240	0.443	0.241
	6	0.040	0.010	0.089	0.044	0.111	0.401

Figure 7. The location BN. The left depicts the macro-level location values in the study area. The right top is the location BN, and the right bottom is the conditional probability table of travel destination location given current location. The values in the CPT are the conditional probabilities of travel destination location at a specified value over current location at a specified value.

Finer-scale utility-based activity location choices. Using random forest, we determine the first four “most important” variables to a specific activity type including work activities, school activities, shopping activities, social activities, unknown activities, and other activities (Figure 8). We uncover close relationships among activity type, environmental restrictions including distance to the nearest endangered area or containment site, and environmental attractions including employment opportunities (restaurants and shopping area), education opportunities (total school enrollment and number of schools), and recreation opportunities (shopping area). The importance measure scores of these variables are computed from random forest and serves as weight to calculate the total utility-based scores of all tracts in the study area for a specific activity type, which finally combines the BN probabilities to simulate an individual’s location choice. Figure 9 shows the total utility-based score of all census tracts in the Miami-Dade region for a specific travel purpose. The results suggest that high scores occur mostly in downtown areas for social activities, other activities, unknown activities and shopping activities. This is interpreted that while people conduct these activities, the probability that they go to the downtown area is greater than the other areas.

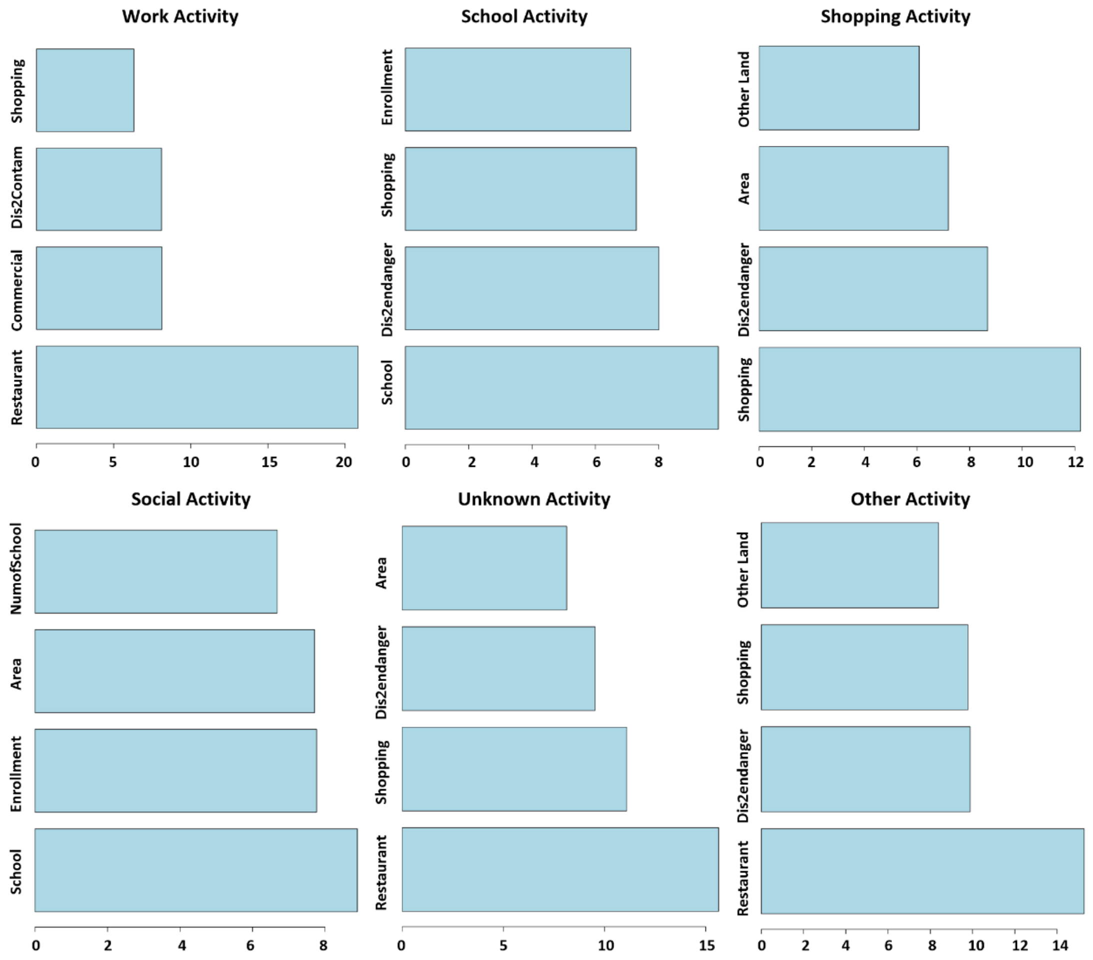


Figure 8. The first four “important” variables’ for a specified activity type, including work activities, school activities, shopping activities, social activities, unknown activities, and other activities, as well as the important measure scores computed from random forest. The x axis is the importance measure score, and the y axis is the variable. A variable with high scores for a specific activity type is interpreted as great contribution of the variable to this activity (Restaurant: the number of restaurants per tract, Commercial: the commercial area per tract, Dis2Contam: the tract to the nearest contamination area distance, Shopping: the shopping area per tract, School: the number of schools per tract, Dis2endager: the tract to the nearest endangered area distance, Enrollment: the total school enrollment per tract, Area: the tract area, Other Land: the total area of other land use types, excluding residential and school, per tract, and Numofschool: the number of schools per tract).

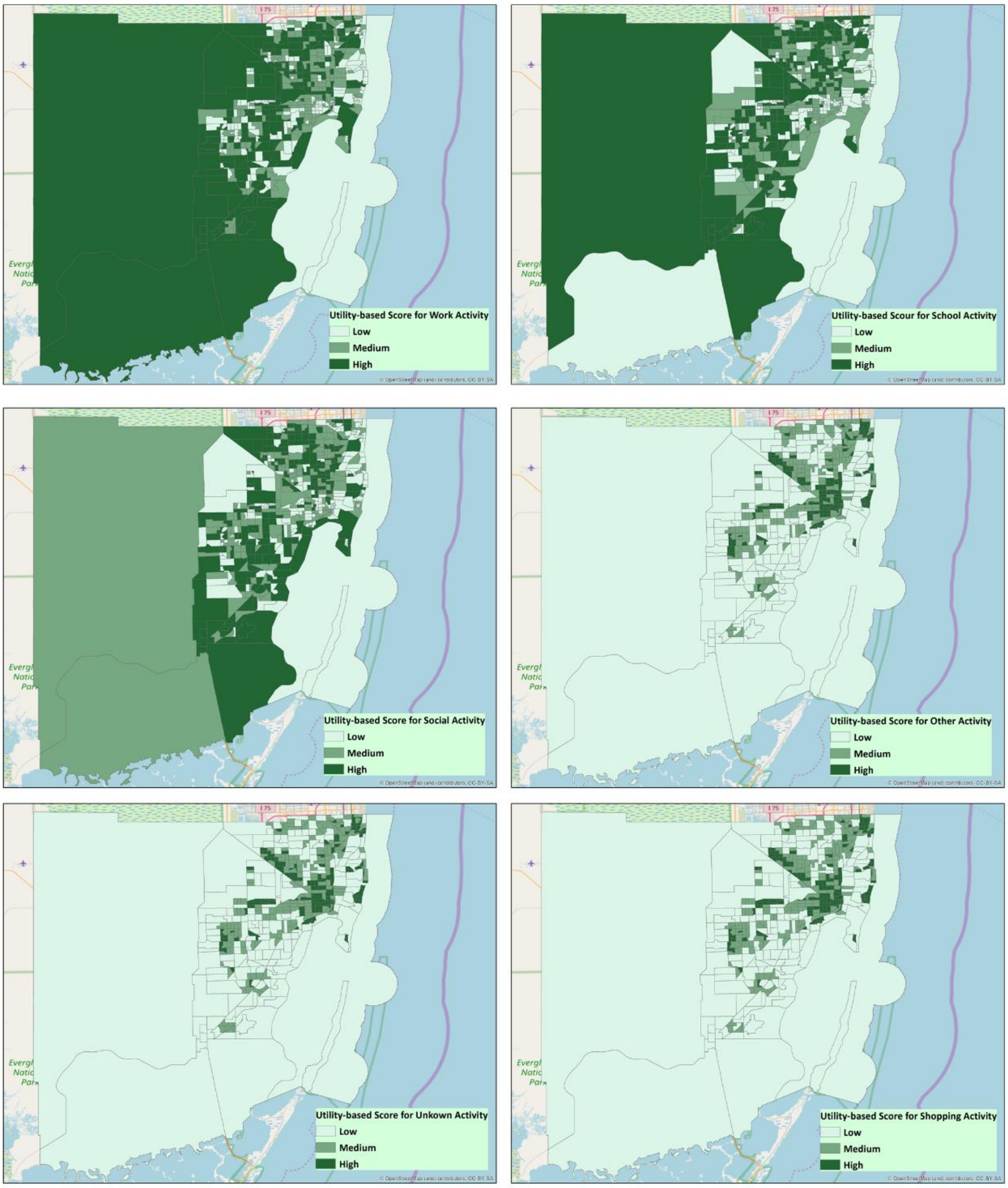


Figure 9. The total utility-based scores of all tracts in the study area for a specific activity type derived from random forest. The scores are discretized into "low", "medium" and "high". A high score of a tract is interpreted as large probability that the tract is selected for a specified activity type. For instance, people are most likely to choose the downtown area to conduct shopping activities, social activities, unknown activities and other activities.

2.5.3 Predictive BNs Validation and Improvement

To validate the 9 BNs, 10-fold cross-validation is utilized. Figure 10 summarizes the results of 10-fold cross-validation. With running cross-validation 200 times, we find that travel purpose and travel mode are replicated at 62%, while travel destination location is only 45%. To improve the BN-ABM prediction, we can include a couple of strategically selected behavioral aspects that are known to improve the prediction in other ABMs, e.g. the home to work distance and the home to school distance. This has already been done in many activity-based models, and this is also supported by the anchor point theory in time geography (Goulias, 2004; Goulias, 2005; Pribyl and Goulias, 2005). Table 4 depicts the independents variables, the training datasets, the test datasets and the summary of the cross-validation results for the BN-ABM and the enhanced BN-ABM. Figure 11 summarizes the cross-validation results of the enhanced model. To include the tract-based home to work distance, the tract-based home to school distance, the tract-based origin to destination location distance, and the index of current travel in the BN-ABM, we see improvements in the travel mode BN (5% up), the location BN (10% up), the travel duration BN (6 minutes less), and the activity duration BN (15 minutes less). In particular, the travel frequency, travel duration and activity duration BNs for unemployed people and children, originally built discretely, are learnt continuously in the improved BN-ABM by including the current time, the tract-based origin to destination location distance, and the index of the travel.

Table 4. The independents variables, the training and test datasets, and the average of the 10-fold cross-validation results for the BN-ABM and the enhanced BN-ABM.

	Travel-activity Attributes	**Independent Variables**	**Training (records)**	**Test (records)**	**Mean Accuracy (%) or Residual**
The BN-ABM	Travel Purpose	Age, number of children in the household, employment status, personal income, current activity, and vehicle use	5,139	600	62%
	Travel Mode	Age, number of children in the household, employment status, employment type, and vehicle use	5,139	600	62%
	Travel Destination Location	Current location, time budgets, travel mode and employment status	5,139	600	45%
	Travel Frequency for Employed People and Students	personal income, time budgets, age and employment status	1,891	200	1 trip
	Travel Duration for Employed People and Students	Current time, current activity, and employment status	2,403	300	18 minutes
	Activity Duration for Employed People and Students	Personal income, employment status and time budgets	458	60	55 minutes

	Travel Frequency for Unemployed People and Children	time budgets and residential type	656	70	53%
	Travel Duration for Unemployed People and Children	Age, travel mode, vehicle use, residential type, and personal income	2,175	200	44%
	Activity Duration for Unemployed People and Children	Time budgets, travel purpose and current activity	320	40	
The enhanced BN-ABM	Travel Purpose	Age, number of children in the household, employment status, personal income, current activity, vehicle use, and **household size**	5,139	600	62%
	Travel Mode	Age, number of children in the household, employment status, vehicle use, and **time budgets**	5,139	600	67%
	Travel Destination Location	Current location, time budgets, travel mode employment status, **home-to-school distance**, and **home-to-work distance**	4,578	500	55%
	Travel Frequency	personal income, time budgets, age, employment status and **current time**	2,547	300	1 trip

	Travel Duration	employment status, travel mode, travel purpose, age, current time, and **tract-based origin-to-destination location distance**	4,578	500	12 minutes
	Activity Duration	employment status, time budgets, personal income, travel purpose, current time and **the index of the travel**	778	80	40 minutes

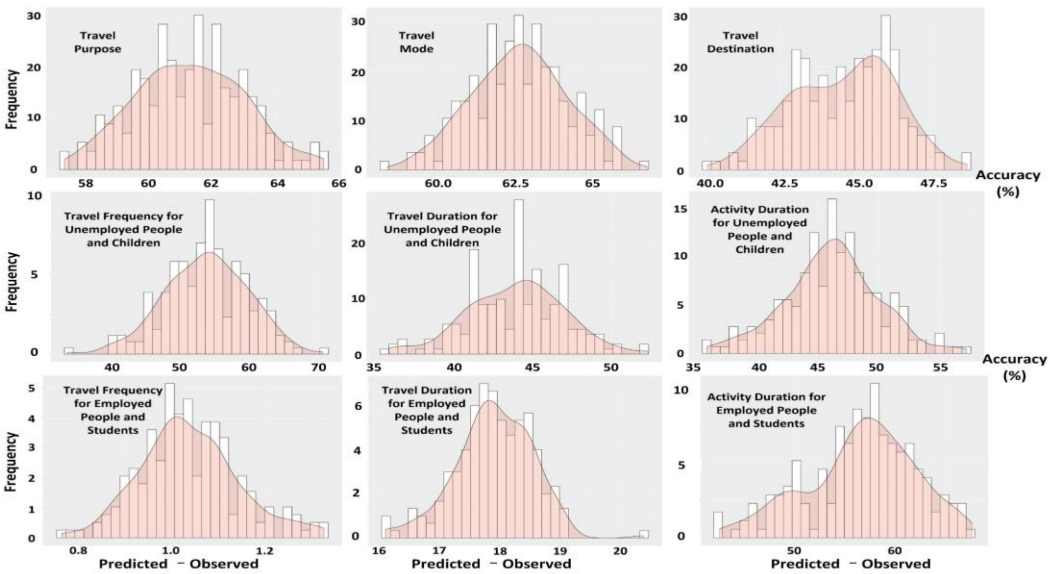


Figure 10. The 10-fold cross-validation for the total 9 BNs, including travel purpose choices, travel mode choices, travel destination location choices, employed people and students' travel frequency choices, employed people and students' travel duration choices, employed people and students' activity duration choices, unemployed people and children's travel frequency choices, unemployed people and children's travel duration choices and unemployed people and children's activity duration choices. With the cross-validation running 200 times, the x axis are the accuracy or residual intervals, and the y axis is the frequency of the cross-validation results for a specified accuracy or residual range. Travel purpose, travel mode, travel destination location, unemployed people and children's travel frequency, unemployed people and children's travel duration and unemployed people and children's activity duration are evaluated by the accuracy, while employed people and students' travel frequency (trip), employed people and students' travel duration (minute) and employed people and students' activity duration (minute) are validated by the difference between the predicted and the observed.

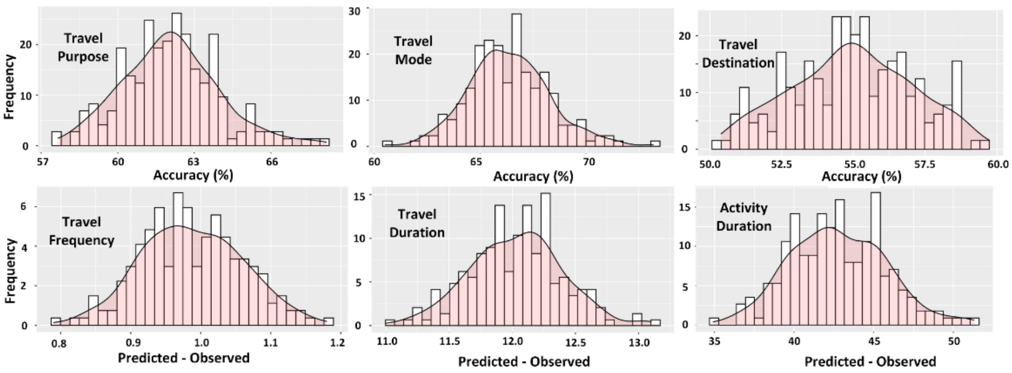


Figure 11. The k-fold cross-validation for the enhanced model, including travel purpose choices, travel mode choices, travel destination location choices, travel frequency choices, travel duration choices and activity duration choices. With the cross-validation running 200 times, the x axis are the accuracy or residual intervals, and the y axis is the frequency of the cross-validation results for a specified accuracy or residual range. Travel purpose, travel mode, and travel destination location are evaluated by the accuracy, while travel frequency (trip), travel duration (minute) and activity duration (minute) are validated by the difference between the predicted and the observed.

2.5.4 One-weekday BN-ABM Simulation

Here we conduct a one-weekday simulation. For each time-budget of an individual, we predict peoples' travel frequency as well as travel purpose, travel mode, travel duration, travel destination location, and activity duration for each travel. Using a predicted activity record as example (Figure 12), an individual leaves home at 7:30 am, drops off his child at 7:50 am, and goes to work at 8:00 am; in the afternoon, he goes back home at 16:00 pm. The transport mode that he uses to conduct these activities as well as the destination locations of these activities are also simulated.

Figure 13 shows the in-travel and out-travel ratios per tract at 8:00 am and 18:00 pm derived from our one-weekday simulation results. We can see that Miami-Dade downtown areas have a greater number of in-travels at 8:00 am and a greater number of out-travels at 18:00 pm, while residential and rural areas experience a contrary trend. Gariazzo et al. presented high-resolution population presence and urban mobility, derived from mobile phone data, in the city of Rome, Italy (Gariazzo et al., 2019). They also found that at the downtown cells, the time pattern of peoples' mobility shows a maximum and a minimum value at approximately 9:00 a.m. and 7:00–8:00 p.m., respectively, corresponding to morning and evening commuting times.

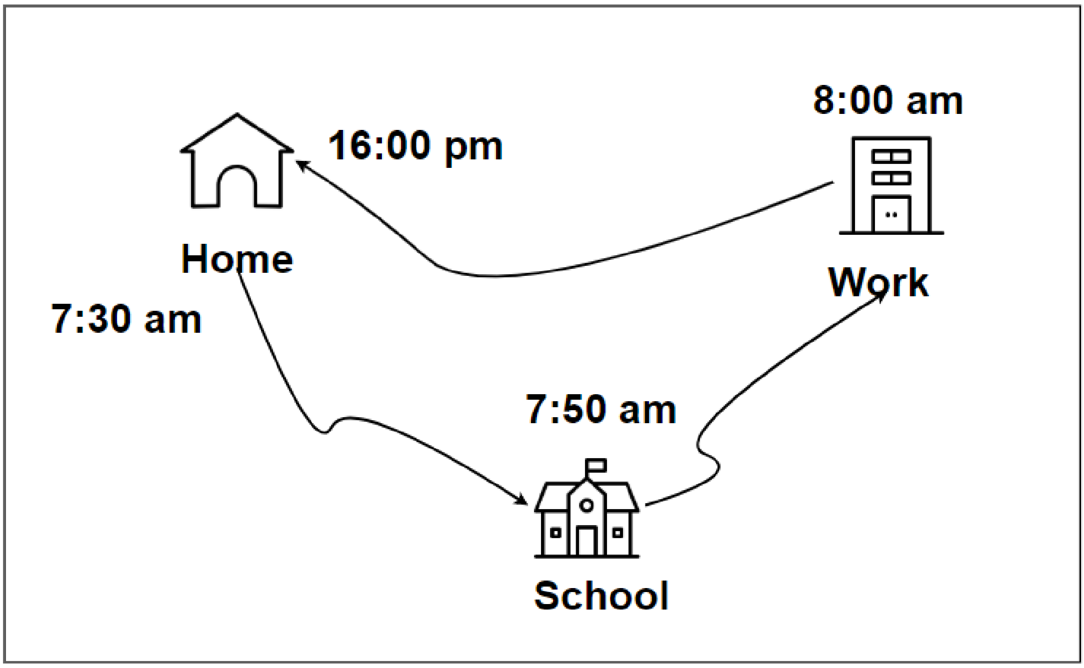


Figure 12. A simple prediction from the BN-ABM.

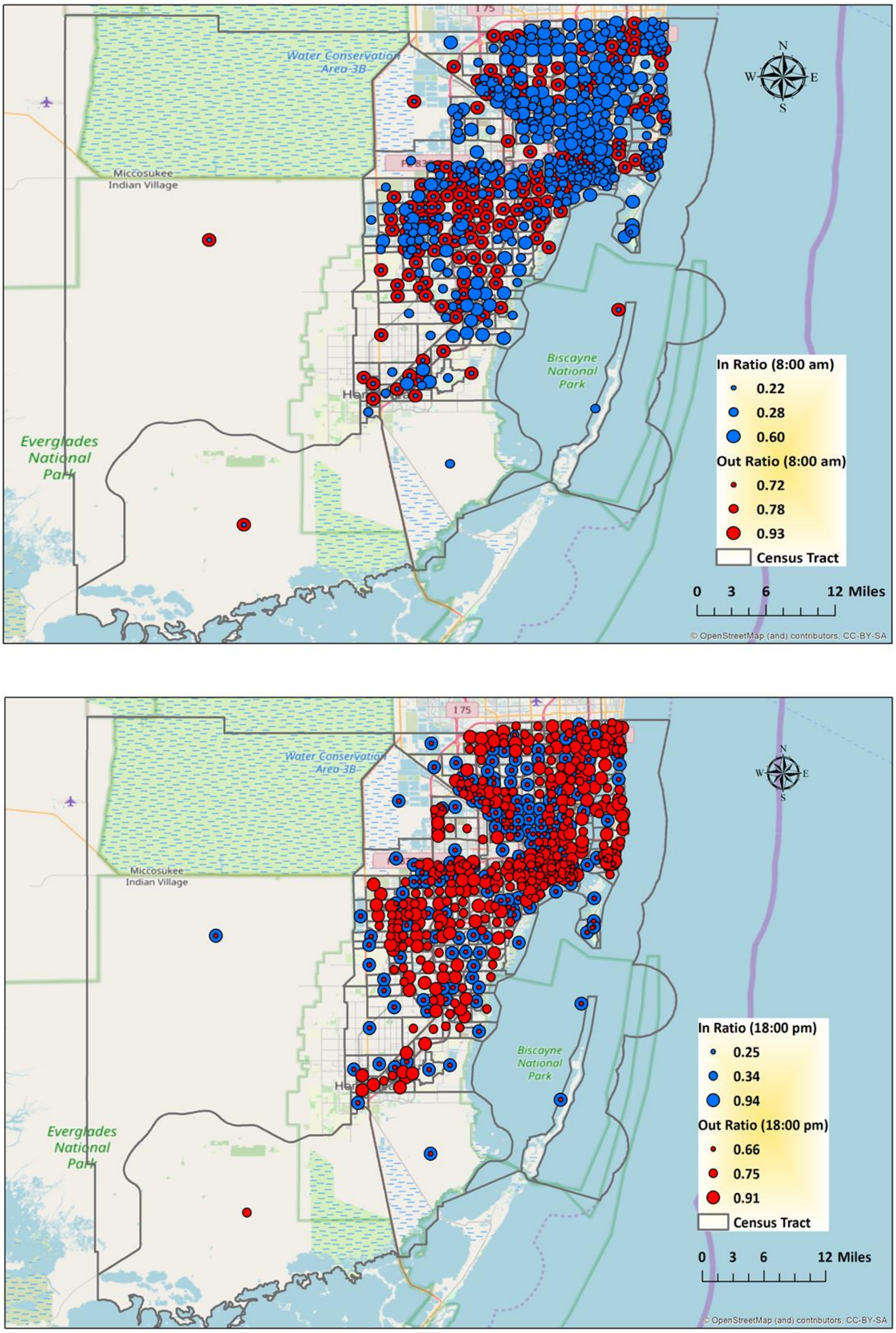


Figure 13. The out/in ratios at 8:00 am and 18:00 pm derived from the one-weekday modeling result (Top: 8 am, and Bottom: 6 pm). The blue circle is the in-ratio of a tract, the red circle is the out-ratio of the tract, and the radius of the circle is the out/in ratio value of the tract.

2.6 Conclusions

In this study we include Bayesian Networks to extend an activity-based model to simulate individual day-varying travels and activities. The case study in Miami-Dade County, Florida demonstrates the efficacy of this proposed, enhanced model in large-scale application. Our one-weekday simulation results suggest that downtown areas in Miami-Dade County have a greater number of in-travels at 8:00 am and a greater number of out-travels at 18:00 pm, while residential and rural areas experience converse trends.

In the model, unemployed people and children are “flexible” on both weekdays and weekends; employed people and students are “semi-flexible” on weekdays and “flexible” on weekends since they have mandatory activities such as work activities or school activities at specific times of weekdays. The model retrieves weekday and weekend time-budgets of an individual based on how “flexible” they are. The BNs embedded in the model then compute conditional probabilities of a travel-activity attribute including travel frequency, travel propose, travel duration, travel mode, travel destination location, and activity duration over a large set of crucial, independent variables, and infer an individual’s most-likely activity at a specified time. The BN-ABM allows for both regular and irregular activities occurring, and such rich activity-based travel modelling component is capable of modeling individual travel dynamics. Another important feature of the BN-ABM is that it is an individual-scale simulation and facilitates tracking individual travelers regarding where they are, what activity they conduct, what transport mode they use to conduct the activity, and when they will go to next activity in a very spatially and temporally explicit way, which adds the ability to test various policy scenarios to the model. For instance, what shall be the effect on peoples' daily travels of a transit expansion in Miami-Dade County? Or the effect of land-use intensification such as regional population growth and labor resettlement within the study area? Or price of travel such as fuel cost, parking pricing and poll-road charging?

There are some components of the BN-ABM that require further improvements. Unemployed people and children experience highly "flexible" activities since there are few long-term, fixed activities that limit their travels and they have a greater number of time-budgets. Today, most open-source BN platforms such as the bnlearn package in R allow for continuous BNs by computing Gaussian regression- based probability density. This simple linear method has a bad performance in estimating unemployed people and children's highly "flexible" travels. A greater probability density computation method for continuous travel-activity attributes can hold extraordinary potential for improving the dependability and accuracy of the BN-ABM. Another important future work is model validation, although we validate the model in a narrower sense. In this study we test the built 9 BNs by using k-fold cross-validation (k=10), but a boarder-sense evaluation of the dependability of our simulation results is missing. Recent studies have presented three validation frameworks including: (1) expanding model to a large-scale region and comparing aggregate simulation results between multiple sites, (2) aggregate analysis between model results and additional datasets such as cellphone data, travel survey data and traffic count data, and (3) comparing model results with another model

(Baqueri et al., 2019; Bassolas et al., 2019; Liu et al., 2018). These examples of activity-based models validation help improving the value of the proposed BN-ABM model. These examples of ABM validation helps to improve the value of the BN-ABM.

Despite these limitations, our simulation results confirm clear advantages of the activity-based modeling framework and methodology in terms of model structure, model development, data collection efforts, and hieratical location decision. Our model can also provide an appropriate tool for a range of stakeholders to explore the potential influence of current and future transport-related policies on public travel demand and help evaluating these policies. Further development of the model and approach outlined here shall ultimately lead to developing the BN-ABM with high dependability.

3. Human Prevention Behavior Modeling

3.1 Introduction

For many vector-borne diseases human prevention behavior is important to the transmission of the diseases as well as disease control and prevention. Mathematical models such as compartmental models have a long history of being applied to study the impact of human prevention behavior on these diseases. These aggregation models stratify a population into board subgroups such as susceptible, exposed, infectious or recovered, and describe the transmission between these compartments by the total number of individuals in the subgroup and health-state transferring rate (e.g., transmission probability, infectious rate or recovery rate). For example, classical compartmental models such as Susceptible-Exposed-Infectious-Recovered (SEIR) models and Susceptible-infectious-Susceptible (SIS) models have been widely used to model the spread of influenza and Sexually Transmitted Infections (STIs) (Mills et al., 2014; Dukic et al., 2012; Liljeros et al., 2003; De Vries et al., 2006), and different assumptions have been made. For influenza, people are not likely to be infectious immediately after infection; for STIs, they assume that all exposed individuals are infectious. However, Zika is more complicated since it is a vector-borne disease that involves two species populations: (1) human hosts and (2) mosquito vectors. Kucharski et al. developed a SEIR model that stratifies hosts into four subgroups: susceptible, exposed, infectious and recovered; and vectors into three subgroups: susceptible, exposed, and infectious. The simulation result of their model shows a good performance (Kucharski et al., 2016).

Although there are fewer efforts on studying Zika, researchers have applied compartmental models for studying other mosquito-borne diseases like Dengue and Malaria (Aron 1988; Yang 2000; Van den Driessche and Watmough 2002; Otero 2011) (Carvalho et al., 2019; Knerer et al., 2015; Nawawi & Aldila, 2020; Ndii, 2020; M. J. Otero et al., 2010; Song et al., 2020; Hyun Mo Yang & Ferreira, 2008). Carvalho et al. evaluated the control strategies of Dengue including the Aedes aegypti mosquito control and vaccination campaign using their compartmental model: (1) the vector mechanical control accomplished by a discrete function that represents the removal of breeding, (2) the chemical control carried out using insecticide and larvicide, and (3) the vaccination studied through the transfer of a fraction of individuals, proportional to the vaccination rate, from the susceptible to the recovered compartments (Carvalho et al., 2019). Nawawi and Aldila assumed that humans infected with Dengue virus and treated in a hospital will be protected (hospitalization), and divided human population into 4 compartments i.e susceptible (S), infected non hospitalized ($In1$), infected hospitalized ($In2$), and recovered (R) compartment in their SIR model (Nawawi & Aldila, 2020). In addition to vector-borne diseases, compartmental models have been applied to many infectious diseases like COVID-19. Tian et al. investigated the controls of the COVID-19 outbreak in China such as the Wuhan travel ban and level 1 response using a SEIR model (Tian et al., 2020). Against this background, the key is to define the nature of these human prevention behaviors on disease prevention and control, which will be studied in this dissertation research.

3.2 Literature Review

Vector-borne disease outbreaks are a major threat to global health, economy, and society (Mlakar et al., 2016; Cao-Lormeau et al., 2016; Cauchemez et al., 2016; Eisen et al., 2017; Flores & O'Neill, 2018; Gubler, 1998; Heukelbach & Werneck, 2016; Malone et al., 2016; Mysorekar & Diamond, 2016; Petersen et al., 2019; Rasmussen et al., 2016; Shaw & Catteruccia, 2019; Swei et al., 2020; van den Berg et al., 2017). In the United States, the Zika virus epidemic in 2015-16 resulted in 5,102 cases and the short term economic impact of US$3.5 billion. Therefore, assessing the emerging intervention strategies for vector-borne diseases is significantly important [87]– [96]. Take the 2016 Zika epidemic in Miami-Dade County, Florida as a case study, we conduct model-based evaluation of the emerging vector-borne disease intervention strategies. A greater understanding of the intervention strategies that successfully combat the 2016 Zika epidemic in Miami-Dade County, Florida will aid many countries that remain suffering from vector-borne diseases (Campos et al., 2015; Hayes, 2009; Cao-Lormeau et al., 2016; N'Dri et al., 2020; Cruvinel et al., 2020; Zhao et al., 2020; Caminade et al., 2019; Grillet et al., 2019).

In 2016, the United States reported an increase in Zika due to the bites of Aedes mosquitoes, especially in the state of Florida (Malone et al., 2016). Miami-Dade County in Florida reported as the most Zika-active area experienced a dramatic decrease in infection after a countywide truck/aerial adulticide/larvicide outdoor spraying applied by Miami-Dade County as well as other controls recommended by the CDC. In particular, the CDC suggested environmental interventions such as draining any water containers including garbage cans and toys and discarding old tires and drums that potentially keep water. These recommendations reduce the living aquatic habitat of the larva mosquitoes. They also suggested individual interventions including using mosquito repellent and regular bed-nets, wearing long clothing, installing screens on windows and doors, and avoiding travelling to mosquito-active areas. These advices reduce/block the contacts between humans and the adult mosquitoes.

Within the exiting literature, mathematical models have become well established in the past two decades to assess emerging vector-borne disease intervention strategies including regular nets, artemisinin-combination therapy (ACT), long-lasting insecticide treated nets (LLINs), indoor residual spraying (IRS), mass screening and treatment (MSAT) and vaccination (Agusto et al., 2013; Bhattarai et al., 2007; Bi et al., 2020; Biswas et al., 2020; Burattini et al., 2008; Counotte et al., 2019; Griffin et al., 2010; Miyaoka et al., 2019). In particular, compartmental models are capable of taking into account these intervention strategies in the transmission cycles of vector-borne diseases and qualifying their impacts on disease control and prevention using ordinary differential equations (Majumder et al., 2020; Padmanabhan et al., 2017; Biswas et al., 2020; Miyaoka et al., 2019; Goswami et al., 2018; Ajelli et al., 2017; Ebenezer Bonyah et al., 2017; Funk et al., 2016; Hyun M Yang, 2000; Aron, 1989).

Therefore, the aim of this study is to examine the nature of various prevention strategies that combats emerging vector-borne disease outbreaks. In comparison of the Activity-ABM, a compartmental model that incorporates the prevention strategies cited above is proposed and applied to the 2016 Zika outbreak event in Miami-Dade County, Florida. The rest of this study is organized as follows. Section 3.2 describes the proposed methodology in detail, specifically an overview of the baseline model and the intervention model as well as the model parameterization. Section 3.4 focuses on the results of applying the proposed model to the 2016 Zika epidemic in Miami-Dade County, Florida, including human infections predicted from the baseline model and the intervention model. Section 3.4 concludes with a summary of findings and discusses problems as well as future works.

3.3 Methodologies

3.3.1 The Baseline Model, SEIR

Model Overview. The SEIR model where human hosts and mosquito vectors transmits virus by interaction and bite, one of the simplest compartmental models, stratifies hosts and vectors into four and three subgroups, in particular, Susceptible (S), Exposed (E), Infectious (I) and Recovery (R) for hosts, and Susceptible (S), Exposed (E), and Infectious (I) for vectors. To build the baseline model, we assume that: 1) after getting infected with Zika, humans do not become infectious immediately; 2) people acquire lifelong immunity after recovery; 3) the population is closed; and 4) in a transmission cycle, mosquitoes die before recovery. Although mosquitoes regarding population, spatiotemporal distribution, movement, reproduction rate and feeding rate are driven by climate factors such as temperature and humidity (Monaghan et al., 2016), the climate impact would be weaken by the outdoor spraying applied in Miami-Dade County. Such large-scale vector control program could kill a great deal of vectors on a short time scale. Compared to dramatic and rapid declines in vector population due to outdoor sprayings, the climate- and environment- driven impact becomes inappreciable.

Originally developed by Kucharski et al. (Kucharski et al., 2016), Figure 14 depicts the details of the SEIR. β^H represents the transmission probability from vectors to humans (contact rate per human to vectors); β^V is the transmission probability from humans to vectors (contact rate per vector to humans); α^H and α^V are the latent periods for humans and vectors; γ stands for the recovery rate of humans; δ is the lifespan of vectors; S^H, E^H, I^H and R^H are the population for susceptible, exposed, infectious and recovery humans; and S^V, E^V and I^V are the population for susceptible, exposed and infectious mosquitoes. Transmission occurs when a susceptible vector bites an infectious host and/or an infectious vector bites a susceptible host, and is formulated as follows:

$$S^H(t+1) = S^H(t) - \beta^H * S^H(t) * I^V / N^H$$

$$E^H(t+1) = E^H(t) + \beta^H * S^H(t) * I^V / N^H - E^H(t) * \alpha^H$$

$$I^H(t+1) = I^H(t) + E^H(t) * \alpha^H - I^H(t) * \gamma$$

$$R^H(t+1) = R^H(t) + I^H(t) * \gamma$$

$$N^H(t) = S^H(t) + E^H(t) + I^H(t) + R^H(t)$$

$$S^V(t+1) = S^V(t) - \beta^V * S^V(t) * I^H / N^V + N^V(t) * \delta - S^V(t) * \delta$$

$$E^V(t+1) = E^V(t) + \beta^V * S^V(t) * I^H / N^V - E^V(t) * \alpha^V - E^V(t) * \delta$$

$$I^V(t+1) = I^V(t) + E^V(t) * \alpha^V - I^H(t) * \delta$$

$$N^V(t) = S^V(t) + E^V(t) + I^V(t)$$

where t is the current time step; $t+1$ is the next time step; N^H is the total population for humans; and N^V is the total population for mosquitoes.

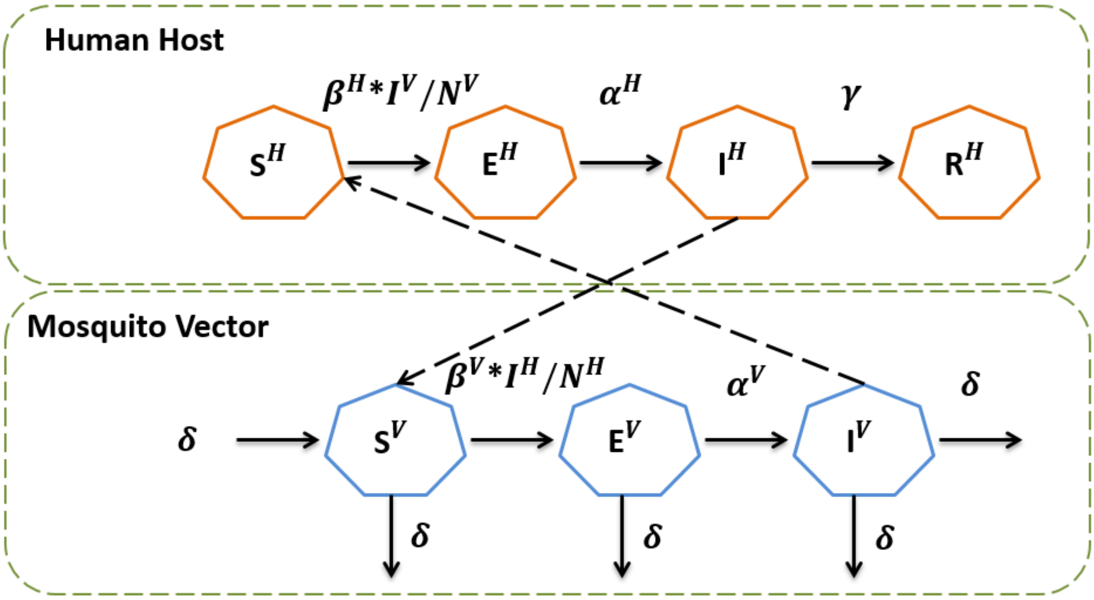


Figure 14. The baseline model. Human host is divided into four compartments, namely susceptible, exposed, infectious and recovered. People who are not currently infected with, but susceptible to Zika are susceptible, people who are infected with Zika but unable to transmit Zika virus are exposed, people who are able to transmit the virus are infectious, and people who recover from Zika disease are recovered. Mosquito vectors are divided into three compartments, including susceptible, exposed and infectious. Mosquitos that may potentially become infected with Zika are susceptible, mosquitoes that are infected with Zika but unable to transmit the virus are exposed, and mosquitos that are able to transmit the virus are infectious.

Baseline Parameters. Table 5 lists the values and sources of the parameters required in the baseline model. The average latent periods for humans α^H and mosquitoes α^V are 5.9 days and 10.5 days (Lessler et al., 2016); the recovery period for humans γ is 5 days (Goswami and Shanmukha, 2020); the average lifespan of mosquitoes δ is 15 days (Kucharski et al., 2016); the transmission probabilities from vector to human β^H and from human to vector β^V are 0.417 and 0.418 (Kucharski et al., 2016).

Table 5. Parameters for the baseline model.

Parameter	Definition	Sources	Values
β^H	Transmission probability of human host	Kucharski et al., 2016	0.417
α^H	Latent period of human host	Lessler et al., 2016	0.169
γ	Recovery rate of human host	Goswami and Shanmukha, 2020	0.200
β^V	Transmission probability of mosquito vector	Kucharski et al., 2016	0.418
α^V	Latent period of mosquito vector	Lessler et al., 2016	0.095
δ	Death/Birth rate of mosquito vector	Kucharski et al., 2016	0.128

Initial States. According to the collected CDC Zika data, the local infection in Miami-Dade Country began on 1 August 2016, when is the initial date of the baseline modeling exercise. According to the United States Census Bureau, the population in Miami-Dade Country on that day was 2,692,990. Estimating the initial states of the vectors is difficult. As Kucharski et al. proposed, the exposed and infectious hosts/vectors are initially equal (Kucharski et al., 2016). On 1 August 2016, Miami-Dade County had 99 travel-related infections and 14 local-acquired cases. We assume that these 99 travel cases aroused the 14 local infections, and estimate 203 exposed (E) and 203 infectious (I) mosquitos.

3.3.2 The Intervention Model, SEIR-IM

Model Overview. In the review of literature, we find that emerging vector-borne disease interventions promote disease prevention and control in the context of human hosts, mosquito vectors, and human-vector contacts (Bi et al., 2020; E. Bonyah et al., 2019; Bouzid et al., 2016; Nepal. et al., 2016; Goswami et al., 2018; Hunter, 2016; Ngonghala et al., 2019; Rather et al., 2017; Singh et al., 2018). In particular, the host-based controls including regular bed-nets usage, wearing long clothing, and avoiding traveling to virus-active areas prevent diseases by completely separating people from virus; the vector-based controls such as outdoor sprayings and LLINs reduce infections by minimizing mosquitoes; the contact-based controls like mosquito repellent usage prevent diseases by reducing human-vector contacts.

According to the nature of these three controls on disease prevention and control, many researchers performed model-based vector-borne disease intervention evaluation by formulating the effects of the interventions in the transmission cycles of the diseases. In Agusto et al., the LLINS control on malaria is a decreasing function of how long people use it since the pesticide treatment on nets loses efficacy due to frequent washing and exposure to sunlight (Agusto et al., 2013). Griffin et al. supposed that IRS decreases mosquito population or blocks human-mosquito contacts because it kills mosquitoes when they rest on the wall and repel them before they feed (Griffin et al., 2010).

Analogously, we formulate the three controls, namely the host-based controls, the vector-based controls, and the contact-based controls, as follows: 1) people who use the host-based controls are not susceptible to Zika; 2) people who use the contact-based controls have a lower human-mosquito contact rate; and 3) the vector-based controls minimize the vector population. Figure 15 illustrates how we formulate these three interventions in the transmission cycles of Zika. The host-based controls reduce the population for susceptible humans SH by the rate d^H. The contact-based controls affect the human-vector contact rates β^H and β^V to be new, lower values β_2^H and β_2^V. The vector-based controls minimize the population for susceptible vectors SV by the rate d^V.

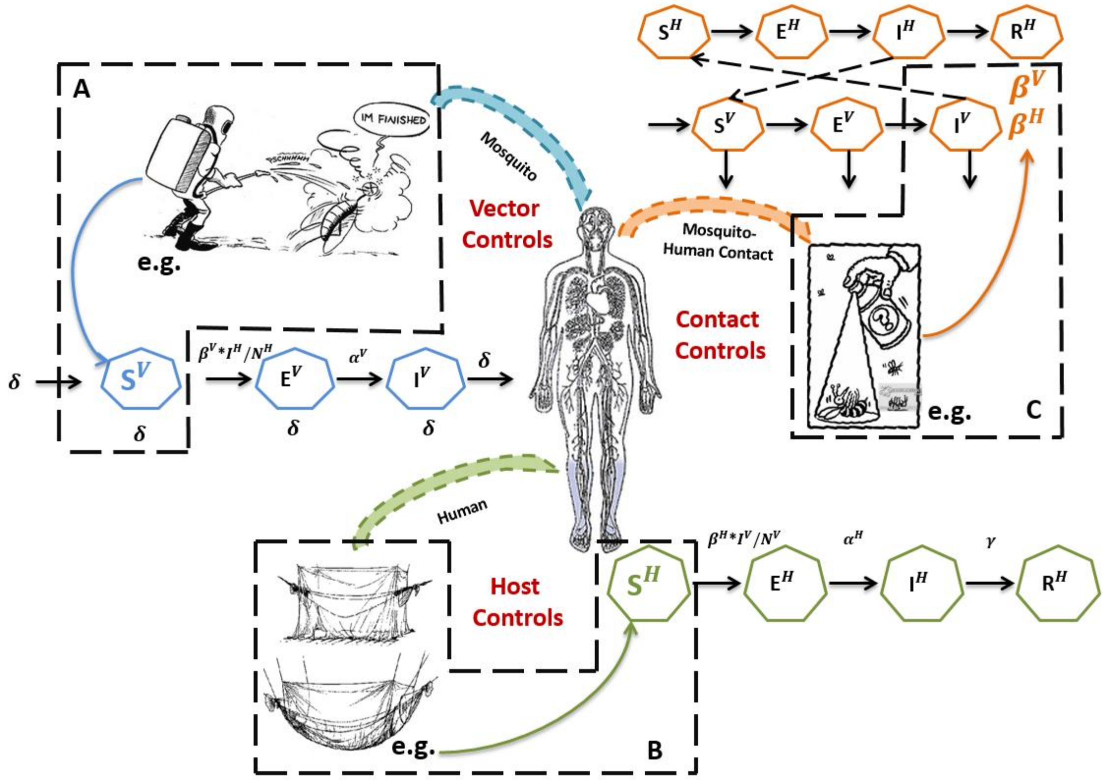


Figure 15. The intervention model. Building on the baseline model, the intervention model takes into account three interventions, including the vector-based controls, the host-based controls, and the contact-based controls. The vector-based controls minimize the vector population. The host-based controls separate humans from virus. The contact-based controls reduce the contacts between humans and mosquitoes.

Intervention Parameters. Table 6 lists the values and sources of the parameters required in the intervention model, where the transmission probabilities from vector to human and from human to vector β_2^H and β_2^V, and the rates d^V and d^H , by which the populations for susceptible vectors and susceptible hosts S^V and S^H decrease due to using the host controls and vector controls are unknown and estimated by fitting the model to the data using MCMC. And the intervention transmissions are formulated as below:

$$S^H(0)' = S^H(0)(1 - d^H)$$

$$E^H(t+1) = E^H(t) + \beta^H{}_2 * I^V * S^H(t) - E^H(t) * \alpha^H$$

$$S^V(0)' = S^V(0)(1 - d^V)$$

$$E^V(t+1) = E^V(t) + \beta^V{}_2 * I^H * S^V(t) - E^V(t) * \alpha^V - E^V(t) * \delta$$

Table 6. Parameters for the intervention model.

Parameters	Definition	Sources	Values (After)	Values (Before)
$\beta^H 2$	New transmission probability for human (contact control)	Modeled	Unknown	0.417
α^H	Latent period for human	Lessler et al., 2016	0.169	0.169
γ	Recovery rate for human	Goswami and Shanmukha, 2020	0.200	0.200
$\beta^V 2$	New transmission probability for mosquito (contact control)	Modeled	Unknown	0.418
α^V	Latent period for vector	Lessler et al., 2016	0.095	0.095
δ	Death/Birth rate for vector	Kucharski et al., 2016	0.128	0.128
d^H	Percentage of human hosts insusceptible to Zika after using host controls	Modeled	Unknown	NA
d^V	Percentage of mosquitoes being killed after using vector controls	Modeled	Unknown	NA

3.3.3 MCMC-based Parameterization and Model Fit for the Invention Model

Method Overview. To fit the intervention model and estimate the unknown parameters, namely the new transmission probabilities from vector to human and from human to vector $\boldsymbol{\beta_2^H}$ and $\boldsymbol{\beta_2^V}$ due to using the contact-based controls, the decreasing rate for humans $\boldsymbol{d^H}$ due to using the host-based controls, and the decreasing rate for vectors $\boldsymbol{d^V}$ due to using the vector-based controls, we use the MCMC. This stochastic approach repeatedly generates random sampling from the potential space of the parameters and summarizes their distributions (Greenland, 2006). This parameterization performs in two stages. First, we generate Markov chains by searching though the parameter space and identifying the most likely search region. Second, we undertake the expectation approximation, summarize the samples and calculate the statistical summary of the sampling (Greenland, 2006). In this study, we use the maximum likelihood estimation, and the likelihood of the four target parameters is formulated as follows:

$$P(D|\theta) = e^{-\sum_{i=1}^{n}(y_i-\tilde{y}_i)^2}$$

where y_i is the i^{th} Zika data, and $\tilde{y}_i$ is the i^{th} modeled data, which are computed from the Eq. (1) – (13). And the posterior distribution of the four target parameters is given:

$$P(\theta|D) = e^{-\sum_{i=1}^{n}(y_i-\tilde{y}_i)^2} * P(\theta)$$

The aim of MCMC is to identify the combination of the four parameters that minimizes $\sum_{i=1}^{n}(y_i - \tilde{y}_i)^2$ and fits the data best. Accordingly, $P(D|\theta)$ and $P(\theta|D)$ needs to be maximized. MCMC starts with an initial user-defined value for the target parameters, computes $P(D|\theta)$, searches the next potential values through the parameter space, and calculates new $P(D|\theta)$. By comparing these two $P(D|\theta)$, we will keep the larger one. By analogy, we construct a Markov chain and calculate the statistic summary of the chain.

3.3.4. Data Sources

In 2016-17, the CDC daily updated the counts of Zika infection by county across Florida, including travel-related cases, locally-acquired cases, pregnant women cases and sexual-transmitted cases. Travel-related Zika cases are non-residents who get infected in Florida while local cases are infected residents. They use Polymerase Chain Reaction technique (PCR) to identify present virus, and Antibody Capture Enzyme-Linked Immunosorbent Assay technique (IgM Antibody) to identify recent past infection. Next they query the patients with positive results about their travel history, close contact, sexual history and mosquito contact rate. Finally, the laboratory and interview results determine whether the infection is travel-related, locally-acquired, congenital or sexual-transmitted. In this study we focus on the local transmission of Zika in Miami-Dade County, and collect the locally-acquired cases during 1 August 2016 to 17 May 2017 available through the CDC.

As the CDC reported, in the 2016 Zika outbreak event of the United States, Florida was the only state with the locally-transmitted cases, and most cases have been within Miami-Dade County. The first Zika case in Florida was reported on 19th January 2016, and was travel-related. As the count of the travel-related cases increased, the first local case was reported on 1 August 2016 in Miami-Dade County, and triggered a local outbreak across the county.

3.4 Results

3.4.1 Human Infections in the Baseline Simulation

Results for the Zika infections by day for human hosts in the baseline simulation are shown in Figure 16, where the x-axis stands for the simulated Zika cases, and the y-axis represents the infection cases reported by the CDC. Within the simulation, the first 60 days (1st August 2016 – 30th September 2016) experienced a good match of the model and the data (R2 = 0.9662), and thus the 61 day (1st October 2016) is the initial date of the intervention modeling exercise. It is noteworthy that October 1st 2016 is at the stage that Miami-Dade County implemented the countywide truck/aerial adulticide/larvicide outdoor spraying.

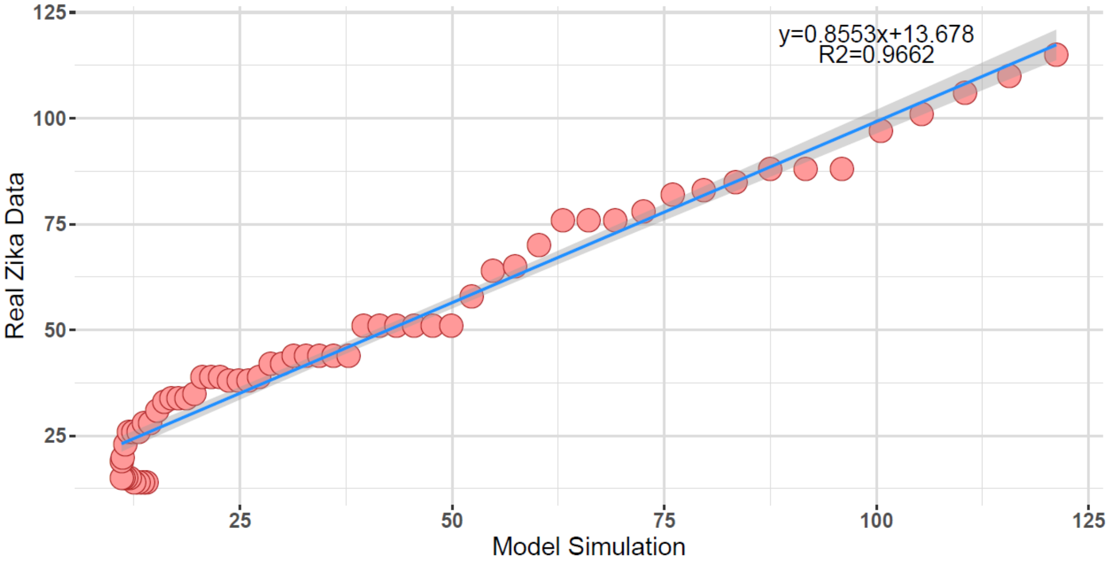


Figure 16. The baseline simulation results, in particular, the comparison between the predicted and the observed. The x axis is the predicted, and the y axis is the data.

Figure 17 depicts the timeline of the 2016 Zika epidemic in Miami-Dade County. Although we collect data from Jan 19 2016 to May 12 2017, the local outbreak began in 1 August 2016. Our baseline modeling result suggests that the following two months (August and September, 2016) experiences few interventions, regardless of individual or public interventions, and October 2016 is the start date of the intervention modeling exercise.

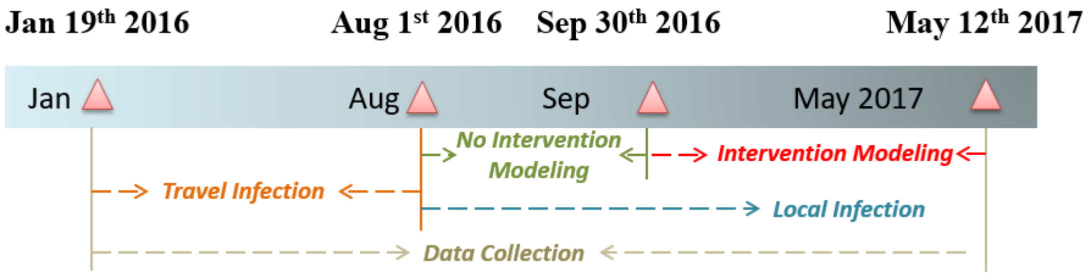


Figure 17. The timeline of the 2016 Zika epidemic in Miami-Dade County, Florida.

3.4.2 Human Infections in the Intervention Simulation

Results for the model fit and parameter estimation of the intervention model SEIR-IM are shown in Figure 18, which are the four well-constructed Markov chains for the intervention parameters $\boldsymbol{\beta^H}$, $\boldsymbol{\beta^V}$, $\boldsymbol{d^H}$ and $\boldsymbol{d^V}$. These four chains converge to the parameter space quickly and display a stable sampling, and the four parameters $\boldsymbol{\beta^H}$, $\boldsymbol{\beta^V}$, $\boldsymbol{d^H}$ and $\boldsymbol{d^V}$ are estimated to be 0.39, 0.18, 0.98 and 0.99.

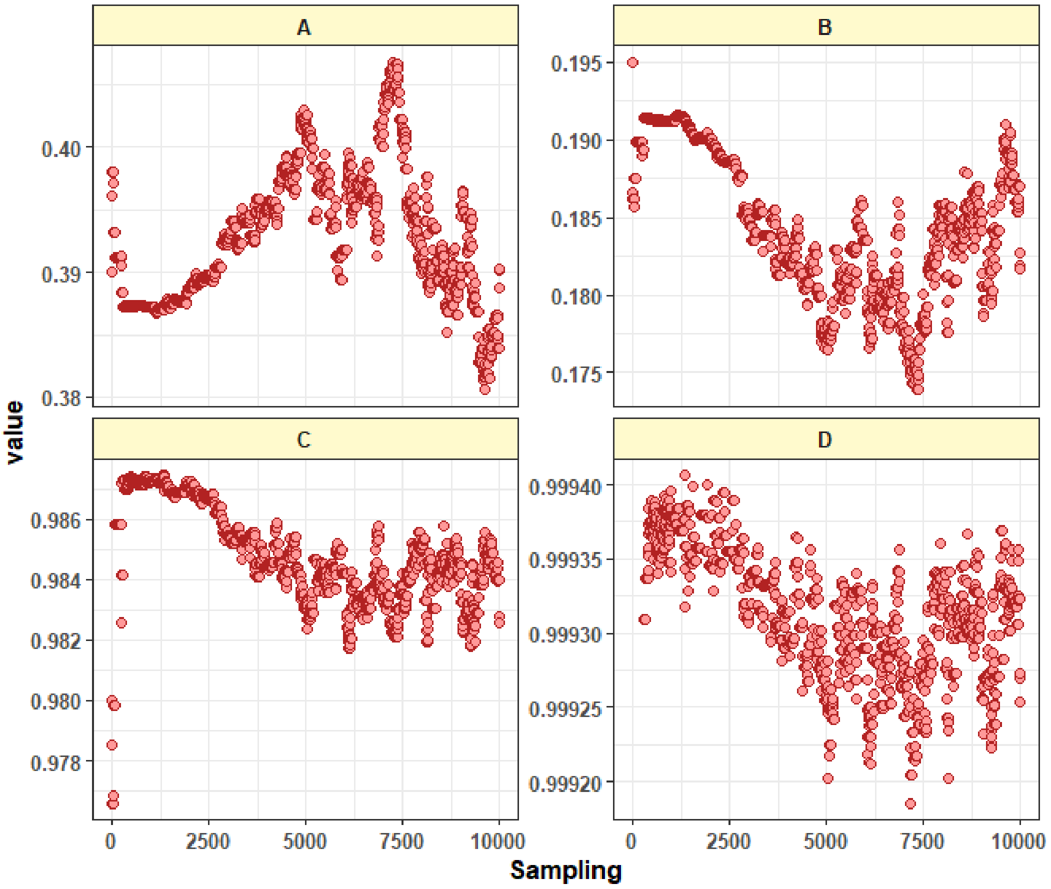


Figure 18. The MCMC samplings for the four intervention parameters (A: β^H the new transmission probability for humans due to using the contact-based controls; B: β^V the new transmission probability for mosquitoes due to using the contact-based controls; C: d^H the percentage of humans who are insusceptible to Zika due to using the host-based controls; and D: d^V the percentage of mosquitoes being killed by using the vector-based controls).

Results for the Zika infections by day for human hosts in the intervention simulation are shown in Figure 19. While the data reaches the peak at around day 150 versus the peak at around day 180 in the intervention simulation, the model clearly tallies with the data.

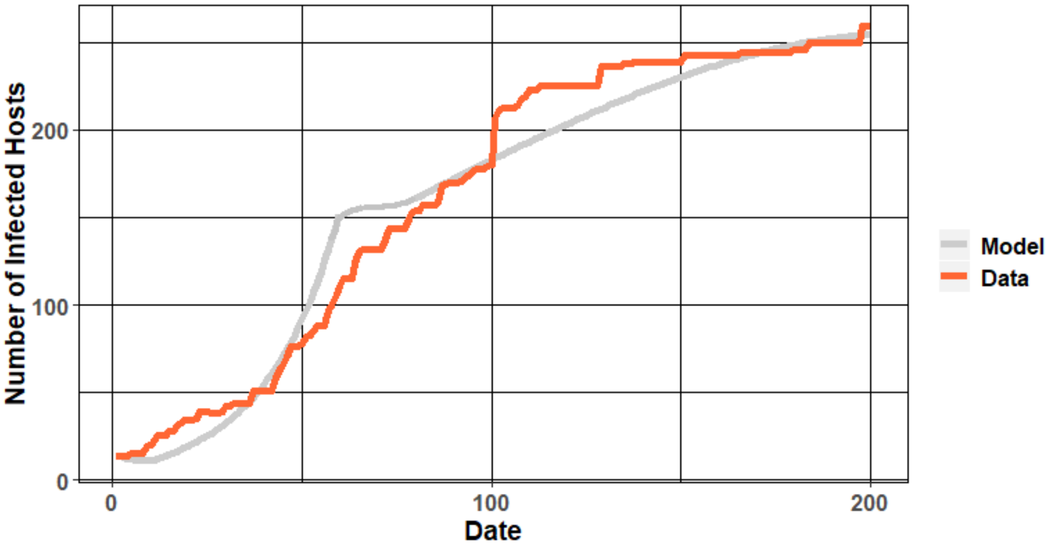


Figure 19. The intervention modeling result, where the x axis is number of days starting from 1 August 2016, and the y axis is the accumulated cases of Zika infection. The grey line is the modeled, and the orange line is the data.

3.5 Conclusions

In this study we propose a novel SEIR intervention model, SEIR-IM to evaluate the emerging interventions that combats vector-borne diseases, and applies the model to the 2016 Zika epidemic in Miami-Dade County, Florida as a case study. We find that vector-borne disease intervention strategies promote disease control and prevention in the context of humans, vectors, and human-vector contact. In particular, the host-based controls such as avoiding traveling to virus-active areas aim to separate people from virus; the vector-based controls such as outdoor sprayings and LLINs aim to minimize vectors; the contact-based controls such as vector repellent aim to reduce the contact between humans and vectors.

To model the impacts of the three interventions, namely the host-based controls, the vector-based controls, and the contact-based controls, on the transmission cycles of vector-borne diseases, we define four intervention parameters in the SEIR-IM. They are the new transmission probability from vector to human β_2^H by using the contact-based controls, the new transmission probability from human to vector β_2^V by using the contact-based controls, the proportion of the humans who are not susceptible to Zika virus by using the host-based controls d^H, and the proportion of the vectors that are killed by using the vector-based controls d^V. Using the MCMC approach, we estimate the four unknown intervention parameters β_2^H, β_2^V, d^H, and d^V to be 0.39, 0.18, 0.98 and 0.99. Although 0.98 usage of the host controls in Miami-Dade County seems overestimated, it is modeled as a representative of all interventions sharing the nature of the bed-net usage for vector-borne diseases control and prevention, for instance, wearing long-sleeved shirts and long pants, using screens on windows and doors, and avoiding traveling to virus-active areas. In general, the proportion of the humans who are insusceptible to Zika due to using the host-based controls, regardless of with or without awareness to completely avoid contact with vectors, are 98%.

Our results confirm findings by others that compartmental models can depict the macro-scale transmission dynamics of diseases based on data accessible at an aggregate scale and revealing valuable general characteristics of the diseases (Goswami & Shanmukha, 2020; Griffin et al., 2010; Hay et al., 2010). Within the simulation, we recognize one general characteristic of vector-borne diseases modeling. At early stage of an outbreak, few people would utilize interventions. In this case, the simplified assumptions of the compartmental modeling are reasonable to model a disease. As the epidemic spreads locally and widely, governments begin applying public interventions, and people start using individual interventions. At that time, the baseline model fails to understand the disease and parameters regarding the interventions applied must be included in order to achieve the disease's modeling. Another reason is that vector-borne diseases have distinctive lifestyles and transmission cycles in comparison to non-communicable diseases, which makes the spread of the diseases complicated and unpredictable. Additional factors such as the biology of the vector itself, host immunity, geography, and climate must also be considered. This is also why the SEIR-IM cannot perform long-term prediction.

In this study we pay little attention to a heterogeneous mixing in a target population as well as individual heterogeneity and stochasticity in probability of infection. In general, our model is incapable of capturing heterogeneity and stochasticity among pathogens, hosts and vectors in respect to climate, biological, geographical, behavioral, social, economic and environmental variables at a local scale. Due to the underlying simplified assumptions, i.e. well-mixed populations in which all individuals have equal chance of contact, the SEIR-IM neglects spatiotemporal variation in human-vector contact and fails examining the transmission dynamics of diseases emerging from complicated interactions among multi-species agents at a local scale.

Despite these limitations, our model provides an appropriate tool for a range of stakeholders to explore the potential influence of emerging interventions on vector-borne disease transmissions and help determining optimal policy or program for elimination of the diseases. Due to the convenient simplified assumptions, our model also requires less in computation ability and memory, and has a good performance in parameter estimation, model fit and model parameterization. These ultimately lead to the built SEIR-IM with the potential goal of global eradication of vector-borne diseases.

4. Model-based Evaluation of Human Mobility and Prevention Behavior

4.1 Introduction

Human mobility and prevention behavior are two key factors to the transmissions of vector-borne diseases. Mathematical models such as aggregate compartmental models and disaggregate individual-based models are useful to study these diseases. However, the compartmental modeling is often limited by over-simplified assumptions, such as the spatially and temporally even distributions of virus transmission rate, human-vector contact rate, human demographics, mobility and behavior. For instance, several studies assume that people either work or study from 9:00 am to 5:00 pm, ignoring temporal variations (e.g., weekday vs. weekend, daytime vs. nighttime) and individual variations (e.g., night shift worker, retired people, or unemployed people), while others simply assume that interaction between humans and mosquitoes is random (Adams & Kapan 2009; Meloni et al., 2011; Belik et al., 2011).

To cope with these limitations discussed above, individual-based models have been developed. Perez and Dragicevic (2009) considered the spread of a communicable disease in an urban environment as a result of individuals' interactions in a geospatial context and developed an Agent-Based Model (ABM[*2]). To represent the spatial heterogeneity and the complexity involved in infectious diseases diffusion, the model endowed human agents with mobility through a transportation network allowing them to move between places. Their results provide an insight into the application of the agent-based modelling approach to calculate the infected agents in specific urban environments and time frames emerging from agents’ interactions. There are two additional reasons that make this modeling method significantly meaningful and realistic. First, chance often greatly affects the outbreak of an infectious disease. In a given population, sometimes we may see an outbreak occur; at other times, outbreaks would not happen under similar conditions (Vynnycky and White, 2010). Second, a susceptible individual may contact more than one infectious individual, but only one of them would have caused the infection (Vynnycky and White, 2010). However, compartmental models are incapable of modeling such two facts.

To model the two facts above: (1) chance, this agent-based modeling method uses the Reed-Frost equation to calculate individuals' risk of the infection, draws a number at random and specifies the range where it is located; and (2) only one effective exposure to virus, an ABM once determines whether an individual is exposed, and ignores their possible, following exposures to virus.

The Reed-Frost equation is defined as follows (Vynnycky and White, 2010):

$$\lambda = 1 - (1 - p)^{I_t}$$

where p is the probability of an effective contact between two individuals in each time step t, and I_t is the number of infectious individuals at time t. A traditional ABM assumes that individuals mix random and even, and p is identical to all individuals. However, the p varies temporally and spatially (e.g. an individual would have high contact probabilities in the daytime or would contact few individuals when they go to work). This is why an agent-based model works better in a small population such as hospital, school or workplace. Therefore, to simulate an infectious disease in a county or coarser level using this method, calculating risk of the infection that is specific to an individual is important and will be studied in this dissertation research.

*2: ABM in Chapter 4 refers to Agent-Based Model

4.2 Literature Review

Human behavior as a key factor has been studied to drive the variation in host-vector contacts (Galvani & May, 2005; Perkins et al., 2013; Reiner et al., 2014; Smith et al., 2007; Steven T. Stoddard et al., 2009). In this section, we conduct a model-based investigation to evaluate the importance of the variation in host-vector contact due to human behavior to the transmission cycles of a vector-borne disease. Such exploration is important to the associated public health intervention strategies.

In the literate of review, agent-based models have become well established in the past two decades by viewing vector-borne disease transmission dynamics as a complex adaptive system (Alderton et al., 2016; Dommar et al., 2014; Jacintho et al., 2010; Jindal & Rao, 2017; Manore et al., 2015; Mniszewski et al., 2014; Mulyani et al., 2017). Alderton et al. (2016) presented a new ABM for investigating the 2013 T.b.rhodesiense human African trypanosomiasis (rHAT) outbreak in Eastern Province, Zambia and explored the influence of multi-hosts' movement including human, cattle and other domestics animals. This rHAT ABM permits incorporating finer-scale human mobility and demographic attributes such as age and gender into the simulation. Dommar et al. (2014). formulated a network-based ABM for understanding the spatiotemporal transmission of a chikungunya outbreak driven by tropical rainfall, human mobility and social structures, where host agents 'live' in the network nodes and are allowed to travel to their neighborhood nodes.

However, the ABMs cited above often ignore the interrelatedness of human behavior and an epidemic as well as dynamic patterns of contact between hosts and vectors. In a disease outbreak event, human mobility as a key behavioral factor may lead to great exposure to vectors across locations that people visit and ultimately high transmission rates (S. T. Stoddard et al., 2013). And on the other hand, increased distributions of prevention behavior such as vaccination (Chen, 2006; Griffin et al., 2010; Perisic & Bauch, 2009a, 2009b), bed-net usage (Barnes et al., 2009; Kleinschmidt et al., 2007; O’Meara et al., 2008) and outdoor sprayings (Griffin et al., 2010; Shanks et al., 2005), and ultimate, expected declines in infection often occur. A greater understanding of such complicated interrelatedness of human behavior and disease transmissions will aid disease prevention and control as well as associated public health policy-makings.

Against this background, we propose a novel agent-based model, Activity-ABM that couples of individual-scale human daily mobility and travel behavior, human prevention behavior, and host-vector contact dynamics with virus transmission cycles. This proposed Activity-ABM can be applied to answer the following questions: What prevention should be the most effective? Where prevention should be targeted? What mobility could generate large amounts of infection in the human population? Who would be the most likely to get infected with virus? The model also addresses modeling host-vector contact dynamics driven by human mobility and prevention behavior. We assume that individual exposure to vectors varies as activities that they perform and preventions that they use. Using a simple example, high host-vector contact rates may occur when people stay at home versus low contact rates when they go to school/work. Individual heterogeneity in human mobility and prevention behavior causes dynamic interaction between hosts and vectors as well as altering interaction between individuals and environments. These dynamics often lead to unexpected, emergent outbreaks. A deeper understanding of such dynamics will also help health-related policy-makings. The rest of this section is organized as follows. Section 4.2 presents the detailed methodology including the overview of the Activity-ABM as well as the four components embedded the Activity-ABM. Section 4.4 focuses on the results for the case study, scenario test and uncertainty analysis. Section 4.5 concludes with a summary of findings and discusses problems as well as future works.

4.3 Methodologies

4.3.1 Overview of the Activity-ABM

The Overview, Design concepts, & Details Protocol (ODD) is a set of universal and standardized guidelines that outline an ABM's purpose, variables, framework, and data (Grimm et al. 2006; Grimm et al. 2010). According to the OOD, this section describes the proposed Activity-ABM model. Figure 20 illustrates the overview of the proposed Activity-ABM that consists of four primary components: (1) human agents' daily mobility and travel behavior, (2) human agents' prevention behavior, (3) mosquito agents, and (4) virus transmission engaged in human agents' behavior, mosquito agents' distribution and human-mosquito contact dynamics.

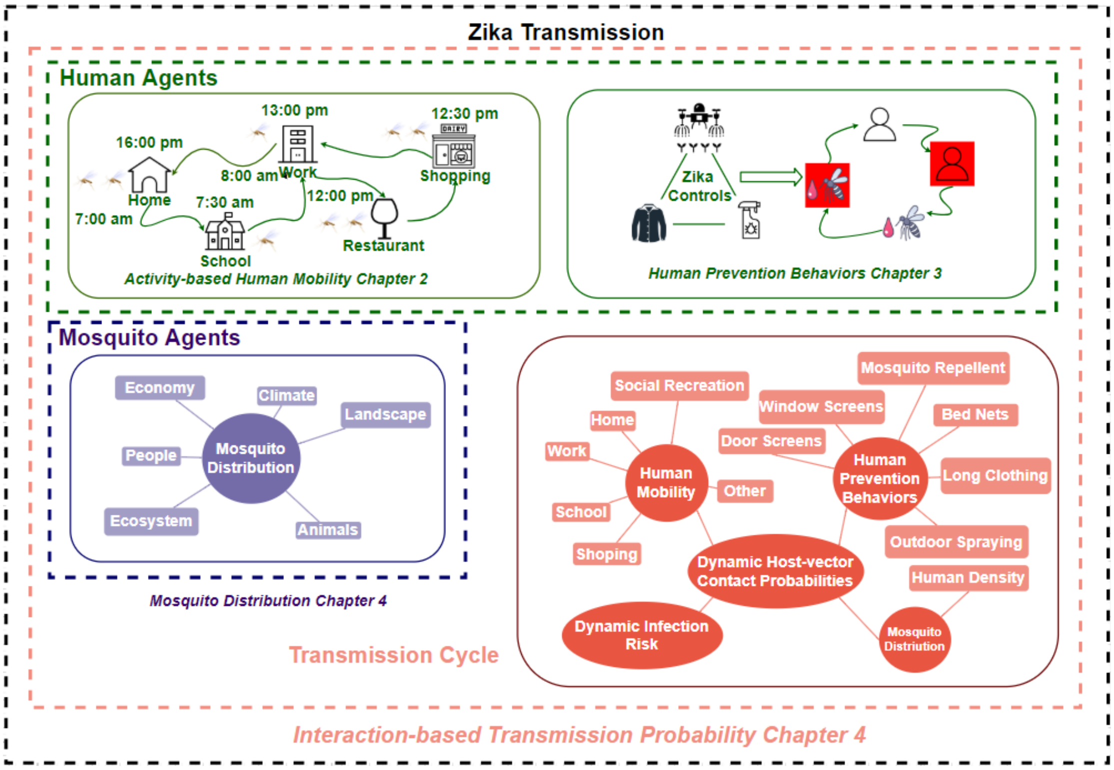


Figure 20. Overview of the Activity-ABM model and conceptual illustration of this model for daily travels of a population, daily prevention behaviors of the population, mosquito distribution, and the sub-models underlying this proposed framework.

The Activity-ABM recognizes the relationship between an epidemic and human behavior at the individual- and population-levels. Therefore, the model begins with an activity-based model that creates a simplified microscopic synthetic population to represent the actual population and generates daily travels of the population at the level of individual travelers. Next, the model creates mosquito agents, and updates the health states of humans and mosquitoes based on their risk of the infection associated with where they are, what activity they perform, what prevention behavior they use and the number of infectious individuals in their neighborhoods. The proposed model serves 4 **purposes**:

1). To simulate the mobility and travel behavior of humans, including travel frequency, travel propose, travel mode, travel duration, travel destination locations, and stay duration. **These travels are simulated on a travel diary survey, the American Community Survey, and many GIS-based environmental and zonal attributes (Table 2). Each human agent features person-, household-, and mobility- level characteristics such as age, income, number of children in the household and activity records (Table 1).**

2). To simulate the individual-level and population-level disease prevention behavior of humans, including the host controls (e.g. travel ban, stay at home and bed-net usage), the vector controls (e.g. outdoor spraying and drain any water containers), and the host-vector contact controls (e.g. mosquito repellent usage). **Lacking the ground data, these prevention behaviors are estimated by model fit, and distributed random. Each human agent features whether they use prevention as well as what prevention they use.**

3) To simulate the distribution of mosquitoes including the number of mosquitoes per census tract and mosquito agents in each tract. **Lacking the ground data, the mosquito population per tract is calculated based on human population from the American Community Survey, and mosquito agents are finally generated**

for each tract.

4). To simulate the transmission between humans and mosquitoes, including the number of infectious individuals in each agent's location, contact probability engaged in their behavior, and risk of the infection. **Each agent features a health state that is updated based on the current time, the current location, the behavior, and the physical activity of the agent.**

Design Concepts. The Activity-ABM views an epidemic as a complex adaptive system where the disease transmissions emerge from complex agents interacting with each other as well as environments. The whole epidemic system's behavior is more complex than aggregation of agents' actions but also adapting to the changing environment. The primary concepts of the model, including adaptation, stochasticity, interaction and observation are discussed as follows:

1). **Stochasticity.** For mosquito agents, birth and death behaviors are random and determined by a birth rate. For both human and vector agents, infections are random chances determined by risk of the infection.

2). **Interaction.** Human agents due to daily mobility interact with the environment. Human agents and vector agents interact with each other in a spatial and temporal explicit manner to transmit the virus.

3). **Observation.** The output of the Activity-ABM are a .txt file of the county-level aggregation of infections by three hours for human hosts, a .txt file of the county-level aggregation of infections by day for human hosts, and a .csv file of 1000 random-selected human agents' mobility and health state per three hours, from which a shapefile file and a point map are generated per day.

Spatial Scale. The model utilizes at the census tract level, and the census tracts are used to query the neighborhood of an individual agent in the simulation. For example, a human agent staying in a census tract, all mosquito agents in the same tract are counted when calculating the person's risk of the infection.

Temporal Scale. If the temporal resolution was very high, more possible contacts between humans and mosquitoes would occur, and the simulation result would be greater than the real cases. If the resolution was coarse, it would increase the change of missing possible host-vector contacts, and cause the simulation result less than the real cases. At the same time, high temporal resolution could increase the demand in computation ability and memory. In this study we determine the temporal scale of the model based on minimizing the model and the data as well as computer memory and computation ability; therefore, time in the model is split into 8 time-steps per day across a 285-day period.

Scenario Test. We build three local-context scenarios that apply each control to 100 random-selected census tracts, and compare the simulation results to identify what prevention is the most effective in the local context (Table 7). In scenario 1, the host-based controls are evaluated. If human agents in the 100 selected census tracts use the host-based controls, they will be insusceptible to Zika infection. In scenario 2, the vector-based controls are evaluated. If mosquito agents in the 100 selected census tracts use the vector-based controls, they will be insusceptible to Zika infection. In scenario 3, the contact-based controls are evaluated. If human agents and mosquito agents in the 100 selected census tracts use the contact-based controls, they will be susceptible to Zika infection with a low probability estimated in the baseline modeling exercise (0.1 (e-5) and 0.15 (e-5), respectively). These results can be explored, in depth, to make the associated public health intervention strategies evidenced-based. For example, how does localized intervention strategies influence the population-based public health? Or the model serves as evidence to identify the best intervention strategy.

Table 7. Description of the scenarios

Scenario	Agents' Attributes Regarding Prevention Behavior	Prevention Behavior
1	Human agent's risk infection (Yes: 0; No 1)	The Host Control
2	Mosquito agent's risk infection (Yes: 0; No 1)	The Vector Control
3	Human/mosquito agent's risk infection (from the baseline modeling exercise)	The Contact Control

Uncertainty Analysis. To assess and evaluate the performance of the Activity-ABM, uncertainty analysis is conducted by fixing all inputs of the baseline model and testing what range of the output the model generates. This section builds a large-scale Activity-ABM where 3,000,000 human agents and 5,000,000 mosquito agents are created and their current location, current activity, host-vector contact probability, risk of the infection and health state are updated in 8 time-steps per day. Such large- and finer- scale modeling causes a great demand in computer memory and computation ability. In the uncertainty analysis the Activity-ABM only runs 5 times.

4.3.2 Human agents in the Activity-ABM

Human agents. Human agents are created using the demographic census data and a traditional travel diary survey. Each human agent is given their home location in the census tract level, and socio-economic and demographic attributes (Table 1). The Activity-ABM then generates their daily mobility and travel routine represented by a list of trips including current activity, travel purpose (next activity), current location, travel destination location, current time (departure time), travel mode, travel duration (arrival time), and random attributes each human agent with what prevention they use.

Human agents' daily mobility and travel behavior. The dynamics of human daily mobility and travel behavior, the activities generated to represent human daily mobility as well as the transport mode, the start time, the duration, the arrival time and the origin-destination locations for each activity have been simulated and predicted by transportation geographers using activity-based models (Goulias et al., 2011; Kitamura

& Fujii, 1998; Veldhuisen et al., 2000; Bhat et al., 2004; Pendyala et al., 2005; W. Davidson et al., 2010; Shiftan & Ben-Akiva, 2011; Scherr et al., 2019; Baqueri et al., 2019; Yasmin et al., 2015; B. Davidson et al., 2011). This activity-based method simulates human daily mobility and forecasts travel demand at the level of individual travelers, and the generated activity-based mobility that refers to traveling between those locations where people conduct activities results in dynamic exposure to vectors and ultimate activity-specific transmission rates (Steven T. Stoddard et al., 2009). For the purpose of studying vector-borne diseases underlying dynamic host-vector contact, ABMs are effective as individual exposure to vectors can be calculated by the sum of exposure through their activity-based daily routine as well as their activity- and prevention- specific risk of the infection.

To simulate a disease outbreak underlying human mobility, Chapter 2 begins with creating a synthetic population that represents the actual population using the Iterative Proportional Updating algorithm proposed by Ye et al. (Ye et al., 2014), and generates individual-scale activities and travels of the population using the Prism-Constrained Activity Simulation Framework proposed by Pendyala et al. (Pendyala et al., 2005). Their framework has been developed to investigate travels on weekdays and assumes that travel patterns of an individual are stable in the short term. However, weekend travels plays a crucial role in the spread of an epidemic (Cooley et al., 2016; Mao, 2011). To generate day-varying activities of an individual, Chapter 2 integrates Bayesian network into the Prism-Constrained activity-based model.

Human agents' prevention behavior. Chapter 3 summarizes vector-borne disease intervention strategies into three categories in the context of host, vector and host-vector contact (Bi et al., 2020; E. Bonyah et al., 2019; Bouzid et al., 2016; Nepal. et al., 2016; Goswami et al., 2018; Hunter, 2016; Ngonghala et al., 2019; Rather et al., 2017; Singh et al., 2018), and defines how they become effective in the transmission cycles of diseases (Agusto et al., 2013; Killeen & Smith, 2007); Griffin et al., 2010; Musso et al., 2015; M. Otero et al., 2011; Hyun M Yang, 2000). In particular, human agents who use the host controls are not susceptible to virus since the host controls such as regular bed-nets usage, wearing long clothing, and avoiding traveling to virus-active areas prevent diseases by completely separating humans from vectors; human agents who use the contact controls have a low human-vector contact rate since the contact controls such as mosquito repellent prevent diseases by reducing human-vector contacts; the vector controls such as outdoor sprayings and long-lasting insecticide treated nets prevent diseases by minimizing vectors.

4.3.3 Mosquito agents in the Activity-ABM

Researchers conducted many studies to model mosquito population and seasonal movement (Depinay et al., 2004; Gu & Novak, 2009; Kraemer et al., 2015; Messina et al., 2016; Monaghan et al., 2016; Samy et al., 2014). In review of these studies, independent variables such as nutrient competition, socioeconomic status, land-cover and land use, resource attraction, predation and climate have been proposed to be related to mosquito distribution and movement (Table 8). Depinay et al. proposed that predation is an important factor to vector distribution; therefore, the Activity-ABM takes into account human population density to create mosquito agents in the study area.

Mosquito agents. We assume that mosquito agents in the model cannot move in a long distance although human agents can move autonomously from a short- to long-distance at any time. At the start of the simulation, 5,000,000 “static” mosquito agents are created according to the human population density available thought the ACS, and each mosquito agent is given their home location in the census tract level. At the end of each simulation day, the model updates the mosquito births and deaths. Births and deaths random occur in the study area at a rate of 0.128 (Kucharski et al., 2016), and the lifespan of mosquito is 15 days (Lessler et al., 2016). Table 9 depicts all agents living in the Activity-ABM as well as their state variables and scales.

Table 8. Literature review of Mosquito Distribution and Movement Modeling

Model	Method	Objective	Source
Individual-based Model (IBM)	Temperature (life span), Moisture (e.g. precipitation and relative humidity), Nutrient Competition (mortality in the larval stage), Predation and Disease, and Dispersal (seeking blood meals and oviposition sites)	Anopheles Population Dynamics	Depinay et al. 2004
Individual-based Model	Landscape (20 houses that are aligned diagonally, vertically or horizontally), and Resource Attraction (hosts and oviposition sites, e.g. random flight when the resource was not within the mosquito's perception range, and directional flight)	Status and Movement of Anopheles Mosquitoes	Gu and Novak 2009
Geographic Information Systems-based Model (GIS)	Temperature, Rainfall and Photoperiodic Responses (using ESRI ArcGIS, Spatial Analyst and Arcobjects that determines the start of spring egg hatching and onset of autumn egg diapause for all grids within the study zone)	Survival and Seasonal Activity of Aedes Albopictus	Medlock et al. 2006
Boosted Regression Trees(BRT)	Temperature, Precipitation, Humidity, Vegetation Indices and Urban land cover (predict the probability of vector occurrence from 0 to 1)	Global Distribution of Aedes Mosquitoes	Kraemer et al. 2015 Messina et al. 2016
Ecological Niche Modeling	Climate, Socioeconomic Status, Land-cover, Mosquito Abundance, and Accessibility (explore what factors driven Zika risk for different zones)	Global Geographic Potential of Zika	Samy et al. 2016
Forecasting Regional Model (FRM)	Remote Sensing-based Normalized Difference Vegetation Index (NDVI), Temperature, Precipitation, and Humidity (multiple linear regression analyses)	Aedes aegypti larval indices	Estallo et al. 2008
Meteorologically Driven Models	Poverty, DENV and CHIKV transmission data, Transportation data, Temperature and Rainfall (daily counts of egg, larval, pupal and adult Ae. Aegypti using Skeeter Buster and DyMSiM)	Seasonal Occurrence and Abundance of Aedes Aegypti	Monaghan et al. 2016

Table 9. Agents and State Variables in the Activity-ABM

Agents	State Variables
Human (individual moving agents) Humans are created by the individuals in the BN-ABM (Chapter 2). In the Activity-ABM, all humans move to different census tracts based on their activity records generated from the BN-ABM (Chapter 2).	Unique ID Activity Records Current location Risk of the infection Health state
Mosquito (individual static agents) Mosquitoes are created in the Activity-ABM.	Unique ID Location Risk of the infection Health state
Environment (Census tract)	Unique ID Number of human agents by health state Number of mosquito agents in health state

4.3.4 Virus Transmission Simulation in the Activity-ABM

The virus transmission cycles between humans and vectors are formulated as follows. The model builds on an earlier compartment model that assumes the acquisition of immunity to diseases after recovery (Kucharski et al., 2016), but is extended to include dynamics in human-vector interaction due to human behavior. Individuals begin susceptible (S) to exposed (E) with risk of the infection determined by effective contact probability between any two individuals and number of infectious individuals in their neighborhoods. Human agents become infectious (I) after 6 days and recovered (R) after 5 days [76], while mosquito agents become infectious (I) after 7 days and their recovery (R) will not be considered in the simulation since the average lifespan of mosquito is 15 days (Kucharski et al., 2016).

Risk of the infection. To compute risk of the infection of an individual in the

Activity-ABM, the Reed-Frost equation is used:

$$P_{-i,j}(t) = 1 - P_{i,j}(t)$$

$$IR_i(t) = 1 - (1 - P_{i,j}(t))^{I_v(t)}$$

where $P_{i,j}(t)$ is the probability of an effective contact between individual i and vector j at time t, $P_{-i,j}(t)$ is the probability that individual i and vector j cannot interact with each other at time t, $I_v(t)$ is the number of infectious vectors at time t in the neighborhood of individual i, and $IR_i(t)$ is risk of the infection for individual i. Earlier Reed-Frost equation assumes that individuals mix random, defines $P_{i,j}(t)$ identical to all individuals in a population, and ignores dynamic interaction among individuals due to their mobility and prevention behavior, for instance, individual mobility on weekdays and weekends, individual mobility during daytime and nighttime, individual mobility in commercial areas and residential areas, and prevention behavior for children, student, employed and unemployed individuals. These dynamics cause host-vector contacts to various extents in space and time and ultimate transmission dynamics of diseases. The proposed Activity-ABM takes into account host-vector contact dynamics by assuming that the effective human-vector contact probability $P_{i,j}(t)$ varies as daily activities and prevention behavior of a human agent, thereby changing their susceptibility to diseases. In the Activity-ABM, the Reed-Frost equation is modified as follows:

$$P_{-i,j}(t) = 1 - P_{i,j,a}(t)$$

$$IR_{i,a}(t) = 1 - (1 - P_{i,j,a}(t))^{I_v(t)}$$

where a is the activity that individual i performs at time t, $P_{i,j,a}(t)$ is the probability of an effective contact between individual i and vector j at time t specific to activity a, $P_{-i,j}(t)$ is the probability that individual i and vector j will not interact with each other at time t, $I_v(t)$ is number of infectious vectors at time t in the individual i's neighborhood, and $IR_{i,a}(t)$ is the risk of the infection for individual i when they conduct activity a. If individual i use prevention, their $p_{i,j}(t)$ will be modified. In particular, $p_{i,j}(t)$ will be 0 if individual i use the host control, or will decrease if he uses the contact control.

Initial states. The CDC reported that the local infection in Miami-Dade Country began on 1 August 2016, when is the initial date of the baseline modeling exercise. According to the United States Census Bureau, the human population in Miami-Dade Country on that day was 2,692,990. Estimating the initial state of the vectors is difficult. As Kucharski et al. proposed, the infected and infectious hosts/vectors are initially equal (Kucharski et al., 2016). On 1 August 2016, Miami-Dade County had 99 travel-related infections and 14 local-acquired cases. The model assumes that the 99 travel cases aroused the 14 local infections, and estimates 203 infected (E) and 203 infectious (I) mosquitos for the initial simulation.

Simulation. Step 0 (initialization) – all human agents and their activity-based mobility, sociodemographic attributes, prevention behavior, and health state, and mosquito agents and their location and health state are initialized and created. Each step, the health states of all human agents and vector agents living in the Activity-ABM are updated, which is based on the census tract that each agent stays in, the number of infectious individuals in the census tract, and the contact probability in regards to the current activity and prevention behavior of the individual.

Baseline, Intervetion and Scenario Modeling Exercise: The Activity-ABM model starts with a baseline modeling exercise that considers only human mobility. To include human-vector contact dynamics due to human mobility, we define three parameters. They are the probability of an effective contact between humans and infectious mosquitoes when people conduct home activities P_{home}, the probability of an effective contact between humans and infectious mosquitoes when people conduct work/school activities $P_{work/school}$, and the probability of an effective contact between humans and infectious mosquitoes when people conduct other activities P_{others}. Table 10 shows all parameters required in this baseline modeling exercise. Next is the intervention model exercise that considers both human mobility and prevention behavior. To include human-vector contact dynamics due to human prevention behavior, we define three parameters. They are the new probability of an effective contact between humans and infectious mosquitoes due to using the contact-based controls $P_{contact}$, the percentage of humans using the host-based controls P_{host}, and the percentage of mosquitos affected by the vector-based controls P_{vector}. Table 11 shows all parameters required in this intervention modeling exercise. Finally, three scenarios are built to evaluate what prevention is the most effective in the local context.

Table 10. The parameters required in the baseline modeling exercise of the Activity-base model.

Parameter	Definition	Sources	Values
Num_mos	Initial population for mosquito agents	Chapter 3	5,000,000
Num_human	Initial population for human agents	The ACS data	2,680,607
Num_infected_mos	Initial population for infected mosquito agents	Chapter 3	100
Num_infectious_mos	Initial population for infectious mosquito agents	Chapter 3	100
Num_infected_humans	Initial population for infected human agents	The CDC data	7
Num_infectious_humans	Initial population for infectious human agents	The CDC data	7
Birth/Death_rate_mos	Mosquito birth/death rate	Kucharski et al., 2016	0.128
EI_human	Latent period for human agents	Lessler et al., 2016	6 (days)
IR_human	Recovery period for human agents	Lessler et al., 2016	5 (days)
EI_mos	Latent period for mosquito agents	Lessler et al., 2016	11 (days)
Life_mos	Life span for mosquito agents	Kucharski et al., 2016	15 (days)
P_{home}	Probability of an effective contact between humans and infectious mosquitoes when people conduct home activities	Modeled	Unknown
$P_{work/school}$	Probability of an effective contact between humans and infectious mosquitoes when people conduct work/school activities	Modeled	Unknown
P_{others}	Probability of an effective contact between humans and infectious mosquitoes when people conduct other activities	modeled	Unknown

Table 11. The parameters required in the intervention modeling exercise of the Activity-base model.

Parameter	Definition	Sources	Values
$P_{contact}$	The new probability of an effective contact between humans and infectious mosquitoes due to using the contact-based controls	**Modeled**	Unknown
P_{host}	The percentage of humans using the host-based controls	**Modeled**	Unknown
P_{vector}	The percentage of mosquitos affected by the vector-based controls	**modeled**	Unknown

4.4 Data Sources

To test the efficacy of the proposed Activity-ABM, this study applies the model to the 2016 Zika outbreak in Miami-Dade County, Florida. The required data are the counts of Zika cases in Miami-Dade County, a traditional travel diary survey, the American Community Survey, and multiple GIS datasets. In the Activity-ABM, the travel diary survey is combined with the ACS data to create a synthetic population that represent the actual population, and used to generate individual daily activities for the entire population. The model also requires the counts of Zika cases to estimate the modeling parameters and validate the simulation results.

4.4.1 Zika Dataset

In 2016-17, the CDC has daily released the counts of Zika cases by county across Florida, including travel-related cases, locally-acquired cases, pregnant women cases and sexual-transmitted cases. This study focuses on the local Zika transmission in Miami-Dade and collects the locally-acquired cases during 1 August 2016 to 17 May 2017 available through the CDC.

4.4.2 Travel Diary Survey Dataset

The 1999 Southeast Florida Household Travel Survey that was collected by the Florida Department of Transportation (FDOT) Districts and metropolitan areas is downloaded. As the study area is Miami-Dade County, the Miami-Dade travel dataset is extracted from the survey including Broward, Miami-Dade and Palm Beach.

4.4.3 Census and Environmental Data

The 2012-2016 ACS 5-year estimates data at the census tract level in Miami-Dade regarding age, household size, household income, number of workers in a household and number of households is downloaded. A set of open GIS environmental and zonal datasets, including environmental endangered sites, contamination areas, dump sites, golf sites, parks, major malls, school enrollment, groceries, restaurants and land cover and land use, are also downloaded via the Miami-Dade County. For the grocery and restaurant data in Miami-Dade County, Yelp Search API is used to access the local businesses and search all groceries or restaurants. They are then aggregated to the total per census tract. The details are shown in Section 2.4.2.

4.5 Results

4.5.1 Mosquito Population

The weights for mosquito agents are shown in Figure 21. According to the 2012-2016 ACS 5-year estimates data, human population density in the south part of Miami-Dade County reaches to the peak, where the maximum mosquito population occurs. At the beginning of the simulation, 5,000,000 “static” mosquito agents are created and distributed based on these calculated weights.

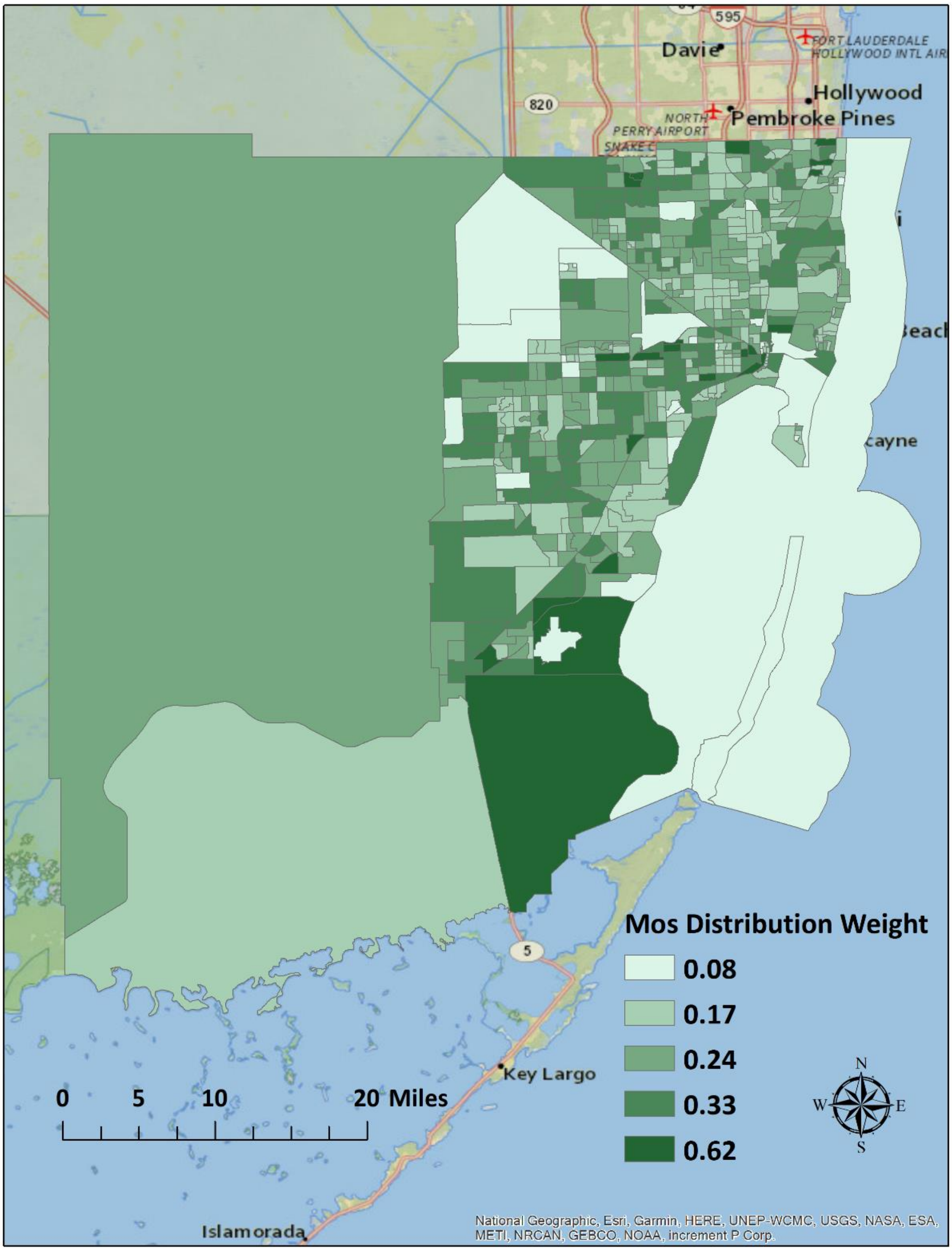


Figure 21. The tract-level weights for mosquito agents in the study area computed from the human population density. A high weight of a tract is interpreted as a large mosquito population in the tract.

4.5.2 Human Infections in the Baseline Modeling Exercise

The county-level aggregation of Zika infections by day for human hosts from the baseline modeling is shown in Figure 22. The baseline modeling parameters, including the effective human-vector contact probabilities for home activity P_{home} , for work/school activity $P_{work/school}$, and for others P_{others}, are estimated by locally minimizing the simulation result and the CDC Zika data. They are estimated to be 0.4 (e-5), 0. 1 (e-5) and 0. 15 (e-5), respectively. Our baseline modeling results confirm findings by others that high risk of Zika infection happens when people stay at home while low risk of infection happens when people go to school/work (Stoddard et al., 2009). Within the simulation, the first 60 days (1 August 2016 – 30 September 2016) experienced a good match of the model and the data (Figure 23). It is noteworthy that October 1st 2016 is at the stage that Miami-Dade County implemented the countywide truck/aerial adulticide/larvicide outdoor spraying. Thus the 61 day (1st October 2016) is the initial date of the intervention modeling exercise.

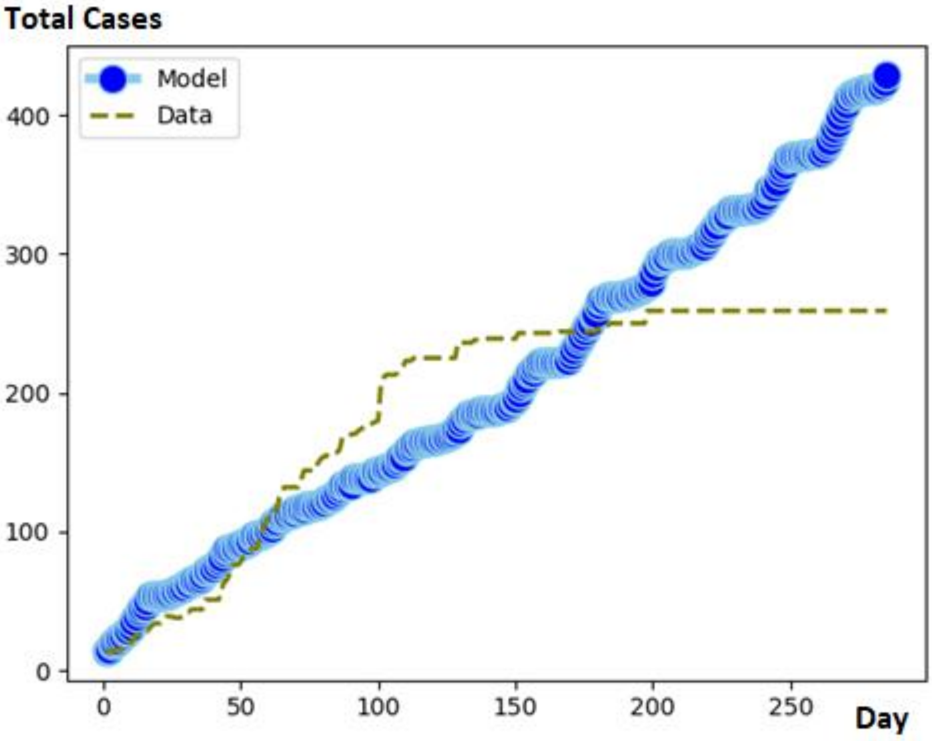


Figure 22. The baseline simulation result across a 285-day period. The x axis is the number of days starting from August 1st 2016, and the y is the accumulated cases

of Zika. The blue line is the model prediction, and the yellow line is the data.

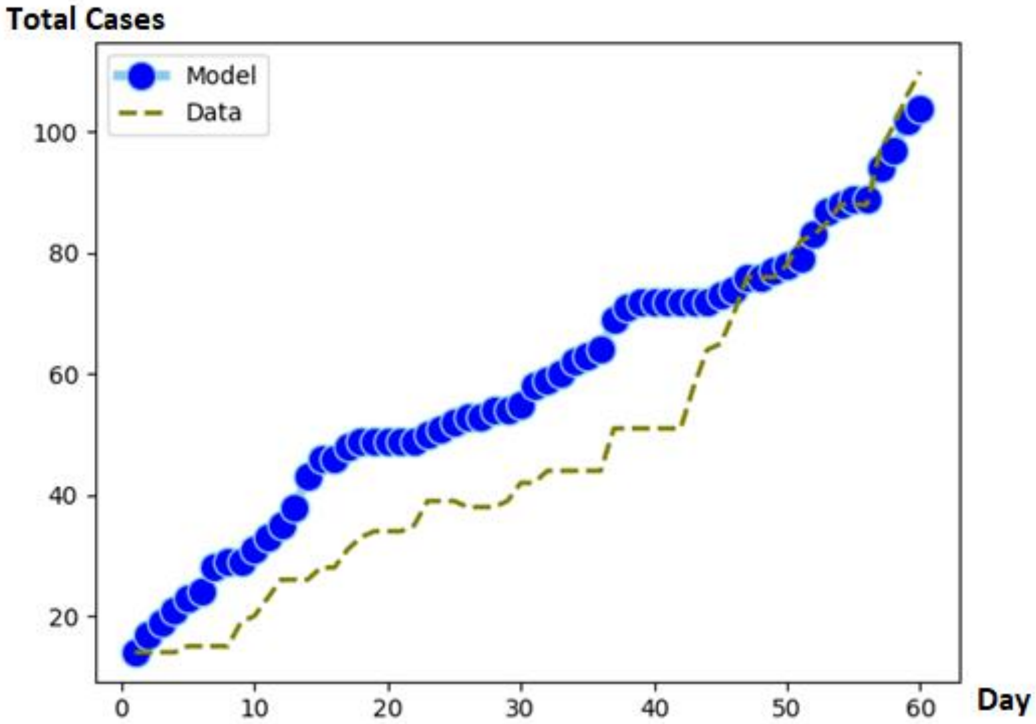


Figure 23. The baseline simulation result for the first 60 days (August 1st to Sept 30th 2016). The x axis is the number of days starting from August 1st 2016, and the y is the accumulated cases of Zika. The blue line is the model prediction, and the yellow line is the data.

4.5.3 Human Infections in the Intervention Modeling Exercise

The county-level aggregation of Zika infections by day for human hosts from the intervention modeling is shown in Figure 24. The intervention modeling parameters, including the new probability of an effective contact between humans and infectious mosquitoes due to using the contact-based controls P_{contact}, the percentage of humans using the host-based controls P_{host}, and the percentage of humans using the host-based controls P_{vector} are estimated be 0.05 (e-5), 0. 6 and 0. 8, respectively.

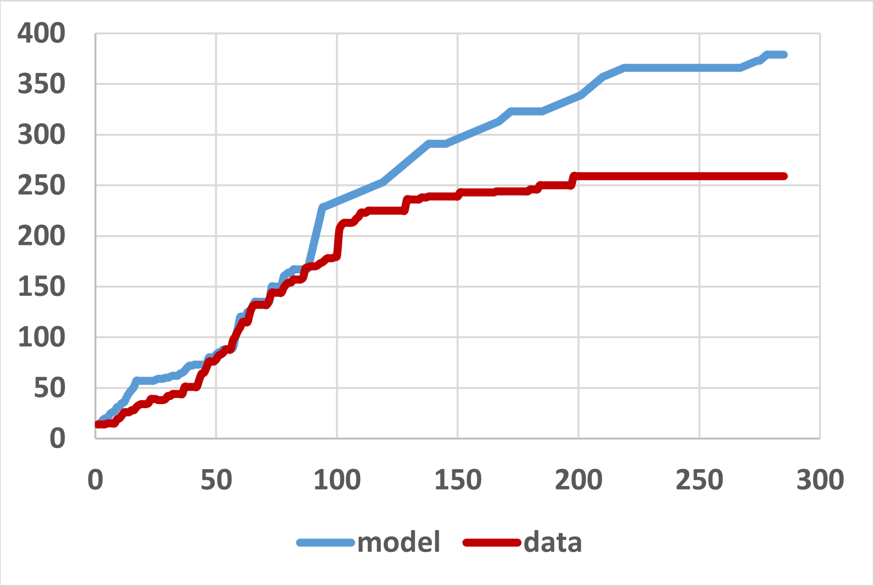


Figure 24. The baseline and intervention simulation result during August 1st 2016 to May 12th 2017. The x axis is the number of days starting from August 1st 2016, and the y is the accumulated cases of Zika. The blue line is the model prediction, and the red line is the data.

4.5.4 Human Infections in the Scenario Modeling Exercise

The county-level aggregation of Zika infections by day for human hosts from the scenario modeling is compared in Figure 25. Across a 100-day period, the human infections in the host scenario are the most, while the fewest infections occur in the vector scenario. The result suggests that the vector controls are the most effective, as the 2016 Zika outbreak in Miami-Dade County ended after an outdoor spraying to control mosquitoes.

Within the simulation, the human infections in the vector scenario are mostly and significantly fewer than the host and contact scenarios. In the first 60 days the number of infections is similar between the contact scenario and the host scenario, while the subsequent simulation shows an increasing difference between these two scenarios, in the host scenario mostly with more human infections. After 100 days, the outbreaks in the vector and contact scenarios end, while the infection in the host scenario still increases.

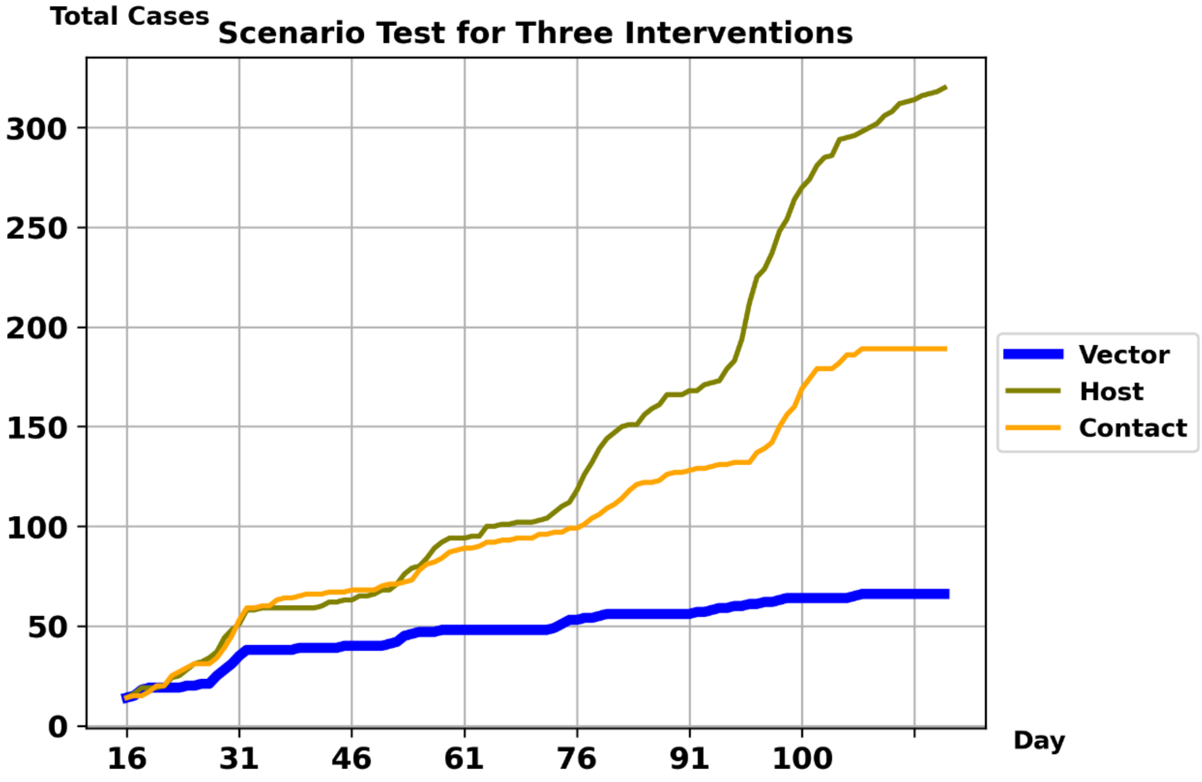


Figure 25. The scenario test for the three controls, including the vector-based controls, the host-based controls, and the host-vector contact-based controls. The x axis is the number of days starting from August 1st 2016, and the y is the accumulated cases of Zika predicted from each scenario. The blue line is the vector-control scenario prediction, the yellow line is the host-control scenario prediction, and the orange line is the contact control scenario prediction.

4.5.5 Human Infections in the Uncertainty Analysis Exercise

The county-level aggregation of Zika infections by day for human hosts from the uncertainty analysis is compared in Figure 26. In this uncertainty analysis, the baseline mode runs five times across a 100-day period. The human infections in the five runs shows an initial period of stability, including a similar 50-day infection increase from the initial population of 3,000,000 humans. Within the 5-run uncertainty analysis, the human infections of the 1st and 3rd runs shares a peak of 65 at around day 30, before being near-stable at around day 60, while the rest 3 runs shares a stable increasing across the simulation period. In this case, it is hard to evaluate the uncertainty of the Activity-ABM since there are only 5 runs for the uncertainty analysis.

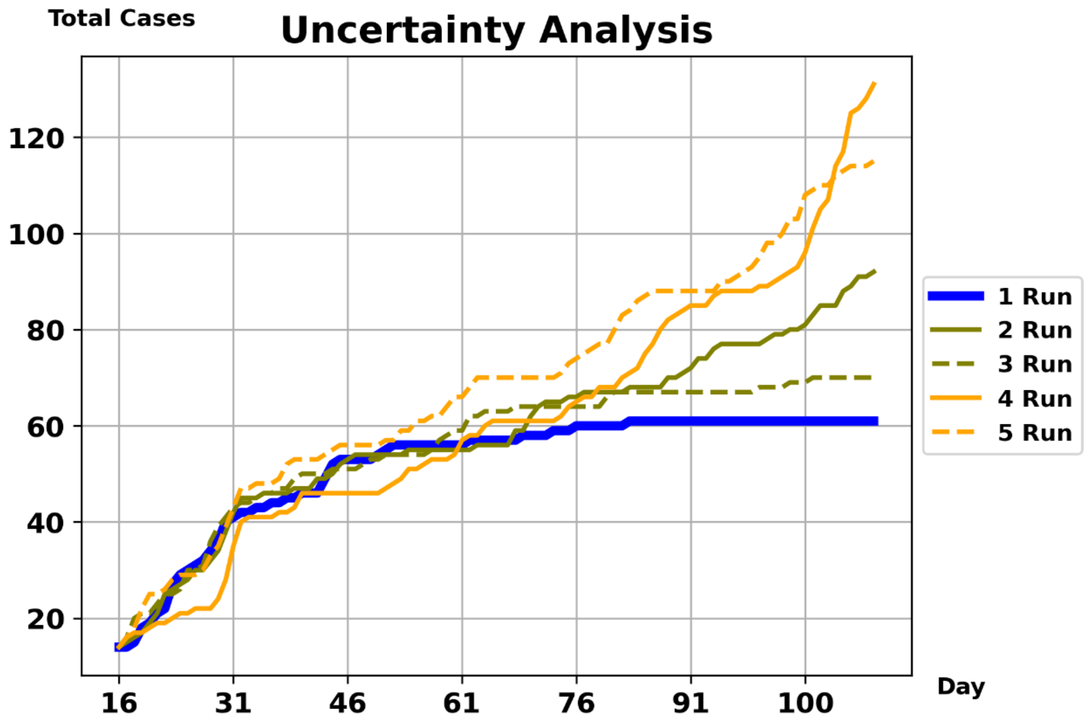


Figure 26. The uncertainty analysis result. The x axis is the number of days starting from August 1st 2016, and the y is the accumulated cases of Zika. The blue line is the model prediction, and the yellow line is the data.

4.6 Conclusions

This section presents a novel model, Activity-ABM that integrates activity-based models and agents-based models to evaluate the effectiveness of the prevention strategies that combats vector-borne diseases. We find that vector-borne disease prevention strategies are primarily related to human mobility and prevention behavior, and promote disease control in the context of humans, vectors, and human-vector contacts. Takes the 2016 Zika epidemic in Miami-Dade County, Florida as a case study, our modeling results suggest that high risk of Zika infection happens when people stay at home while low risk of infection happens when people go to school/work, and the vector-based controls are the most effective. This case study also demonstrates the efficacy of the proposed, enhanced model for a large-scale application.

To understand human-vector contact dynamics due to human mobility, we define three parameters in the baseline modeling exercise, including the effective human-vector contact probability for home activities P_{home}, the effective human-vector contact probability for work/school activities $P_{work/school}$, and the effective human-vector contact probability for other activities P_{others}. By locally minimizing the simulation results with the CDC data, we estimate these three baseline parameters P_{home}, $P_{work/school}$, and P_{others} to be 0.4 (e-5), 0. 1 (e-5) and 0. 15 (e-5). Based on this baseline modeling results, we can see that high risk of Zika infection often happens when people stay at home while low risk of infection often happens when people go to school/work (Stoddard et al., 2009). We also define three parameters to include human prevention behaviors, namely the host-based controls, the vector-based controls, and the contact-based controls. They are the new probability of an effective contact between humans and infectious mosquitoes due to using the contact-based controls P_{contact}, the percentage of humans using the host-based controls P_{host}, and the percentage of humans using the host-based controls P_{vector}, and are estimated be 0.05 (e-5), 0. 6 and 0. 8.

To evaluate the effectiveness of the three prevention behaviors, we build three scenarios that apply the host-based controls, the vector-based controls or the contact-based controls in same locations. Within the scenario simulation across a 100-day period, we find that the vector-based controls cause 76 human infections and the outbreak ends by day 85; the contact-based controls cause 178 human infections and the outbreak ends by day 90; the host-based controls cause 325 human infections and the outbreak still occurs by the end of the simulation period. Our scenario results suggest that in the local context the vector-based controls are the most effective.

Our model also allows for individual heterogeneity and stochasticity among pathogens, vectors and hosts as well as host-vector-environment interactions embedded in the transmission cycles of an epidemic. These interactions and variations are crucial to disease prevention and control because they often lead to unexpected and emergent outbreaks. Another important distinguishing feature of the Activity-ABM is that it is an individual-scale model and facilitates tracking the health state of a human agent who has prevention behavior and human infections of the locations that apply prevention behavior in a spatially and temporally explicit manner. It adds the ability to test various public health intervention scenarios and to identify the best localized intervention strategy for a population. For instance, what intervention should be the most effective? Where interventions should be targeted? So that local managers can make evidence-based decisions about what program to support, government and health organizations can make proven policy and funding decisions, and practitioners can devise evidence-inspired programs. The model can also test various modeling initials, for instance, a specified, initial distribution of human/mosquito infections, and a specified, initial distribution of mosquitoes (e.g. vegetation-based or precipitation-based).

However, two issues raise for the model. In this study, we conduct a large-scale application of the Activity-ABM, including 5,000,000 mosquito agents, 3,000,000 human agents, 8 time-step modeling per day, a 285-day simulation period, and 519 census-tract locations. Such finer-, individual- and large- scale modeling has great demand in computation ability and memory. Although we carry out the asynchronous multiprocessing, one simulation across a 100-day period still takes 2-3 days, and a 285-day simulation needs one week or more. Therefore, model fitting and parameter estimation is significantly difficult. Another limitation of this model is that agents in an ABM are defined to be heterogeneous and thus cause this agent-based modeling approach's high dependency in data. Within the existing literature ABMs are often built on a detailed, comprehensive survey (Alderton et al., 2016; Dommar et al., 2014; Jacintho et al., 2010; Jindal & Rao, 2017; Manore et al., 2015; Mniszewski et al., 2014; Mulyani et al., 2017). Such data is expensive, and never available to the public, and ultimately, limits the application of ABMs.

Despite these limitations, our model provides an appropriate tool for a range of stakeholders to explore the potential influence of emerging interventions on vector-borne disease transmissions and help determining optimal policy or program for elimination of the diseases. The case study also demonstrates the efficacy of our model for large-scale application, and the data required in the model are always available to the public. These ultimately, therefore, leads to the proposed Activity-ABM model with high value.

5. Summaries, Contributions, Limitations and Future Works

5.1 Research Summaries

To examine the role of dynamics in patterns of contact between hosts and vectors engaged in human behavior in the transmission cycle of an epidemic, this dissertation proposes an activity-based ABM that couples of individual-scale human daily mobility and travel behavior, human prevention behavior, and host-vector contact dynamics with virus transmission cycles, and applies the model to the 2016 Zika virus in Miami-Dade County, Florida as a case study. To evaluate the performance of the model, Chapter 3 builds a compartmental model (SEIR), and Chapter 5.2 presents detailed comparison of these two models regarding model assumption, model fit, parameter estimation and model application. An important feature of the Activity-ABM is that it is a local-, large- and individual- scale modeling framework and facilitates tracking the health state of an individual traveler through time and space, which adds the ability to test various policy scenarios to the model. To evaluate what control should be the most effective in the local context, Chapter 4 builds three scenarios that random selects 100 locations (census tracts) that apply only the host controls, the vector controls or the contact controls, and evaluates how effective these controls are. Such investigation helps public health intervention strategy-makings that attempt to improve human health in the population level, using a simple example, prospective planning of financial resources for epidemiologically relevant and cost intensive diseases like dengue. The rest of this section is organized as follows. Chapter 5.1 concludes with a summary for the findings from Chapter 2-4. Chapter 5.2 discusses contributions and limitations.

5.1.1 Human Daily Travel Modeling

Chapter 2 generates the daily travels and activities for the entire population in the study area – Miami-Dade County, Florida using activity-based microsimulation method that has been developed for transportation modeling and planning. An important distinguishing feature of the activity-based model is its ability to test various policy scenarios by tracking travel-activity patterns of an individual in a spatially and temporally explicit way. Earlier activity-based models have been designed to study weekday travels by assuming that individual travels are stable in the short term. However, people could have different travels between weekdays and weekends and even across days of a week. Compared to weekday travels, weekend travels with significantly different patterns are crucial disease control and prevention. Ignoring such variation could result in the simulation that is not representative of the underlying population. This section aims at extending an activity-based model to model dynamics in individual daily travels by defining activity scheduling changes of an individual as "daily and uncertain changes". The proposed activity-based model computes probability distributions for six travel-activity attributes i.e. travel frequency, travel duration, travel mode, travel destination location, travel propose, and activity duration, and interprets the alternating predictive results underlying different time-budgets on weekdays and weekends as indicating an activity scheduling change. To conduct this task, Bayesian Networks are built to learn the probability distribution for each travel-activity attribute and infers the probability that a specific activity attribute arises at a given time. This proposed BN-ABM framework is tested by using a case study in Miami-Dade County, Florida, and the result demonstrates the efficacy of the enhanced model.

5.1.2 Human Prevention Behavior Modeling

Chapter 3 reviews emerging human (vector-borne diseases) prevention behavior, and examines how they become effective in the transmission cycles of the diseases. In August 2016, Miami-Dade County implemented Zika intervention strategies to combat a dramatic increase in the infection. Encouragingly, there was a significant decrease; howbeit, the effectiveness of these interventions remains unclear, and many countries in the world still suffer from many vector-borne diseases such as Dengue, West Nile Virus and Zika. To evaluate these intervention measures, a Susceptible–Exposed–Infectious–Recovered Intervention Model is proposed and applied to the 2016 Zika outbreak in Miami-Dade County, Florida as a case study. Within the exiting literature, we find that Zika intervention measures control the infection in the context of host, vector and host-vector contact. According to the nature of the three categorized controls in disease prevention and control, the SEIR model is extended to evaluate the three interventions, and then is parameterized using the Markov Chain Monte Carlo. The modeling results successfully suggest that the three interventions result in a remarkable decline of the Zika infection in the study area, as reported by the daily-updated cases from the CDC.

5.1.3 Model-based Evaluation of Human Mobility and Prevention Behavior

To evaluate the importance of variation in human-vector contact due to human behavior including mobility and prevention behavior, Chapter 4 develops an activity and agent-based model, Activity-ABM. It couples human prevention behavior (Chapter 3), individual human daily mobility and travel behavior (Chapter 2), dynamic human-mosquito contact (Chapter 4), and virus transmission cycles (Chapter 3). Take the 2016 Zika epidemic in Miami-Dade County, Florida as a case study, the model illustrates how human-mosquito contact dynamics engaged in daily regular travels and activities of individual humans as well as a variety of disease prevention behaviors influence the transmissions of vector-borne diseases. For instance, Chapter 4 estimates the effective human-mosquito contact probability ($P_{H,V}$) of 0.2 (e-5) both in home and for multiple activities (e.g. shopping and social recreation activities) and 0.1 (e-5) at work/school. The model also shows what prevention behavior is the most effective by building three scenarios. The scenario testing results suggest that the vector controls such as outdoor sprayings cause the fewest infections for humans, as the 2016 Zika outbreak in Miami-Dade County ended after an outdoor spraying to control mosquitoes. Practically, the proposed Activity-ABM will aid determining what mobility generates large amounts of infection in the human population as well as what behavior should be the most effective to control diseases. Combined with human behavior, the model will also facilitate identifying key locations where prevention should be targeted. These may provide targets for evidence-based public health interventions and disease prevention and control.

5.2 Research Contributions and Limitations

This dissertation highlights the role of space in health research by integrating demographics of a population, individual daily mobility and travel behavior, prevention behavior at the level of both individual and population and diffusion of an epidemic, specifically the finer-scale spatiotemporal transmission dynamics of a vector-borne disease. Similar behavior-based health studies have been conducted; however, this dissertation research is designed to consider both mobility and prevention behavior and investigate the impacts of dynamics in patterns of contact between hosts and vectors engaged in individual daily travels and disease prevention behaviors. Finally, the proposed model is tested by a large-scale application.

5.2.1 Theoretical Contribution

Highlight the role of space in health research. Space has long been instinctively linked to health research in terms of scale, human mobility and interaction etc. Recent developments in geospatial data acquisition techniques are enabling geographers to increase their interest in the transmission, prevention and control, and public health intervention of many diseases (Richardson et al., 2013). This dissertation based on interdisciplinary spatial and temporal data including health, environment, social, and demography data, Global Positioning System (GPS) data, and approaches in geography and related fields including agent-based modeling and activity-based transportation modeling, is generating advances in behavior, interaction and infectious diseases studies.

For vector-borne diseases human behavior is one key geographic factor to drive variation in patterns of contact between hosts and vectors, and ultimately infections to various extents in space and time. In particular, movements of infected humans can increase the dispersal of parasites, and this human travel-mediated spread of parasites could become global concerns (Wesolowski et al., 2012). Many advanced approaches have been developed to define and measure the interactions between humans and mosquitoes engaged in their behavior: “many-to-many”, “one-to-many” and “one-to-one”. Actually, this is a modeling-scale issue that we focus on population-population transmission, individual-population transmission or individual-individual transmission. Adams and Kapan (2009) assumed that a large mosquito population causes a high infection probability and measured the interaction using human population in travel, i.e. travel rate to a given zone and mosquito size in a zone. Wesolowski et al. (2012) proposed a travel network where an individual travels between different zones or nodes and defined the interaction as a function of the mosquito population in the zone. Funk et al. (2010) developed an individual-based model where human agents get infected by interacting with an infected mosquito, and defined a parameter called “bite-success-rate” (also known as contact rate in an epidemic mathematical model) to measure the interaction. If an individual is successfully bitten by a mosquito, the mosquito must be within a sensible range. In this case, the interaction is viewed as a spatial colocation of humans and mosquitoes by biting. Kiszewski and Darling (2010) proposed another way to connect human and mosquito populations in the transmission cycle of an epidemic: the interaction duration of humans and mosquitoes. If an individual stays in an area with mosquitos for a long time, the infection probability is large. In this case, the infection probability is a function of the stay duration, i.e., an exponential function of time and contact rate per time. Against this background, this thesis models the interaction using the "one-to-one" overlapping of humans and mosquitoes engaged in human behavior and mosquito distribution. Humans can move autonomously from a short- to long- distance at any time, but mosquitoes cannot move in a long distance, for instance, Matheson et al. (2017) assumed that the mosquitoes in a local scale can only move in 5 meters. This is why mosquitoes are designed as "static" agents in the Activity-ABM. On the other hand, we are accessible to mosquitoes at any time in a mosquito area except for when mosquitoes sleep or we use prevention strategies. Matheson et al. (2017) assumed that the accessible period to mosquitoes for humans is from 9:00 pm to 5:00 am based on the habitual cycle of mosquitoes, and others presumed that the accessible period only happens when people travel (Adams & Kapan, 2009; Funk et al., 2010; Wesolowski et al., 2012). Lacking such information or data in the study area, this thesis defines the entire simulation period as the accessible period.

Spatial scale is also important as it could cause the variation in results from the same model utilized at different levels of spatial resolution – the spatial effect of the modifiable areal unit problem (MAUP) (Kwan, 2020; Kwan, 2009). This thesis research uses two different views to deal with the MAUP. One way is to identify the best spatial scale at which the model operates to minimize the difference between modeling results and data. Another view that mitigates the MAUP is to use scale-independent modeling measures. Since vector-borne diseases are primarily transmitted by interacting with infected vectors, the interaction modeling component is the key to the proposed model and it is designed to be scale-independent. Further, individuals who live in the same unit are modelled to experience different levels of exposure to vector, regardless of where they live or how much time they spend within the area. Such dynamics in exposure to vector is assumed to primarily depend on peoples' activity-based mobility and prevention behavior, not the areas where they live. Such taking into account the impacts of human behavior, dynamic human-vector interaction and spatial scales on the transmission cycle of an epidemic will hold extraordinary potential for creating new discovery pathways in disease prevention and control, and contribute to the behavior-based spatial epidemiologic theory.

Contribute to methodologies in multiple fields. Another intellectual merit of this dissertation is its expected contribution to the methodologies for day-varying human mobility and travel behavior modeling as well as dynamic multiple-species interaction simulation. Previous studies often ignore daily variation in individual travels as well as dynamic interactions among them, which could result in simulation results that are not representative of the underlying population.

People are often endowed with travels and activities varying between weekdays and weekends and even across days of a week, which leads to disease transmission to decrease or increase. The study by Hens et al. (2009) estimated a 10~20% reduction in influenza infections during weekend when compared to weekdays using a population-based prospective survey of mixing patterns in eight European countries. Decreasing weekend travels and activities due to workplaces, school, and many other locations of higher transmission closed may expect disease transmission to decrease (Mao, 2011). Some studies have been performed to explore the impacts of weekends as well as holidays on decreasing disease transmission (Cauchemez et al., 2008; Eames et al., 2011, 2012; Hens et al., 2009; Mao, 2011). In order to generate day-varying travels and activities of a population at the level of individual travelers, this thesis proposes a novel activity-based modeling framework, BN-ABM that integrates Time Geography, ABM, and Bayesian network. This proposed BN-ABM generates and forecasts complete dynamic activity scheduling for a population by taking into account individual fixed and mandatory activities as well as semi-dynamic time-budgets varying between weekdays and weekends, which has the potential to be used in transportation modeling and planning. The BN modeling component embed in the BN-ABM defines daily travels and activities of an individual as “daily and uncertain changes”, computes probability distributions for each travel-activity attribute, and interprets the alternating predictive results underlying time-budgets on weekdays and weekends as indicating their daily travel changes.

In addition to the dynamics of human daily mobility and travel behavior discussed above, the variations in individual preference in human prevention behavior (human response) are also important as it causes their exposure to vector to various extents in space and time and reduces or amplifies the infections. Further, individual prevention behavior choice thoroughly varies as the source of health information available to them, such as public news by websites, TV stations, newspapers and other media platforms, and their attitudes, beliefs and perceptions of infection risk, which explains the clustered occurrence of people susceptible to or infected with the diseases, or infectious or recovered (Funk et al., 2010). One reason is the dynamic human-vector interaction due to the variation in individual preference in human prevention behavior. In order to take into account such dynamics in human-vector interaction, this thesis builds the BN-ABM based on the assumption that individual exposure to vector varies as activities that they perform and prevention behavior that they use, and adjust the interaction-based risk of the infection modeling component. This method can be applied to many communicable diseases.

Integrate time geography, complex system theory and spatial epidemiology. For vector-borne diseases dynamic interaction between humans and vectors as well as altering interaction between individuals and their specific environments plays an important role in minimizing exposure to vector and the transmission of the diseases. Traditional methods such as statistical regression analysis are unable to examine these dynamic interactions engaged in the transmission cycles of the diseases. A complex system consists of large numbers of interacting entities, and explores and draws out these dynamic interactions by creating interacting agents and defining rules that guide an agent’s behavior as well as interaction with each other, which traditional geographic methods fail to capture. This thesis views the transmission of an epidemic as a complex adaptive system that emerges from complex interdependent processes in which individuals interact with each other and their environment and in which both individuals and environments adapt and change over time (Auchincloss & Diez Roux, 2008b), which motivates us to consider health research as the dynamics processes characterized by interactions and relationships between agents, environment, emergence and adaption. In particular, integrating complexity theory into health systems, we assume that the population in a given place are not separated but interrelated, and they can be influenced by external environments (Cilliers & Spurrett, 1999), which is usually reflected and modeled in communicable diseases that spread among people in the same (geographic) community as well as though transportation networks – interactions. Complexity theory also presumes that health systems are dynamic, nonlinear and have the capability to organize and reorganize themselves, which is a good example of the outbreak and re-outbreak of diseases – emergence (Griffiths & Sweeney, 2002). And learning from experiences, these dynamic and nonlinear health systems adjust their present behaviors – adaption. This is why health behaviors are stable and established but occasionally are in a slight state of change (Griffiths & Sweeney, 2002). The population-level dynamics of the diseases ultimately emerge from these micro-scale interactions and adaptations (Auchincloss & Diez Roux, 2008b). Another important distinguished feature is that the adoption behavior of complex systems dynamic models allows us to take into account the causes of the diseases at multiple levels, reciprocal relations and interrelation between causes that characterize the causation of the diseases (S. Galea et al., 2010; Sandro Galea et al., 2009).

To generate and construct daily activity scheduling of a population at the levels of individual travelers engaged in the transmission cycle of an epidemic, this dissertation formulates Time geography, often derived from the ontology that individual activities and travel paths become captured within a set of constraints in space and time, in the proposed BN-ABM model. Time geography, originally proposed by the Swedish geographer Torsten Hägerstrand in the mid-1960s to explore migration patterns in Swedish, describes a powerful conceptual framework to capture peoples' life paths and understand their spatial behaviors within constraints (Hägerstrand, 1970). Later, a lot of efforts have been made to computationally represent time geography entities and relationships, such as time-space prisms, capability constraints, coupling constraints, and authority constraints (Miller, 2005; Hägerstrand, 1970). *'Capability constraints'* are those that limit individual activities due to biological structure/transportation tools. Some capability constraints are time-oriented i.e. individuals have to sleep for a minimum number of hours. Others are distance-oriented and creates individual concentric rings of accessibility in their surroundings. The radii of the rings based on the ability that individuals move can create a series of tubes to visualize their mobility area, i.e. the inner tube where their arms can reach, the middle tube where they can communicate with each other or see other staff, and the outer tube where they can reach but have to make sure that they can return for the next activity (Hägerstrand, 1970). *'Coupling constraints'* define where, when, and how long individuals join activities, also known as bundles. It refers a group of individual paths sharing the same space and time, and provides a way to measure interactions between individuals i.e. in a restaurant, the waiters and customers form a bundle. Although individuals have the freedom to choose where they work or go to school, after that they have to obey the arrangement and requirement of their companies or schools. They have to work or go school during a given period and thus share common paths. *'Authority constraints'* are those areas or domain under control of a given individual or group. These areas are where other individuals cannot access. Domain can be also viewed to protect resources i.e. natural or artificial ecosystem (Hägerstrand, 1970), and is a cylinder where individuals cannot access or have to access with some invitation or payment. These three constraints always interact in many ways to model human mobility and travel behavior. An individual's choice of a specific activity pattern is viewed as being an allocation problem involving limited resources of time and space to achieve the highest quality of life (McNally & Rindt, 2000), and all human activities have spatial and temporal dimensions: activities occur at particular places for limited durations (Rainham et al., 2010). On a weekday, from Monday to Friday when people go to work/school, an employed individual or student always has a fixed activity schedule, probably from 8:00 am to 3:00 pm (except for lunch time). During this period, their activity area is fixed and they interact more with their colleges/classmates; therefore, their prisms are mornings before work/school, lunch hours and evenings after work/school, and they as well as their colleges/classmates mainly form the bundles. On a weekend, from Saturday to Sunday, an individual has more flexible time; therefore, their prisms are the whole weekend, and they as well as their families and friends mainly form the bundles. How can we model such dynamics in peoples' daily movement? Some studies have provided some potential solutions. Bhat and Koppelman (1999) collected 63,114 geo-tagged tweets from 116 unique users in Santa Barbara, California, created their activity spaces based on the minimum bounding geometry theory, and compared their activity spaces between weekday and weekend. They located a significant difference in downtown areas (downtown Santa Barbara and old town Goleta): during weekday the downtown area is highly visited, but during weekends individual activities are very limited in Isla Vista. It suggested that during weekday people are highly engaged with work, home and school, but during weekend people mainly stay at home and join some leisure activities. Pendyala et al. (2005) based on a travel diary survey built an activity-based model to simulate human daily movement. In their model, for employed individuals and students, there are three “flexible” weekday prisms, also called “open periods”, are determined to model their daily movement; for unemployed individuals and children, there is only one weekday prism. For weekend prisms, there is only one weekday prism. Against this background, this dissertation research introduces Hägerstrand’s Time geography into the BN-ABM by constructing individual time budgets limited by time (weekdays vs. weekends) and individual choices of a specific travel-activity pattern limited by their demographics and socio-economic characteristics as well as their specific surroundings.

5.2.2 Practical Contribution

Investigate finer- and larger- scale spatiotemporal transmission dynamics of an epidemic. This dissertation conducts model-based investigation to understand the role of human mobility and prevention behavior in the transmission cycle of a vector-borne disease and evaluate the efficiency of the associated public health interventions. The developed model is built for the entire Miami-Dade County, involves 3 million human agents and 5 million mosquito agents, and runs in 8 time-steps per day across a

285-day period. Meanwhile, the model utilizes at the census track level and includes 519 locations. Each step an aggregate infection for human hosts by county also emerges. The proposed model can be applied to many vector-borne and communicable diseases, and the assumptions underlying the model need to be adjusted.

Implications for disease prevention and control. Modeling and exploring the impact of human behavior on the transmission of an epidemic can support decision-makings for infectious disease prevention and control. It facilitates the strategic decision-making processes in the field of health care and public health, in particular, prospective planning of financial resources for epidemiologically relevant and cost intensive diseases like Zika and dengue. To conduct this task, this dissertation research focuses on modeling finer-scale spatiotemporal transmission dynamics of an epidemic, and building three scenarios. This scenario test examines the effectiveness of various prevention strategies regarding human mobility and prevention behavior, in particular, recommend people which strategy should be the most effective to prevent diseases. More public health policy-related questions can be answered. For instance, where prevention should be targeted? What mobility could generate large amounts of infection in the human population? Who would be the most likely to get infected with virus?

Transportation modeling and planning. The human mobility and travel behavior modeling component (BN-ABM) embedded in the Activity-ABM can be used to estimate and forecast travel demand at the level of individual travelers. It can track travel-activity patterns of an individual in a spatially and temporally explicit way, and thus is capable of answering various transportation policy-related questions. For instance, what shall be the effect on peoples' daily travels of a transit expansion in Miami-Dade? Or the effect of land-use intensification such as regional population growth and labor resettlement within the study area? Or price of travel such as fuel cost, parking pricing and poll-road charging?

Promote evidence-based public health policies. A public health intervention is a policy or effort that intends to improve human health in the population level. Informing health-related decision-makings such as introduction of vaccination and implementation of outdoor sprayings using evidence-based approaches has received increasing attentions. The billions of U.S. tax dollars spent on the support of human health in the population level reveals the necessary in choosing the programs and policies that are the most effective to prevent diseases. This dissertation has the potential to informing these decisions using evidence, and serves as evidence to determine the best available program and policy by building various scenarios.

Applicable to a general disease and the interventions. The Susceptible-Exposed-Infectious-Recovered model and the activity and individual-based model built in this dissertation research can be extended to model a general disease and to evaluate the public health interventions associated with the disease. Tian et al. estimated the effect of the transmission control measures for an outbreak of a novel coronavirus [agent of coronavirus disease 2019 (COVID-19)] in China by building a SEIR model (Tian et al., 2020). Their model describes the transmission rate of the COVID-19 virus decreasing proportionally as the control measures, including suspending intracity public transport, closing entertainment venues, banning public gatherings, and banning travel to and from Wuhan City. Our SEIR model also holds extraordinary potential for modeling the COVID-19 outbreaks and evaluating the associated interventions. To achieve this aim, new discovery pathways in measuring the dynamic transmission rates among humans due to the interventions has to be included in the model.

5.2.3 Limitations and Future Works

Although the case study in Miami-Dade County demonstrates the efficacy of the Activity-ABM, there are some components of the Activity-ABM that require further improvements.

Human Daily Mobility and Travel Behavior Modeling Component. In the model, human mobility and travel behavior regarding travel frequency, activity duration and travel duration for unemployed people and children has been originally designed to be continuous, but are trained and leant discretely. Since fewer long-term fixed activities such as work activities and school activities limit their travel routines, unemployed individuals and children have higher flexibility in daily travels and activities and a wider range of time budgets compared to employed individuals and students. Today, most open-source BN platforms such as the *bnlearn* package in R allow modeling human mobility and travel behavior continuously using simple linear Gaussian regression that has poor performance in modeling such ambiguous travels discussed above. Therefore, training continuous BNs for these “flexible” individuals including unemployed people and children by exploring conditional relationships between travel-activity attributes and independent variables rather than building simple regression relationships among them is essential as it improves the accuracy of the human mobility and travel behavior modeling component embedded in the Activity-ABM as well as the dependability of the Activity-ABM. Another important future work is to validate the generated travels and activities in a broader sense. This dissertation research validates the 9 BNs for travel-activity attributes by dividing the survey data into training and testing datasets. The training dataset is to learn the BNs, while the test dataset is to validate the BNs. However, the dependability and accuracy of the generated mobility or how well the generated travels and activities fit into the real world is not examined and discussed here. In review of the literature, three types of validation have been proposed, including: (1) applying model to multiple sites and comparing aggregate simulation results between these sites, (2) aggregate analysis between simulation results and additional datasets e.g. cellphone data and traffic count data, and (3) comparing simulation results and another model (Baqueri et al., 2019; Bassolas et al., 2019; Liu et al., 2018). Integration of these validation frameworks into an activity-based model will aid improving the value of the BN-ABM embedded in the Activity-ABM as well as developing the BN-ABM with high dependability.

Human Prevention Behavior Modeling Component. To generate the individual- and population- level prevention behavior for the study area, this dissertation research randomly determines what prevention an individual uses and where population-level prevention is targeted in a disease outbreak event. Apparently, it is problematic due to the simple "random distribution" assumption. A future, additional survey regarding individual preference in prevention choices and a field dataset regarding sites where community prevention is applied will be crucial to improve the performance of the Activity-ABM. In addition, this dissertation distributes mosquitoes in space based on human population. Within the existing literature, a great deal of additional factors e.g. nutrient competition, land cover and land use, resource attraction, predation climate and socioeconomic status have been proposed to influence the distribution and movement of mosquito (Table 8). Therefore, additional mosquito field data can be collected in future to improve the model.

The Coupling-of Component in the Activity-ABM model. Mathematical methods such as compartmental models and agent-based models have been widely adopted to simulate the transmission of many emerging vector-borne diseases including Dengue and Malaria, and to mitigate risks and impacts by elucidating transmission dynamics of diseases underlying various assumptions and scenarios. This dissertation research develops a novel agent-based model, Activity-ABM (Chapter 4). To evaluate the proposed Activity-ABM, Chapter 3 builds a SEIR compartmental model, and the pros and cons as well as future work of the model are discussed as follows.

Although compartment models are capable of describing the transmission of an epidemic at the population level based on the data accessible at the aggregation scale, these models fail examining the transmission dynamics of the diseases emerging from complicated interaction among multi-species individual agents, agent-environmental interaction, and multi-variate local-scale factors due to the underlying simplified assumptions. Using a simple example, during the outbreak of an epidemic, people often change their behavior in space and time (e.g., avoiding travelling to virus-active areas or applying interventions while outside), the extent to which these changes vary depends on their perception of infection risk. It leads to variation in exposure to virus and ultimate, unexpected infections to various extents in space and time. The classical compartmental models fail to capture the transmission dynamics of an epidemic engaged in these behavioral changes as well as associated interaction dynamics. The Activity-ABM has been developed to address these limitations discussed above. However, this dissertation research conducts a large-scale application which includes millions of agents, and finer-scale updating of their behaviors, actions, locations and complicated interactions with all agents in the same location. It requires intensive computation and memory, and makes model fit and parameter estimation significantly difficult. Although this dissertation research integrates the Python asynchronous multiprocessing into the simulation to improve the computation ability of the Activity-ABM, one simulation i.e. across a 285-day period still takes one week or more. Therefore, exploiting high performance of ABMs, for instance, integration of CyberGIS (Tang and Wang, 2009) shall ultimately be an important future work to develop the Activity-ABM with better performance in model simulation, model fit and parameterization, and scenario tests.

Reference

1. Abbink, P., Stephenson, K. E., & Barouch, D. H. (2018). Zika virus vaccines. Nature Reviews Microbiology, 16(10), 594–600. https://doi.org/10.1038/s41579-018-0039-7

2. Adams, B., & Kapan, D. D. (2009). Man Bites Mosquito: Understanding the Contribution of Human Movement to Vector-Borne Disease Dynamics. PLoS ONE, 4(8), e6763. https://doi.org/10.1371/journal.pone.0006763

3. Agusto, F. B., Del Valle, S. Y., Blayneh, K. W., Ngonghala, C. N., Goncalves, M. J., Li, N., Zhao, R., & Gong, H. (2013). The impact of bed-net use on malaria prevalence. Journal of Theoretical Biology, 320, 58–65. https://doi.org/10.1016/j.jtbi.2012.12.007

4. Ajelli, M., Moise, I. K., Hutchings, T. C. S. G., Brown, S. C., Kumar, N., Johnson, N. F., & Beier, J. C. (2017). Host outdoor exposure variability affects the transmission and spread of Zika virus: Insights for epidemic control. PLOS Neglected Tropical Diseases, 11(9), e0005851. https://doi.org/10.1371/journal.pntd.0005851

5. Alderton, S., Macleod, E. T., Anderson, N. E., Schaten, K., Kuleszo, J., Simuunza, M., Welburn, S. C., & Atkinson, P. M. (2016). A Multi-Host Agent-Based Model for a Zoonotic, Vector-Borne Disease. A Case Study on Trypanosomiasis in Eastern Province, Zambia. PLOS Neglected Tropical Diseases, 10(12), e0005252. https://doi.org/10.1371/journal.pntd.0005252

6. Arentze, T. A., Ettema, D., & Timmermans, H. J. P. (2011). Estimating a model of dynamic activity generation based on one-day observations: Method and results. Transportation Research Part B: Methodological, 45(2), 447–460. https://doi.org/10.1016/j.trb.2010.07.005

7. Armstrong, P., Hennessey, M., Adams, M., Cherry, C., Chiu, S., Harrist, A., Kwit, N., Lewis, L., McGuire, D. O., Oduyebo, T., Russell, K., Talley, P., Tanner, M., & Williams, C. (2016). Travel-Associated Zika Virus Disease Cases Among U.S. Residents—United States, January 2015–February 2016. 65(11), 4.

8. Aron, J. L. (1989). Mathematical modeling of immunity to malaria. Mathematical and Computer Modelling, 12(9), 1180. https://doi.org/10.1016/0895-7177(89)90251-3

9. Auchincloss, A. H., & Diez Roux, A. V. (2008a). A New Tool for Epidemiology: The Usefulness of Dynamic-Agent Models in Understanding Place Effects on Health. American Journal of Epidemiology, 168(1), 1–8. https://doi.org/10.1093/aje/kwn118

10. Auchincloss, A. H., & Diez Roux, A. V. (2008b). A New Tool for Epidemiology: The Usefulness of Dynamic-Agent Models in Understanding Place Effects on

Health. American Journal of Epidemiology, 168(1), 1–8. https://doi.org/10.1093/aje/kwn118

11. Auld, J., & Mohammadian, A. (2012). Activity planning processes in the Agent-based Dynamic Activity Planning and Travel Scheduling (ADAPTS) model. Transportation Research Part A: Policy and Practice, 46(8), 1386–1403. https://doi.org/10.1016/j.tra.2012.05.017

12. Bañuelos, S., Martinez, M. V., Mitchell, C., & Prieto-Langarica, A. (2019). Using mathematical modelling to investigate the effect of the sexual behaviour of asymptomatic individuals and vector control measures on Zika. Letters in Biomathematics, 6(1), 1–19. https://doi.org/10.1080/23737867.2019.1624631

13. Bar-Gera, H., Konduri, K.C., Sana, B., Ye, X. & Pendyala, R.M. (2009). Estimating survey weights with multiple constraints using entropy optimization methods. Proceedings of 88th Annual Meeting of the Transportation Research Board, National Research Council, Washington, D.C.

14. Baqueri, S. F. A., Adnan, M., Kochan, B., & Bellemans, T. (2019). Activity-based model for medium-sized cities considering external activity–travel: Enhancing FEATHERS framework. Future Generation Computer Systems, 96, 51–63. https://doi.org/10.1016/j.future.2019.01.055

15. Barnes, K. I., Chanda, P., & Ab Barnabas, G. (2009). Impact of the large-scale deployment of artemether/lumefantrine on the malaria disease burden in Africa: Case studies of South Africa, Zambia and Ethiopia. Malaria Journal, 8(S1), S8. https://doi.org/10.1186/1475-2875-8-S1-S8

16. Bassolas, A., Ramasco, J. J., Herranz, R., & Cantú-Ros, O. G. (2019). Mobile phone records to feed activity-based travel demand models: MATSim for studying a cordon toll policy in Barcelona. Transportation Research Part A: Policy and Practice, 121, 56–74. https://doi.org/10.1016/j.tra.2018.12.024

17. Beckx, C., Int Panis, L., Arentze, T., Janssens, D., Torfs, R., Broekx, S., & Wets, G. (2009). A dynamic activity-based population modelling approach to evaluate exposure to air pollution: Methods and application to a Dutch urban area. Environmental Impact Assessment Review, 29(3), 179–185. https://doi.org/10.1016/j.eiar.2008.10.001

18. Behjati, S., & Beigy, H. (2018). An order-based algorithm for learning structure of Bayesian networks. In International Conference on Probabilistic Graphical Models(pp. 25-36).

19. Belik, V., Geisel, T., & Brockmann, D. (2011). Natural human mobility patterns and spatial spread of infectious diseases. Physical Review X, 1(1), 011001.

20. Beltrame, A., Zammarchi, L., Zuglian, G., Gobbi, F., Angheben, A., Marchese, V., Degani, M., Mantella, A., Bianchi, L., Montagnani, C., Galli, L., Bassetti, M., Bartoloni, A., & Bisoffi, Z. (2015). Schistosomiasis Screening of Travelers from

Italy with Possible Exposure in Corsica, France. Emerging Infectious Diseases, 21(10), 1887–1889. https://doi.org/10.3201/eid2110.150869

21. Kwan, M. P. (2013). Beyond space (as we knew it): Toward temporally integrated geographies of segregation, health, and accessibility: Space–time integration in geography and GIScience. Annals of the Association of American Geographers, 103(5), 1078-1086.

22. Bhat, C. R. (2005). A multiple discrete–continuous extreme value model: Formulation and application to discretionary time-use decisions. Transportation Research Part B: Methodological, 39(8), 679–707. https://doi.org/10.1016/j.trb.2004.08.003

23. Bhat, C. R., Guo, J. Y., Srinivasan, S., & Sivakumar, A. (2004). Comprehensive econometric microsimulator for daily activity-travel patterns. Transportation Research Record, 1894(1), 57-66.

24. Bhat, C. R., & Koppelman, F. S. (1999). Activity-based modeling of travel demand. In Handbook of transportation Science (pp. 35-61). Springer, Boston, MA.

25. Bhattarai, A., Ali, A. S., Kachur, S. P., Mårtensson, A., Abbas, A. K., Khatib, R., Al-mafazy, A., Ramsan, M., Rotllant, G., Gerstenmaier, J. F., Molteni, F., Abdulla, S., Montgomery, S. M., Kaneko, A., & Björkman, A. (2007). Impact of Artemisinin-Based Combination Therapy and Insecticide-Treated Nets on Malaria Burden in Zanzibar. PLoS Medicine, 4(11), e309. https://doi.org/10.1371/journal.pmed.0040309

26. Bi, K., Chen, Y., (John) Wu, C.-H., & Ben-Arieh, D. (2020). A memetic algorithm for solving optimal control problems of Zika virus epidemic with equilibriums and backward bifurcation analysis. Communications in Nonlinear Science and Numerical Simulation, 84, 105176. https://doi.org/10.1016/j.cnsns.2020.105176

27. Bingenheimer, J. B., & Raudenbush, S. W. (2004). Statistical and Substantive Inferences in Public Health: Issues in the Application of Multilevel Models. Annual Review of Public Health, 25(1), 53–77. https://doi.org/10.1146/annurev.publhealth.25.050503.153925

28. Biswas, S. K., Ghosh, U., & Sarkar, S. (2020). Mathematical model of zika virus dynamics with vector control and sensitivity analysis. Infectious Disease Modelling, 5, 23–41. https://doi.org/10.1016/j.idm.2019.12.001

29. Bogoch, I. I., Brady, O. J., Kraemer, M. U. G., German, M., Creatore, M. I., Kulkarni, M. A., Brownstein, J. S., Mekaru, S. R., Hay, S. I., Groot, E., Watts, A., & Khan, K. (2016). Anticipating the international spread of Zika virus from Brazil. The Lancet, 387(10016), 335–336. https://doi.org/10.1016/S0140-6736(16)00080-5

30. Bonyah, E., Khan, M. A., Okosun, K. O., & Gómez-Aguilar, J. F. (2019). On the co-infection of dengue fever and Zika virus. Optimal Control Applications and

Methods, 40(3), 394–421. https://doi.org/10.1002/oca.2483

31. Bonyah, Ebenezer, Khan, M. A., Okosun, K. O., & Islam, S. (2017). A theoretical model for Zika virus transmission. PLOS ONE, 12(10), e0185540. https://doi.org/10.1371/journal.pone.0185540

32. Bouzid, M., Brainard, J., Hooper, L., & Hunter, P. R. (2016). Public Health Interventions for Aedes Control in the Time of Zikavirus– A Meta-Review on Effectiveness of Vector Control Strategies. PLOS Neglected Tropical Diseases, 10(12), e0005176. https://doi.org/10.1371/journal.pntd.0005176

33. Burattini, M. N., Chen, M., Chow, A., Coutinho, F. A. B., Goh, K. T., Lopez, L. F., Ma, S., & Massad, E. (2008). Modelling the control strategies against dengue in Singapore. Epidemiology and Infection, 136(3), 309–319. https://doi.org/10.1017/S0950268807008667

34. Caminade, C., McIntyre, K. M., & Jones, A. E. (2019). Impact of recent and future climate change on vector-borne diseases: Climate change and vector-borne diseases. Annals of the New York Academy of Sciences, 1436(1), 157–173. https://doi.org/10.1111/nyas.13950

35. Campos, G. S., Bandeira, A. C., & Sardi, S. I. (2015). Zika Virus Outbreak, Bahia, Brazil. Emerging Infectious Diseases, 21(10), 1885–1886. https://doi.org/10.3201/eid2110.150847

36. Cao-Lormeau, V.-M., Blake, A., Mons, S., Lastère, S., Roche, C., Vanhomwegen, J., Dub, T., Baudouin, L., Teissier, A., Larre, P., Vial, A.-L., Decam, C., Choumet, V., Halstead, S. K., Willison, H. J., Musset, L., Manuguerra, J.-C., Despres, P., Fournier, E., … Ghawché, F. (2016). Guillain-Barré Syndrome outbreak associated with Zika virus infection in French Polynesia: A case-control study. The Lancet, 387(10027), 1531–1539. https://doi.org/10.1016/S0140-6736(16)00562-6

37. Carvalho, S. A., da Silva, S. O., & Charret, I. da C. (2019). Mathematical modeling of dengue epidemic: Control methods and vaccination strategies. Theory in Biosciences, 138(2), 223–239. https://doi.org/10.1007/s12064-019-00273-7

38. Cauchemez, S., Besnard, M., Bompard, P., Dub, T., Guillemette-Artur, P., Eyrolle-Guignot, D., Salje, H., Van Kerkhove, M. D., Abadie, V., Garel, C., Fontanet, A., & Mallet, H.-P. (2016). Association between Zika virus and microcephaly in French Polynesia, 2013–15: A retrospective study. The Lancet, 387(10033), 2125–2132. https://doi.org/10.1016/S0140-6736(16)00651-6

39. Cauchemez, S., Valleron, A.-J., Boëlle, P.-Y., Flahault, A., & Ferguson, N. M. (2008). Estimating the impact of school closure on influenza transmission from Sentinel data. Nature, 452(7188), 750–754. https://doi.org/10.1038/nature06732

40. Chen, F. H. (2006). A Susceptible-infected Epidemic Model with Voluntary Vaccinations. Journal of Mathematical Biology, 53(2), 253–272. https://doi.org/10.1007/s00285-006-0006-1

41. Cilliers, P., & Spurrett, D. (1999). Complexity and post-modernism: Understanding complex systems. South African Journal of Philosophy, 18(2), 258–274. https://doi.org/10.1080/02580136.1999.10878187

42. Cirillo, C., & Axhausen, K. W. (2010). Dynamic model of activity-type choice and scheduling. Transportation, 37(1), 15–38. https://doi.org/10.1007/s11116-009-9218-8

43. Clark, A. F., & Doherty, S. T. (2008). Examining the Nature and Extent of the Activity-Travel Preplanning Decision Process. Transportation Research Record: Journal of the Transportation Research Board, 2054(1), 83–92. https://doi.org/10.3141/2054-10

44. Cooley, P. C., Bartsch, S. M., Brown, S. T., Wheaton, W. D., Wagener, D. K., & Lee, B. Y. (2016). Weekends as social distancing and their effect on the spread of influenza. Computational and Mathematical Organization Theory, 22(1), 71–87. https://doi.org/10.1007/s10588-015-9198-5

45. Counotte, M. J., Althaus, C. L., Low, N., & Riou, J. (2019). Impact of age-specific immunity on the timing and burden of the next Zika virus outbreak [Preprint]. Epidemiology. https://doi.org/10.1101/661223

46. Cruvinel, V. R. N., Zolnikov, T. R., Takashi Obara, M., Oliveira, V. T. L. de, Vianna, E. N., Santos, F. S. G. do, Oliveira, K. C. de, & Scott, J. A. (2020). Vector-borne diseases in waste pickers in Brasilia, Brazil. Waste Management, 105, 223–232. https://doi.org/10.1016/j.wasman.2020.02.001

47. Daly, R., Shen, Q., & Aitken, S. (2011). Learning Bayesian networks: Approaches and issues. The Knowledge Engineering Review, 26(2), 99–157. https://doi.org/10.1017/S0269888910000251

48. Davidson, B., Vovsha, P., & Freedman, J. (2011). New Advancements in Activity-Based Models. 20.

49. Davidson, W., Vovsha, P., Freedman, J., & Donnelly, R. (2010). CT-RAMP Family of Activity-Based Models. 15.

50. Department of Natural Sciences (Mathematics), School of Science, Kathmandu University, Kavre, Nepal., Phaijoo, G. R., Gurung., D. B., & Department of Natural Sciences (Mathematics), School of Science, Kathmandu University, Kavre, Nepal. (2016). MATHEMATICAL MODEL ON ANALYSIS OF AWARENESS IN CONTROLLING DENGUE DISEASE. International Journal of Advanced Research, 4(7), 999–1006. https://doi.org/10.21474/IJAR01/1177

51. Depinay, J. M. O., Mbogo, C. M., Killeen, G., Knols, B., Beier, J., Carlson, J., ... & Toure, A. M. (2004). A simulation model of African Anopheles ecology and population dynamics for the analysis of malaria transmission. Malaria journal, 3(1), 29.

52. Dommar, C. J., Lowe, R., Robinson, M., & Rodó, X. (2014). An agent-based model driven by tropical rainfall to understand the spatio-temporal heterogeneity of a chikungunya outbreak. Acta Tropica, 129, 61–73. https://doi.org/10.1016/j.actatropica.2013.08.004

53. Dukic, V., Lopes, H. F., & Polson, N. G. (2012). Tracking epidemics with Google flu trends data and a state-space SEIR model. Journal of the American Statistical Association, 107(500), 1410-1426.

54. De Vries, R., Van Bergen, J. E., De Jong-van den Berg, L. T., Postma, M. J., & PILOT-CT Study Group. (2006). Systematic screening for Chlamydia trachomatis: estimating cost-effectiveness using dynamic modeling and Dutch data. Value in Health, 9(1), 1-11.

55. Eames, K. T. D., Tilston, N. L., Brooks-Pollock, E., & Edmunds, W. J. (2012). Measured Dynamic Social Contact Patterns Explain the Spread of H1N1v Influenza. PLoS Computational Biology, 8(3), e1002425. https://doi.org/10.1371/journal.pcbi.1002425

56. Eames, K. T. D., Tilston, N. L., & Edmunds, W. J. (2011). The impact of school holidays on the social mixing patterns of school children. Epidemics, 3(2), 103–108. https://doi.org/10.1016/j.epidem.2011.03.003

57. Eisen, R. J., Kugeler, K. J., Eisen, L., Beard, C. B., & Paddock, C. D. (2017). Tick-Borne Zoonoses in the United States: Persistent and Emerging Threats to Human Health. ILAR Journal, 58(3), 319–335. https://doi.org/10.1093/ilar/ilx005

58. Eubank, S., Guclu, H., Anil Kumar, V. S., Marathe, M. V., Srinivasan, A., Toroczkai, Z., & Wang, N. (2004). Modelling disease outbreaks in realistic urban social networks. Nature, 429(6988), 180–184. https://doi.org/10.1038/nature02541

59. Ferraris, P., Yssel, H., & Missé, D. (2019). Zika virus infection: An update. Microbes and Infection, 21(8–9), 353–360. https://doi.org/10.1016/j.micinf.2019.04.005

60. Flores, H. A., & O’Neill, S. L. (2018). Controlling vector-borne diseases by releasing modified mosquitoes. Nature Reviews Microbiology, 16(8), 508–518. https://doi.org/10.1038/s41579-018-0025-0

61. Funk, S., Kucharski, A. J., Camacho, A., Eggo, R. M., Yakob, L., Murray, L. M., & Edmunds, W. J. (2016). Comparative Analysis of Dengue and Zika Outbreaks Reveals Differences by Setting and Virus. PLOS Neglected Tropical Diseases, 10(12), e0005173. https://doi.org/10.1371/journal.pntd.0005173

62. Funk, S., Salathé, M., & Jansen, V. A. A. (2010). Modelling the influence of human behaviour on the spread of infectious diseases: A review. Journal of The Royal Society Interface, 7(50), 1247–1256. https://doi.org/10.1098/rsif.2010.0142

63. Galea, S., Riddle, M., & Kaplan, G. A. (2010). Causal thinking and complex system approaches in epidemiology. International Journal of Epidemiology, 39(1), 97–106. https://doi.org/10.1093/ije/dyp296

64. Galea, Sandro, Hall, C., & Kaplan, G. A. (2009). Social epidemiology and complex system dynamic modelling as applied to health behaviour and drug use research. International Journal of Drug Policy, 20(3), 209–216. https://doi.org/10.1016/j.drugpo.2008.08.005

65. Galvani, A. P., & May, R. M. (2005). Dimensions of superspreading. Nature, 438(7066), 293–295. https://doi.org/10.1038/438293a

66. Gámez, J. A., Mateo, J. L., & Puerta, J. M. (2011). Learning Bayesian networks by hill climbing: Efficient methods based on progressive restriction of the neighborhood. Data Mining and Knowledge Discovery, 22(1–2), 106–148. https://doi.org/10.1007/s10618-010-0178-6

67. Gariazzo, C., Pelliccioni, A., & Bogliolo, M. P. (2019). Spatiotemporal analysis of urban mobility using aggregate mobile phone derived presence and demographic data: A case study in the city of Rome, Italy. Data, 4(1), 8.

68. Goswami, N. K., Srivastav, A. K., Ghosh, M., & Shanmukha, B. (2018). Mathematical modeling of zika virus disease with nonlinear incidence and optimal control. Journal of Physics: Conference Series, 1000, 012114. https://doi.org/10.1088/1742-6596/1000/1/012114

69. Goswami, N., & Shanmukha, B. (2020). A Mathematical Analysis of Zika Virus Transmission with Optimal Control Strategies. Computational Methods for Differential Equations.

70. Goulias, K.G. (2004). Transportation planning and modeling, Chapter 29. In Handbook of Transportation Engineering (Editor M. Kutz), McGraw-Hill, New York, NY. Pp. 29.3-29-25.

71. Goulias, K.G. (2005). Trace Data for Activity-based Travel Demand Forecasting Models.

72. Goulias, K. G., Bhat, C. R., Pendyala, R. M., Chen, Y., Paleti, R., Konduri, K. C., Huang, G., & Hu, H.-H. (2011). Simulator of activities, greenhouse emissions, networks, and travel (SimAGENT) in Southern California: Design, implementation, preliminary findings, and integration plans. 2011 IEEE Forum on Integrated and Sustainable Transportation Systems, 164–169. https://doi.org/10.1109/FISTS.2011.5973624

73. Greenland, S. (2006). Bayesian perspectives for epidemiological research: I. Foundations and basic methods. International Journal of Epidemiology, 35(3), 765–775. https://doi.org/10.1093/ije/dyi312

74. Griffin, J. T., Hollingsworth, T. D., Okell, L. C., Churcher, T. S., White, M., Hinsley,

W., Bousema, T., Drakeley, C. J., Ferguson, N. M., Basáñez, M.-G., & Ghani, A. C. (2010). Reducing Plasmodium falciparum Malaria Transmission in Africa: A Model-Based Evaluation of Intervention Strategies. PLoS Medicine, 7(8), e1000324. https://doi.org/10.1371/journal.pmed.1000324

75. Griffiths, F., & Sweeney, K. (2002). Complexity and Healthcare: An Introduction. Radcliffe Publishing Ltd.

76. Grillet, M. E., Hernández-Villena, J. V., Llewellyn, M. S., Paniz-Mondolfi, A. E., Tami, A., Vincenti-Gonzalez, M. F., Marquez, M., Mogollon-Mendoza, A. C., Hernandez-Pereira, C. E., Plaza-Morr, J. D., Blohm, G., Grijalva, M. J., Costales, J. A., Ferguson, H. M., Schwabl, P., Hernandez-Castro, L. E., Lamberton, P. H. L., Streicker, D. G., Haydon, D. T., … Alarcón-de Noya, B. (2019). Venezuela's humanitarian crisis, resurgence of vector-borne diseases, and implications for spillover in the region. The Lancet Infectious Diseases, 19(5), e149–e161. https://doi.org/10.1016/S1473-3099(18)30757-6

77. Grimm, V., Berger, U., Bastiansen, F., Eliassen, S., Ginot, V., Giske, J., ... & Huth, A. (2006). A standard protocol for describing individual-based and agent-based models. Ecological modelling, 198(1-2), 115-126.

78. Grimm, V., Berger, U., DeAngelis, D. L., Polhill, J. G., Giske, J., & Railsback, S. F. (2010). The ODD protocol: a review and first update. Ecological modelling, 221(23), 2760-2768.

79. Gu, W., & Novak, R. J. (2009). Agent-based modelling of mosquito foraging behaviour for malaria control. Transactions of the Royal Society of Tropical Medicine and Hygiene, 103(11), 1105–1112. https://doi.org/10.1016/j.trstmh.2009.01.006

80. Gubler, D. (1998). Resurgent Vector-Borne Diseases as a Global Health Problem. Emerging Infectious Diseases, 4(3), 442–450. https://doi.org/10.3201/eid0403.980326

81. Habib, K. M. N., & Miller, E. J. (2008). Modelling daily activity program generation considering within-day and day-to-day dynamics in activity-travel behaviour. Transportation, 35(4), 467–484. https://doi.org/10.1007/s11116-008-9166-8

82. Hägerstrand, T. (1970). What about people in regional science?. Papers of the Regional Science Association, 24, 7-21.

83. Hay, S. I., Sinka, M. E., Okara, R. M., Kabaria, C. W., Mbithi, P. M., Tago, C. C., Benz, D., Gething, P. W., Howes, R. E., Patil, A. P., Temperley, W. H., Bangs, M. J., Chareonviriyaphap, T., Elyazar, I. R. F., Harbach, R. E., Hemingway, J., Manguin, S., Mbogo, C. M., Rubio-Palis, Y., & Godfray, H. C. J. (2010). Developing Global Maps of the Dominant Anopheles Vectors of Human Malaria. PLoS Medicine, 7(2), e1000209. https://doi.org/10.1371/journal.pmed.1000209

84. Hayes, E. B. (2009). Zika Virus Outside Africa. Emerging Infectious Diseases, 15(9), 1347–1350. https://doi.org/10.3201/eid1509.090442

85. Hens, N., Ayele, G. M., Goeyvaerts, N., Aerts, M., Mossong, J., Edmunds, J. W., & Beutels, P. (2009). Estimating the impact of school closure on social mixing behaviour and the transmission of close contact infections in eight European countries. BMC Infectious Diseases, 9(1), 187. https://doi.org/10.1186/1471-2334-9-187

86. Hernán, M. Á., Brumback, B., & Robins, J. M. (2000). Marginal Structural Models to Estimate the Causal Effect of Zidovudine on the Survival of HIV-Positive Men: Epidemiology, 11(5), 561–570. https://doi.org/10.1097/00001648-200009000-00012

87. Heukelbach, J., & Werneck, G. L. (2016). Surveillance of Zika virus infection and microcephaly in Brazil. The Lancet, 388(10047), 846–847. https://doi.org/10.1016/S0140-6736(16)30931-X

88. Hunter, P. (2016). Challenges and options for disease vector control: The outbreak of Zika virus in South America and increasing insecticide resistance among mosquitoes have rekindled efforts for controlling disease vectors. EMBO Reports, 17(10), 1370–1373. https://doi.org/10.15252/embr.201643233

89. Jacintho, L. F., Batista, A. F., Ruas, T. L., Marietto, M. G., & Silva, F. A. (2010). An agent-based model for the spread of the Dengue fever: a swarm platform simulation approach. In Proceedings of the 2010 Spring Simulation Multiconference(pp. 1-8).

90. Jindal, A., & Rao, S. (2017). Agent-based modeling and simulation of mosquito-borne disease transmission. In Proceedings of the 16th Conference on Autonomous Agents and MultiAgent Systems (pp. 426-435).

91. Kama, M., Aubry, M., Naivalu, T., Vanhomwegen, J., Mariteragi-Helle, T., Teissier, A., Paoaafaite, T., Hué, S., Hibberd, M. L., Manuguerra, J.-C., Christi, K., Watson, C. H., Nilles, E. J., Aaskov, J., Lau, C. L., Musso, D., Kucharski, A. J., & Cao-Lormeau, V.-M. (2019). Sustained Low-Level Transmission of Zika and Chikungunya Viruses after Emergence in the Fiji Islands. Emerging Infectious Diseases, 25(8), 1535–1538. https://doi.org/10.3201/eid2508.180524

92. Kang, C., Gao, S., Lin, X., Xiao, Y., Yuan, Y., Liu, Y., & Ma, X. (2010, June). Analyzing and geo-visualizing individual human mobility patterns using mobile call records. In Geoinformatics, 2010 18th International Conference on (pp. 1-7). IEEE.

93. Killeen, G. F., & Smith, T. A. (2007). Exploring the contributions of bed nets, cattle, insecticides and excitorepellency to malaria control: a deterministic model of mosquito host-seeking behaviour and mortality. Transactions of the Royal Society of Tropical Medicine and Hygiene, 101(9), 867-880.

94. Kim, S., & Kim, Y. (2019). Spatially Filtered Multilevel Analysis on Spatial Determinants for Malaria Occurrence in Korea. International Journal of Environmental Research and Public Health, 16(7), 1250. https://doi.org/10.3390/ijerph16071250

95. Kindhauser, M. K., Allen, T., Frank, V., Santhana, R. S., & Dye, C. (2016). Zika: The origin and spread of a mosquito-borne virus. Bulletin of the World Health Organization, 94(9), 675-686C. https://doi.org/10.2471/BLT.16.171082

96. Kiszewski, A. E., & Darling, S. T. (2010). Estimating a mosquito repellent's potential to reduce malaria in communities. J VECTOR BORNE DIS, 5.

97. Kitamura, R., & Fujii, S. (1998). Two computational process models of activity-travel behavior. Theoretical foundations of travel choice modeling, 251-279.

98. Kleinschmidt, I., La Grange, J. J. P., Ridl, F. C., Barnes, K. I., Durrheim, D. N., Maharaj, R., Maartens, F., Kunene, S., Barreto, A., Sharp, B. L., Mthembu, J. D., Seocharan, I., Morris, N., Martin, C. L., & Streat, E. (2007). SEVEN YEARS OF REGIONAL MALARIA CONTROL COLLABORATION—MOZAMBIQUE, SOUTH AFRICA, AND SWAZILAND. The American Journal of Tropical Medicine and Hygiene, 76(1), 42–47. https://doi.org/10.4269/ajtmh.2007.76.42

99. Knerer, G., Currie, C. S. M., & Brailsford, S. C. (2015). Impact of combined vector-control and vaccination strategies on transmission dynamics of dengue fever: A model-based analysis. Health Care Management Science, 18(2), 205–217. https://doi.org/10.1007/s10729-013-9263-x

100. Konduri, K.C., D. You, Garikapati, V.M., & Pendyala, R.M. (2016). Application of an Enhanced Population Synthesis Model that Accommodates Controls at Multiple Geographic Resolutions. Transportation Research Record, Journal of the Transportation Research Board (forthcoming).

101. Kraemer, M. U., Sinka, M. E., Duda, K. A., Mylne, A. Q., Shearer, F. M., Barker, C. M., Moore, C. G., Carvalho, R. G., Coelho, G. E., Van Bortel, W., Hendrickx, G., Schaffner, F., Elyazar, I. R., Teng, H.-J., Brady, O. J., Messina, J. P., Pigott, D. M., Scott, T. W., Smith, D. L., … Hay, S. I. (2015). The global distribution of the arbovirus vectors Aedes aegypti and Ae. Albopictus. ELife, 4, e08347. https://doi.org/10.7554/eLife.08347

102. Kucharski, A. J., Funk, S., Eggo, R. M., Mallet, H.-P., Edmunds, W. J., & Nilles, E. J. (2016). Transmission Dynamics of Zika Virus in Island Populations: A Modelling Analysis of the 2013–14 French Polynesia Outbreak. PLOS Neglected Tropical Diseases, 10(5), e0004726. https://doi.org/10.1371/journal.pntd.0004726

103. Kwan, M.-P. (2009). From place-based to people-based exposure measures. Social Science & Medicine, 69(9), 1311–1313. https://doi.org/10.1016/j.socscimed.2009.07.013

104. Larrañaga, P., Karshenas, H., Bielza, C., & Santana, R. (2013). A review on

evolutionary algorithms in Bayesian network learning and inference tasks. Information Sciences, 233, 109–125. https://doi.org/10.1016/j.ins.2012.12.051

105. Laurila, J. K., Gatica-Perez, D., Aad, I., Bornet, O., Do, T. M. T., Dousse, O., et al. (2012). The mobile data challenge: Big data for mobile computing research. In Pervasive Computing (No. EPFL-CONF-192489).

106. Lessler, J., Ott, C. T., Carcelen, A. C., Konikoff, J. M., Williamson, J., Bi, Q., ... & Chaisson, L. H. (2016). Times to key events in Zika virus infection and implications for blood donation: a systematic review. Bulletin of the World Health Organization, 94(11), 841.

107. Liljeros, F., Edling, C. R., & Amaral, L. A. N. (2003). Sexual networks: implications for the transmission of sexually transmitted infections. Microbes and infection, 5(2), 189-196.

108. Liu, F., Gao, Z., Jia, B., Yan, X., Janssens, D., & Wets, G. (2018). Validating Activity-Based Travel Demand Models Using Mobile Phone Data. In M. Khatib & N. Salman (Eds.), Mobile Computing—Technology and Applications. InTech. https://doi.org/10.5772/intechopen.75810

109. Mallet, H.P., Vial, A.L., & Musso, D. B. (2015). epidémie a virus ZIKA en Polynésie Francaise 2013–2014. Bulletin d'Information Sanitaires, Epidemiologiques et Statistiques.

110. Majumder, S., Rahman, T., Sigamani, A., & Hossan, S. (2020). Therapeutic and Alternate Preventive Measures to Combat Dengue Epidemic in the Indian Subcontinent. 16.

111. Malayath, M., & Verma, A. (2013). Activity based travel demand models as a tool for evaluating sustainable transportation policies. Research in Transportation Economics, 38(1), 45–66. https://doi.org/10.1016/j.retrec.2012.05.010

112. Malone, R. W., Homan, J., Callahan, M. V., Glasspool-Malone, J., Damodaran, L., Schneider, A. D. B., Zimler, R., Talton, J., Cobb, R. R., Ruzic, I., Smith-Gagen, J., Janies, D., Wilson, J., & Zika Response Working Group. (2016). Zika Virus: Medical Countermeasure Development Challenges. PLOS Neglected Tropical Diseases, 10(3), e0004530. https://doi.org/10.1371/journal.pntd.0004530

113. Manore, C. A., Hickmann, K. S., Hyman, J. M., Foppa, I. M., Davis, J. K., Wesson, D. M., & Mores, C. N. (2015). A network-patch methodology for adapting agent-based models for directly transmitted disease to mosquito-borne disease. Journal of Biological Dynamics, 9(1), 52–72. https://doi.org/10.1080/17513758.2015.1005698

114. Mao, L. (2011). Agent-based simulation for weekend-extension strategies to mitigate influenza outbreaks. BMC Public Health, 11(1), 522. https://doi.org/10.1186/1471-2458-11-522

115. Marcos-Marcos, J., Olry de Labry-Lima, A., Toro-Cardenas, S., Lacasaña, M., Degroote, S., Ridde, V., & Bermudez-Tamayo, C. (2018). Impact, economic evaluation, and sustainability of integrated vector management in urban settings to prevent vector-borne diseases: A scoping review. Infectious Diseases of Poverty, 7(1), 83. https://doi.org/10.1186/s40249-018-0464-x

116. Massad, E., Tan, S.-H., Khan, K., & Wilder-Smith, A. (2016). Estimated Zika virus importations to Europe by travellers from Brazil. Global Health Action, 9(1), 31669. https://doi.org/10.3402/gha.v9.31669

117. McNally, M. G. (2000). The four step model. Handbook of transport modelling, 1, 35-41.

118. McNally, M. G., & Rindt, C. R. (2000). The activity-based approach. Handbook of transport modelling, 1, 35-52.

119. Meloni, S., Perra, N., Arenas, A., Gómez, S., Moreno, Y., & Vespignani, A. (2011). Modeling human mobility responses to the large-scale spreading of infectious diseases. Scientific reports, 1, 62.

120. Messina, J. P., Kraemer, M. U., Brady, O. J., Pigott, D. M., Shearer, F. M., Weiss, D. J., Golding, N., Ruktanonchai, C. W., Gething, P. W., Cohn, E., Brownstein, J. S., Khan, K., Tatem, A. J., Jaenisch, T., Murray, C. J., Marinho, F., Scott, T. W., & Hay, S. I. (2016). Mapping global environmental suitability for Zika virus. ELife, 5, e15272. https://doi.org/10.7554/eLife.15272

121. Miller, E. J., & Roorda, M. J. (2003). Prototype model of household activity-travel scheduling. Transportation Research Record, 1831(1), 114-121.

122. Miller, H. J. (2005). A Measurement Theory for Time Geography. Geographical Analysis, 37(1), 17–45. https://doi.org/10.1111/j.1538-4632.2005.00575.x

123. Mills, C. E., Robins, J. M., & Lipsitch, M. (2004). Transmissibility of 1918 pandemic influenza. Nature, 432(7019), 904.

124. Miyaoka, T. Y., Lenhart, S., & Meyer, J. F. C. A. (2019). Optimal control of vaccination in a vector-borne reaction–diffusion model applied to Zika virus. Journal of Mathematical Biology, 79(3), 1077–1104. https://doi.org/10.1007/s00285-019-01390-z

125. Mlakar, J., Korva, M., Tul, N., Popović, M., Poljšak-Prijatelj, M., Mraz, J., Kolenc, M., Resman Rus, K., Vesnaver Vipotnik, T., Fabjan Vodušek, V., Vizjak, A., Pižem, J., Petrovec, M., & Avšič Županc, T. (2016). Zika Virus Associated with Microcephaly. New England Journal of Medicine, 374(10), 951–958. https://doi.org/10.1056/NEJMoa1600651

126. Mniszewski, S. M., Manore, C. A., Bryan, C., Del Valle, S. Y., & Roberts, D. (2014). Towards a hybrid agent-based model for mosquito borne disease. In Summer Computer Simulation Conference:(SCSC 2014): 2014 Summer Simulation Multi-

Conference: Monterey, California, USA, 6-10 July 2014. Summer Computer Simulation Conference (2014: Monterey, Calif.) (Vol. 2014). NIH Public Access.

127. Monaghan, A. J., Morin, C. W., Steinhoff, D. F., Wilhelmi, O., Hayden, M., Quattrochi, D. A., Reiskind, M., Lloyd, A. L., Smith, K., Schmidt, C. A., Scalf, P. E., & Ernst, K. (2016). On the Seasonal Occurrence and Abundance of the Zika Virus Vector Mosquito Aedes Aegypti in the Contiguous United States. PLoS Currents. https://doi.org/10.1371/currents.outbreaks.50dfc7f46798675fc63e7d7da563da76

128. Mulyani, H., Djatna, T., & Sitanggang, I. S. (2017). Agent Based Modeling on Dynamic Spreading Dengue Fever Epidemic. TELKOMNIKA (Telecommunication Computing Electronics and Control), 15(3), 1380. https://doi.org/10.12928/telkomnika.v15i3.4511

129. Musso, D., Cao-Lormeau, V. M., & Gubler, D. J. (2015). Zika virus: Following the path of dengue and chikungunya? The Lancet, 386(9990), 243–244. https://doi.org/10.1016/S0140-6736(15)61273-9

130. Mysorekar, I. U., & Diamond, M. S. (2016). Modeling Zika Virus Infection in Pregnancy. New England Journal of Medicine, 375(5), 481–484. https://doi.org/10.1056/NEJMcibr1605445

131. Nawawi, J., & Aldila, D. (2020). Mathematical assessment on the effect of hospitalization in dengue intervention. 030002. https://doi.org/10.1063/5.0012142

132. Ndii, M. Z. (2020). Modelling the Use of Vaccine and Wolbachia on Dengue Transmission Dynamics. Tropical Medicine and Infectious Disease, 5(2), 78. https://doi.org/10.3390/tropicalmed5020078

133. N’Dri, B. P., Heitz-Tokpa, K., Chouaïbou, M., Raso, G., Koffi, A. J., Coulibaly, J. T., Yapi, R. B., Müller, P., & Utzinger, J. (2020). Use of Insecticides in Agriculture and the Prevention of Vector-Borne Diseases: Population Knowledge, Attitudes, Practices and Beliefs in Elibou, South Côte d’Ivoire. Tropical Medicine and Infectious Disease, 5(1), 36. https://doi.org/10.3390/tropicalmed5010036

134. Ngonghala, C. N., Ryan, S. J., Tesla, B., Demakovskys, L. R., Mordecai, E. A., Murdock, C. C., & Bonds, M. H. (2019). Effects of Temperature on Zika Dynamics and Control [Preprint]. Ecology. https://doi.org/10.1101/855072

135. Nurul Habib, K. M., Morency, C., & Trépanier, M. (2012). Integrating parking behaviour in activity-based travel demand modelling: Investigation of the relationship between parking type choice and activity scheduling process. Transportation Research Part A: Policy and Practice, 46(1), 154–166. https://doi.org/10.1016/j.tra.2011.09.014

136. O’Meara, W. P., Bejon, P., Mwangi, T. W., Okiro, E. A., Peshu, N., Snow, R. W., Newton, C. R., & Marsh, K. (2008). Effect of a fall in malaria transmission on morbidity and mortality in Kilifi, Kenya. The Lancet, 372(9649), 1555–1562.

https://doi.org/10.1016/S0140-6736(08)61655-4

137. Otero, M., Barmak, D. H., Dorso, C. O., Solari, H. G., & Natiello, M. A. (2011). Modeling dengue outbreaks. Mathematical Biosciences, 232(2), 87–95. https://doi.org/10.1016/j.mbs.2011.04.006

138. Otero, M. J., Barmak, D. H., Dorso, C. O., Solari, H. G., & Natiello, M. A. (2010). Modeling Dengue Outbreaks. ArXiv:1012.1281 [Physics, q-Bio]. http://arxiv.org/abs/1012.1281

139. Padmanabhan, P., Seshaiyer, P., & Castillo-Chavez, C. (2017). Mathematical modeling, analysis and simulation of the spread of Zika with influence of sexual transmission and preventive measures. Letters in Biomathematics, 4(1), 148–166. https://doi.org/10.1080/23737867.2017.1319746

140. Pendyala, R. M., Kitamura, R., Kikuchi, A., Yamamoto, T., & Fujii, S. (2005). Florida activity mobility simulator: overview and preliminary validation results. Transportation Research Record, 1921(1), 123-130.

141. Perez, L., & Dragicevic, S. (2009). An agent-based approach for modeling dynamics of contagious disease spread. International Journal of Health Geographics, 8(1), 50. https://doi.org/10.1186/1476-072X-8-50

142. Perisic, A., & Bauch, C. T. (2009a). Social Contact Networks and Disease Eradicability under Voluntary Vaccination. PLoS Computational Biology, 5(2), e1000280. https://doi.org/10.1371/journal.pcbi.1000280

143. Perisic, A., & Bauch, C. T. (2009b). A simulation analysis to characterize the dynamics of vaccinating behaviour on contact networks. BMC Infectious Diseases, 9(1), 77. https://doi.org/10.1186/1471-2334-9-77

144. Perkins, T. A., Scott, T. W., Le Menach, A., & Smith, D. L. (2013). Heterogeneity, Mixing, and the Spatial Scales of Mosquito-Borne Pathogen Transmission. PLoS Computational Biology, 9(12), e1003327. https://doi.org/10.1371/journal.pcbi.1003327

145. Petersen, L. R., Beard, C. B., & Visser, S. N. (2019). Combatting the Increasing Threat of Vector-Borne Disease in the United States with a National Vector-Borne Disease Prevention and Control System. The American Journal of Tropical Medicine and Hygiene, 100(2), 242–245. https://doi.org/10.4269/ajtmh.18-0841

146. Petersen, L. R., Jamieson, D. J., Powers, A. M., & Honein, M. A. (2016). Zika Virus. New England Journal of Medicine, 374(16), 1552–1563. https://doi.org/10.1056/NEJMra1602113

147. Pierson, T. C., & Diamond, M. S. (2018). The emergence of Zika virus and its new clinical syndromes. Nature, 560(7720), 573–581. https://doi.org/10.1038/s41586-018-0446-y

148. Pribyl, O., & Goulias, K.G. (2005). Simulation of daily activity patterns. Chapter 3 in Progress in Activity-Based Analysis (Ed. Harry Timmermans), Elsevier, pp. 43-65.

149. Rainham, D., McDowell, I., Krewski, D., & Sawada, M. (2010). Conceptualizing the healthscape: Contributions of time geography, location technologies and spatial ecology to place and health research. Social Science & Medicine, 70(5), 668–676. https://doi.org/10.1016/j.socscimed.2009.10.035

150. Rasmussen, S. A., Jamieson, D. J., Honein, M. A., & Petersen, L. R. (2016). Zika Virus and Birth Defects—Reviewing the Evidence for Causality. New England Journal of Medicine, 374(20), 1981–1987. https://doi.org/10.1056/NEJMsr1604338

151. Rather, I. A., Kumar, S., Bajpai, V. K., Lim, J., & Park, Y.-H. (2017). Prevention and Control Strategies to Counter ZIKA Epidemic. Frontiers in Microbiology, 8. https://doi.org/10.3389/fmicb.2017.00305

152. Reiner, R. C., Stoddard, S. T., & Scott, T. W. (2014). Socially structured human movement shapes dengue transmission despite the diffusive effect of mosquito dispersal. Epidemics, 6, 30–36. https://doi.org/10.1016/j.epidem.2013.12.003

153. Reiskind, M., Lloyd, A. L., Smith, K., Schmidt, C. A., Scalf, P. E., & Ernst, K. (2016). On the Seasonal Occurrence and Abundance of the Zika Virus Vector Mosquito Aedes Aegypti in the Contiguous United States. PLoS currents, 8.

154. Richardson, D. B., Volkow, N. D., Kwan, M.-P., Kaplan, R. M., Goodchild, M. F., & Croyle, R. T. (2013). Spatial Turn in Health Research. Science, 339(6126), 1390–1392. https://doi.org/10.1126/science.1232257

155. Rodriguez-Morales, A. J., García-Loaiza, C. J., Galindo-Marquez, M. L., Sabogal-Roman, J. A., Marin-Loaiza, S., Lozada-Riascos, C. O., & Diaz-Quijano, F. A. (2016). Zika infection GIS-based mapping suggest high transmission activity in the border area of La Guajira, Colombia, a northeastern coast Caribbean department, 2015–2016: Implications for public health, migration and travel. Travel Medicine and Infectious Disease, 14(3), 286–288. https://doi.org/10.1016/j.tmaid.2016.03.018

156. Ruiz, T., & Roorda, M. J. (2008). Analysis of Planning Decisions during the Activity-Scheduling Process. Transportation Research Record: Journal of the Transportation Research Board, 2054(1), 46–55. https://doi.org/10.3141/2054-06

157. Samy, A. M., van de Sande, W. W. J., Fahal, A. H., & Peterson, A. T. (2014). Mapping the Potential Risk of Mycetoma Infection in Sudan and South Sudan Using Ecological Niche Modeling. PLoS Neglected Tropical Diseases, 8(10), e3250. https://doi.org/10.1371/journal.pntd.0003250

158. Scherr, W., Joshi, C., Manser, P., Frischknecht, N., & Métrailler, D. (2019). An Activity-based Travel Demand Model of Switzerland Based on Choices and

Constraints. 13.

159. Shanks, G. D., Hay, S. I., Omumbo, J. A., & Snow, R. W. (2005). Malaria in Kenya's Western Highlands. Emerging Infectious Diseases, 11(9), 1425–1432. https://doi.org/10.3201/eid1109.041131

160. Shaw, W. R., & Catteruccia, F. (2019). Vector biology meets disease control: Using basic research to fight vector-borne diseases. Nature Microbiology, 4(1), 20–34. https://doi.org/10.1038/s41564-018-0214-7

161. Shiftan, Y., & Ben-Akiva, M. (2011). A practical policy-sensitive, activity-based, travel-demand model. The Annals of Regional Science, 47(3), 517–541. https://doi.org/10.1007/s00168-010-0393-5

162. Singh, R. K., Dhama, K., Khandia, R., Munjal, A., Karthik, K., Tiwari, R., Chakraborty, S., Malik, Y. S., & Bueno-Mar í R. (2018). Prevention and Control Strategies to Counter Zika Virus, a Special Focus on Intervention Approaches against Vector Mosquitoes—Current Updates. Frontiers in Microbiology, 9, 87. https://doi.org/10.3389/fmicb.2018.00087

163. Smith, D. L., McKenzie, F. E., Snow, R. W., & Hay, S. I. (2007). Revisiting the Basic Reproductive Number for Malaria and Its Implications for Malaria Control. PLoS Biology, 5(3), e42. https://doi.org/10.1371/journal.pbio.0050042

164. Song, H., Tian, D., Shan, C., 1 Complex Systems Research Center, Shanxi University, Taiyuan 030006, China, 2 Shanxi Key Laboratory of Mathematical Techniques and Big Data Analysis on disease Control and Prevention, Shanxi University, Taiyuan 030006, China, & 3 Department of Mathematics and Statistics, The University of Toledo, Toledo 43606, USA. (2020). Modeling the effect of temperature on dengue virus transmission with periodic delay differential equations. Mathematical Biosciences and Engineering, 17(4), 4147–4164. https://doi.org/10.3934/mbe.2020230

165. Soulakellis, N., Kontos, T., Sifakis, N., & Iossifidis, C. (2019). Aerosol Optical Thickness Mapper (AOT-Mapper): A Geo-Information Software for AOT Mapping at Urban Scale Using Landsat TM or ETM+ Satellite Images. In H. Briassoulis, D. Kavroudakis, & N. Soulakellis (Eds.), The Practice of Spatial Analysis (pp. 343–358). Springer International Publishing. https://doi.org/10.1007/978-3-319-89806-3_16

166. Stoddard, S. T., Forshey, B. M., Morrison, A. C., Paz-Soldan, V. A., Vazquez-Prokopec, G. M., Astete, H., Reiner, R. C., Vilcarromero, S., Elder, J. P., Halsey, E. S., Kochel, T. J., Kitron, U., & Scott, T. W. (2013). House-to-house human movement drives dengue virus transmission. Proceedings of the National Academy of Sciences, 110(3), 994–999. https://doi.org/10.1073/pnas.1213349110

167. Stoddard, Steven T., Morrison, A. C., Vazquez-Prokopec, G. M., Paz Soldan, V., Kochel, T. J., Kitron, U., Elder, J. P., & Scott, T. W. (2009). The Role of Human Movement in the Transmission of Vector-Borne Pathogens. PLoS Neglected Tropical Diseases, 3(7), e481. https://doi.org/10.1371/journal.pntd.0000481

168. Swei, A., Couper, L. I., Coffey, L. L., Kapan, D., & Bennett, S. (2020). Patterns, Drivers, and Challenges of Vector-Borne Disease Emergence. Vector-Borne and Zoonotic Diseases, 20(3), 159–170. https://doi.org/10.1089/vbz.2018.2432

169. Tang, W., & Wang, S. (2009). HPABM: A hierarchical parallel simulation framework for spatially-explicit agent-based models. Transactions in GIS, 13(3), 315-333.
170. Tatem, A. J., Huang, Z., Narib, C., Kumar, U., Kandula, D., Pindolia, D. K., ... & Lourenço, C. (2014). Integrating rapid risk mapping and mobile phone call record data for strategic malaria elimination planning. Malaria journal, 13(1), 52.

171. Tian, H., Liu, Y., Li, Y., Wu, C.-H., Chen, B., Kraemer, M. U. G., Li, B., Cai, J., Xu, B., Yang, Q., Wang, B., Yang, P., Cui, Y., Song, Y., Zheng, P., Wang, Q., Bjornstad, O. N., Yang, R., Grenfell, B. T., … Dye, C. (2020). An investigation of transmission control measures during the first 50 days of the COVID-19 epidemic in China. Science, 368(6491), 638–642. https://doi.org/10.1126/science.abb6105

172. Matheson, T. S., Satterthwaite, B., & Callender Highlander, H. (2017). Modeling the spread of the Zika virus at the 2016 olympics. Spora: A Journal of Biomathematics, 3(1), 3.

173. van den Berg, H., Manuweera, G., & Konradsen, F. (2017). Global trends in the production and use of DDT for control of malaria and other vector-borne diseases. Malaria Journal, 16(1), 401. https://doi.org/10.1186/s12936-017-2050-2

174. Van den Driessche, P., & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical biosciences, 180(1-2), 29-48.

175. Vanwambeke, S. O., Van Benthem, B. H., Khantikul, N., Burghoorn-Maas, C., Panart, K., Oskam, L., ... & Somboon, P. (2006). Multi-level analyses of spatial and temporal determinants for dengue infection. International journal of health geographics, 5(1), 5.

176. Veldhuisen, J., Timmermans, H., & Kapoen, L. (2000). RAMBLAS: A Regional Planning Model Based on the Microsimulation of Daily Activity Travel Patterns. Environment and Planning A: Economy and Space, 32(3), 427–443. https://doi.org/10.1068/a325

177. Vianna, P., Gomes, J. do A., Boquett, J. A., Fraga, L. R., Schuch, J. B., Vianna, F. S. L., & Schuler-Faccini, L. (2018). Zika Virus as a Possible Risk Factor for Autism Spectrum Disorder: Neuroimmunological Aspects. Neuroimmunomodulation, 25(5–6), 320–327. https://doi.org/10.1159/000495660

178. Wesolowski, A., Eagle, N., Tatem, A. J., Smith, D. L., Noor, A. M., Snow, R. W., & Buckee, C. O. (2012). Quantifying the Impact of Human Mobility on Malaria. Science, 338(6104), 267–270. https://doi.org/10.1126/science.1223467

179. Vovsha, P., Bradley, M., & Bowman, J. L. (2005). Activity-based travel forecasting models in the United States: progress since 1995 and prospects for the future.

180. Vynnycky, E., & White, R. (2010). An introduction to infectious disease modelling. Oxford University Press.

181. Wilson, A. L., Courtenay, O., Kelly-Hope, L. A., Scott, T. W., Takken, W., Torr, S. J., & Lindsay, S. W. (2020). The importance of vector control for the control and elimination of vector-borne diseases. PLOS Neglected Tropical Diseases, 14(1), e0007831. https://doi.org/10.1371/journal.pntd.0007831

182. Woolhouse, M. E. J., Dye, C., Etard, J.-F., Smith, T., Charlwood, J. D., Garnett, G. P., Hagan, P., Hii, J. L. K., Ndhlovu, P. D., Quinnell, R. J., Watts, C. H., Chandiwana, S. K., & Anderson, R. M. (1997). Heterogeneities in the transmission of infectious agents: Implications for the design of control programs. Proceedings of the National Academy of Sciences, 94(1), 338–342. https://doi.org/10.1073/pnas.94.1.338

183. Yang, Hyun M. (2000). Malaria transmission model for different levels of acquired immunity and temperature-dependent parameters (vector). Revista de Saúde Pública, 34(3), 223–231. https://doi.org/10.1590/S0034-89102000000300003

184. Yang, Hyun Mo, & Ferreira, C. P. (2008). Assessing the effects of vector control on dengue transmission. Applied Mathematics and Computation, 198(1), 401–413. https://doi.org/10.1016/j.amc.2007.08.046

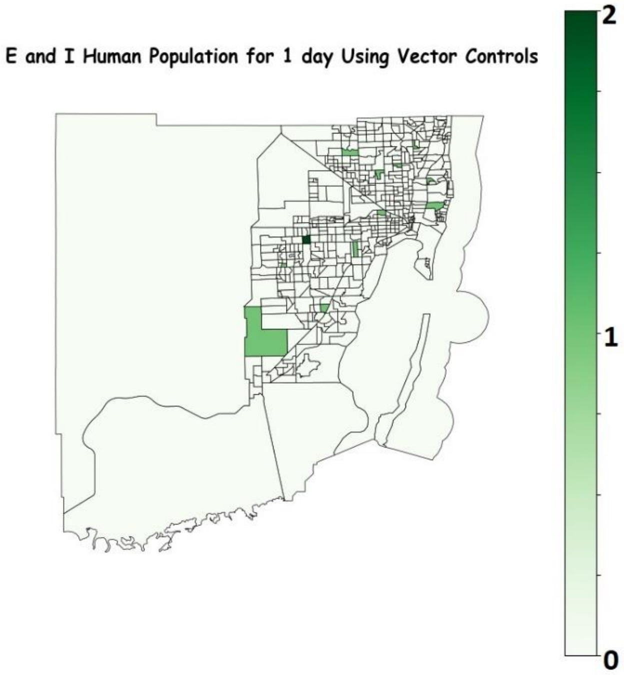
185. Yasmin, F., Morency, C., & Roorda, M. J. (2015). Assessment of spatial transferability of an activity-based model, TASHA. Transportation Research Part A: Policy and Practice, 78, 200–213. https://doi.org/10.1016/j.tra.2015.05.008

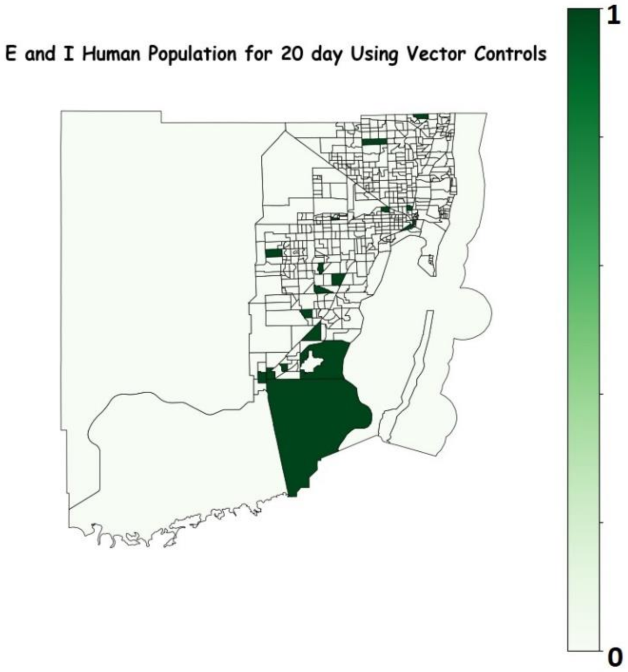
186. Ye, X., Konduri, K., Pendyala, R. M., Sana, B., & Waddell, P. (2009, January). A methodology to match distributions of both household and person attributes in the generation of synthetic populations. In 88th Annual Meeting of the Transportation Research Board, Washington, DC.

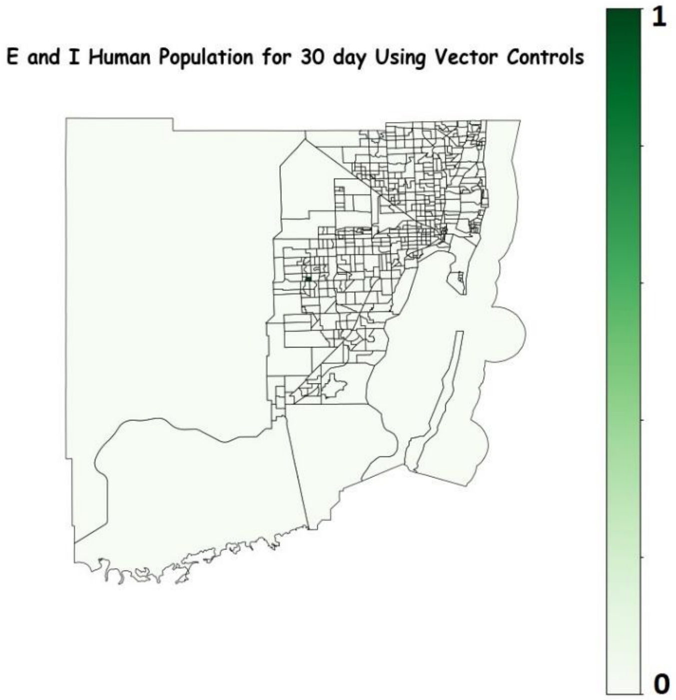
187. Yuan, C., & Malone, B. (2012). An improved admissible heuristic for learning optimal Bayesian networks. arXiv preprint arXiv:1210.4913.

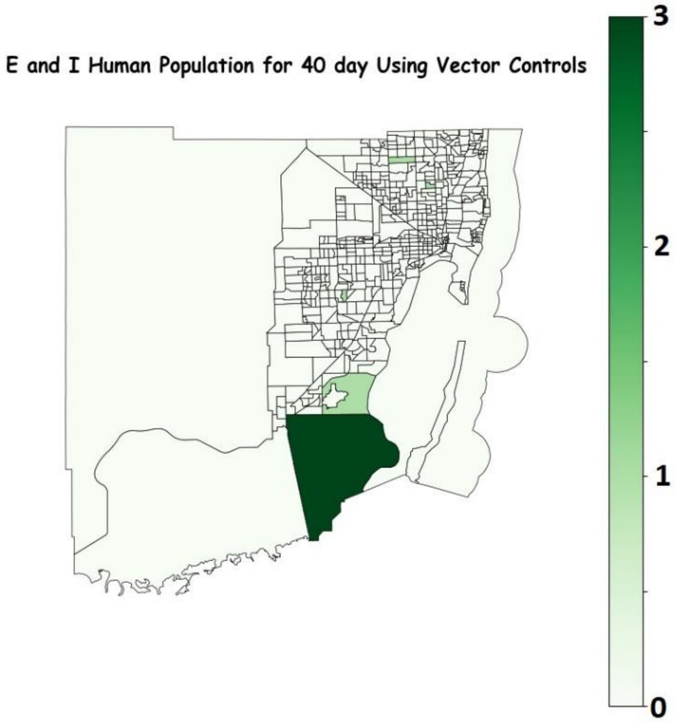
188. Zhao, S., Musa, S. S., Hebert, J. T., Cao, P., Ran, J., Meng, J., He, D., & Qin, J. (2020). Modelling the effective reproduction number of vector-borne diseases: The yellow fever outbreak in Luanda, Angola 2015–2016 as an example. PeerJ, 8, e8601. https://doi.org/10.7717/peerj.8601

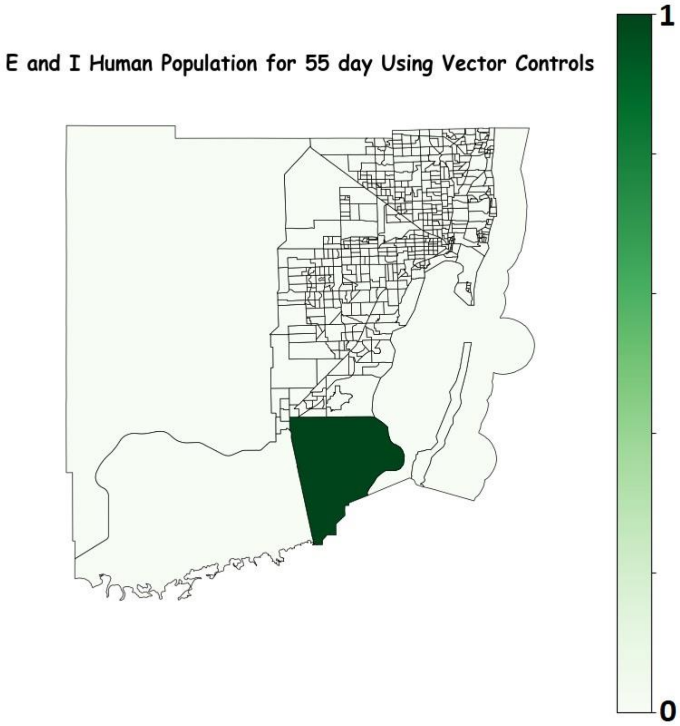
Appendix


E and I Human Population for 1 day Using Vector Controls
2
1
0

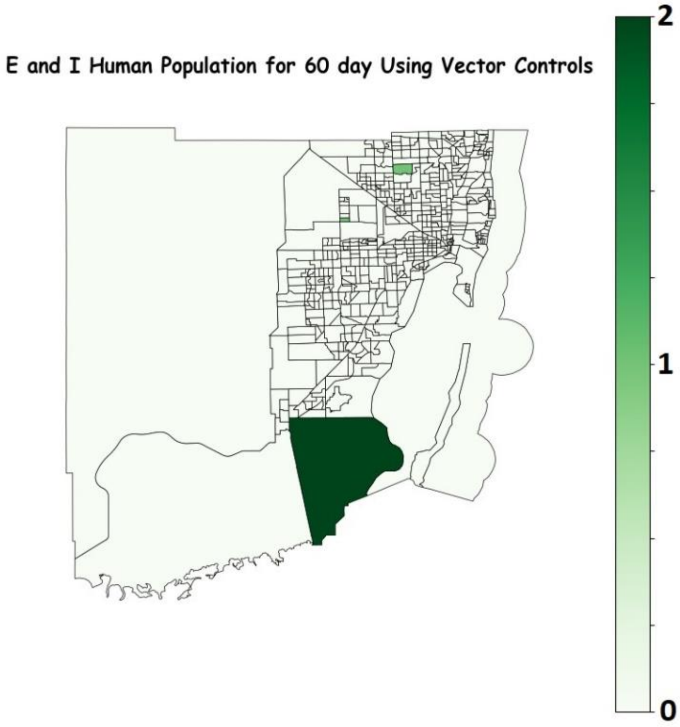

E and I Human Population for 20 day Using Vector Controls
1
0


E and I Human Population for 30 day Using Vector Controls

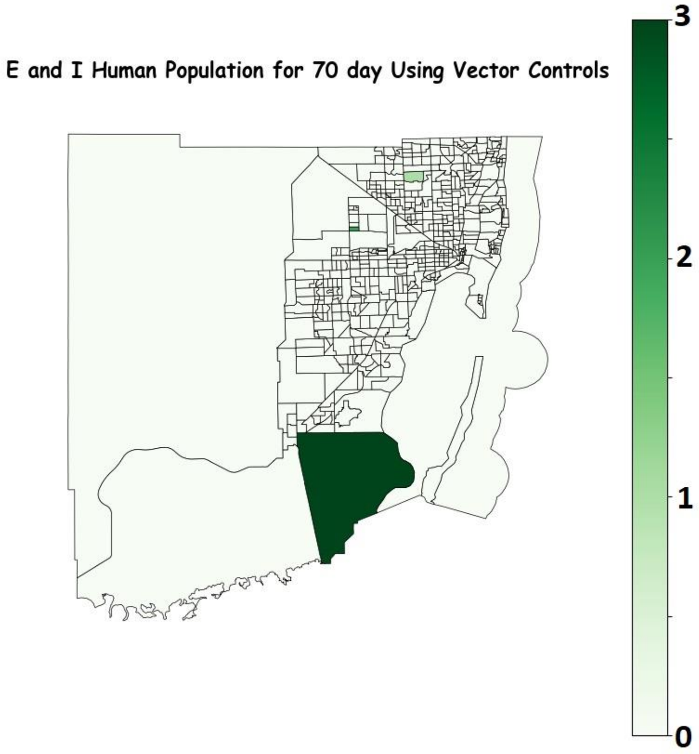

E and I Human Population for 40 day Using Vector Controls



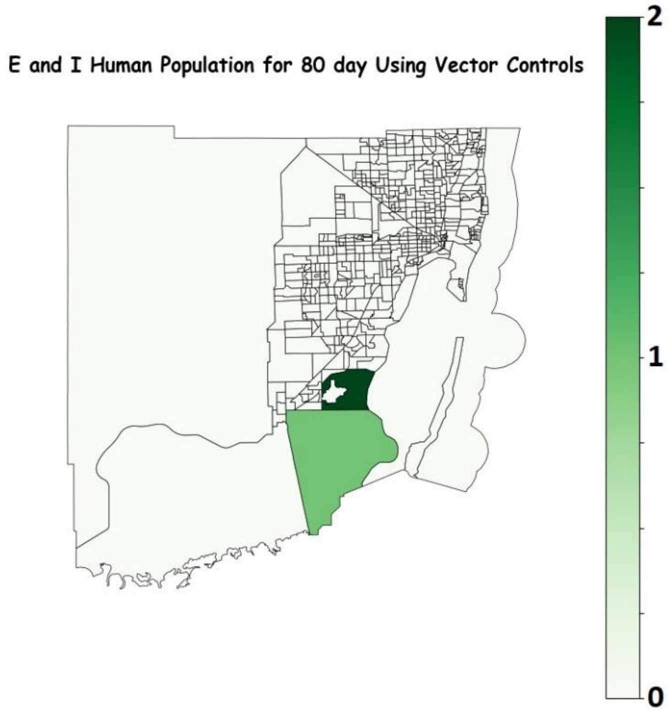
E and I Human Population for 55 day Using Vector Controls



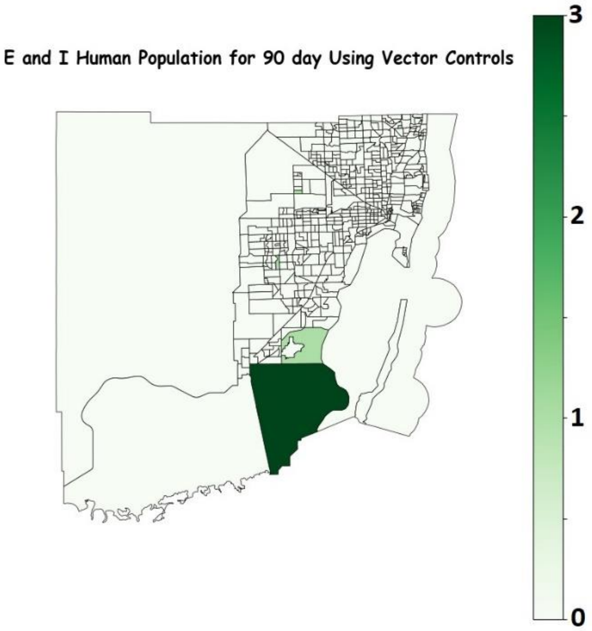
E and I Human Population for 60 day Using Vector Controls



E and I Human Population for 70 day Using Vector Controls
3
2
1
0



E and I Human Population for 80 day Using Vector Controls
2
1
0



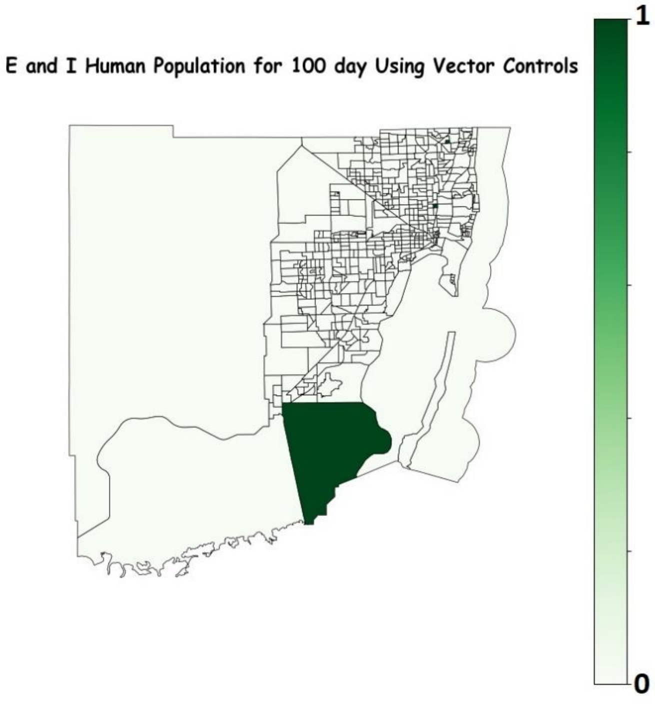
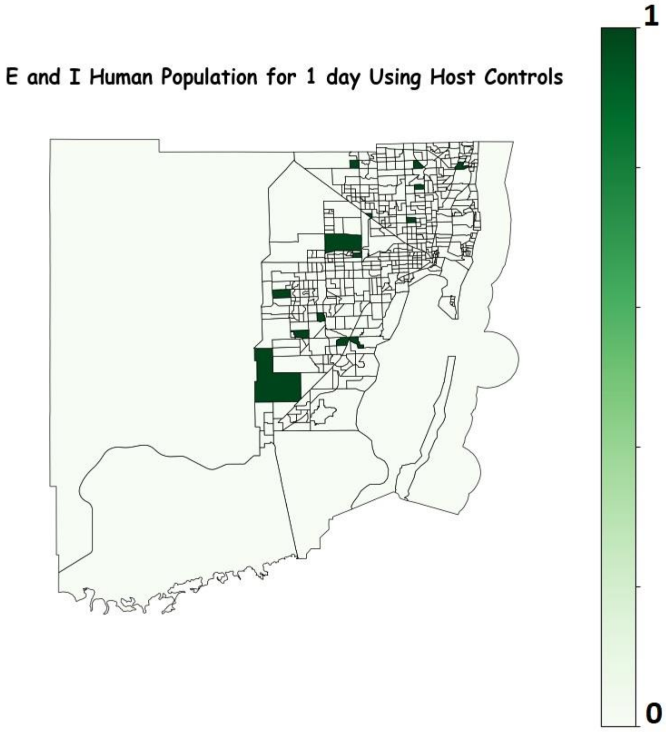
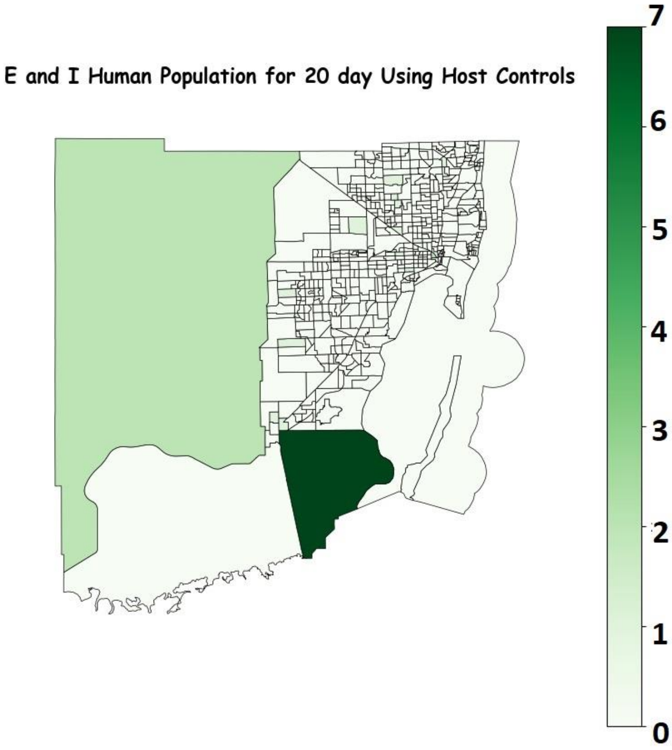


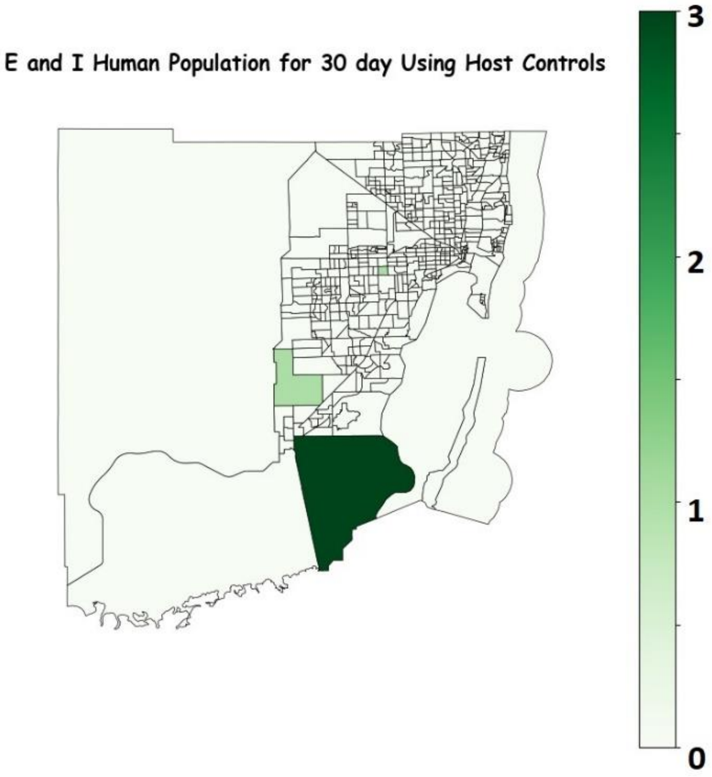
Figure S1. The Day 1, Day 20, Day 30, Day 40, Day 55, Day 60, Day 70, Day 80, Day 90 and Day 100 scenario results for the vector-based controls. The color represents the accumulated cases of Zika infection predicted in the vector control scenario.

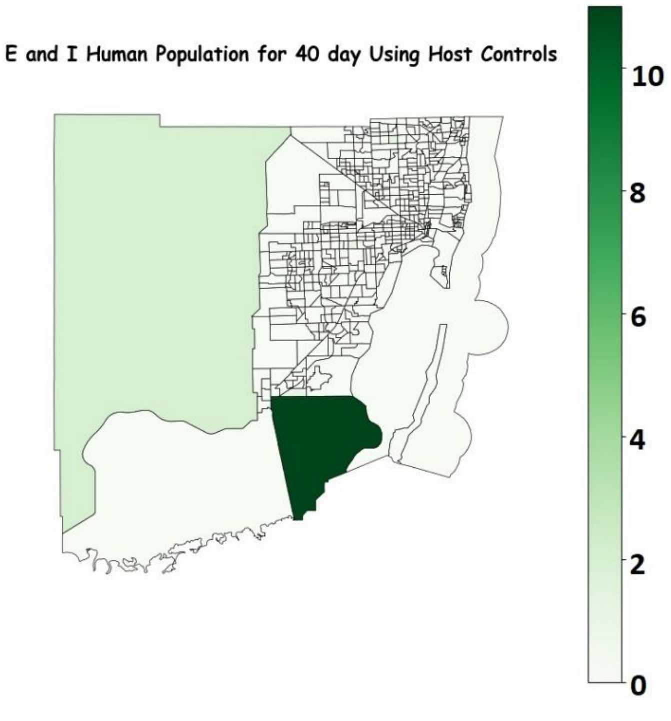


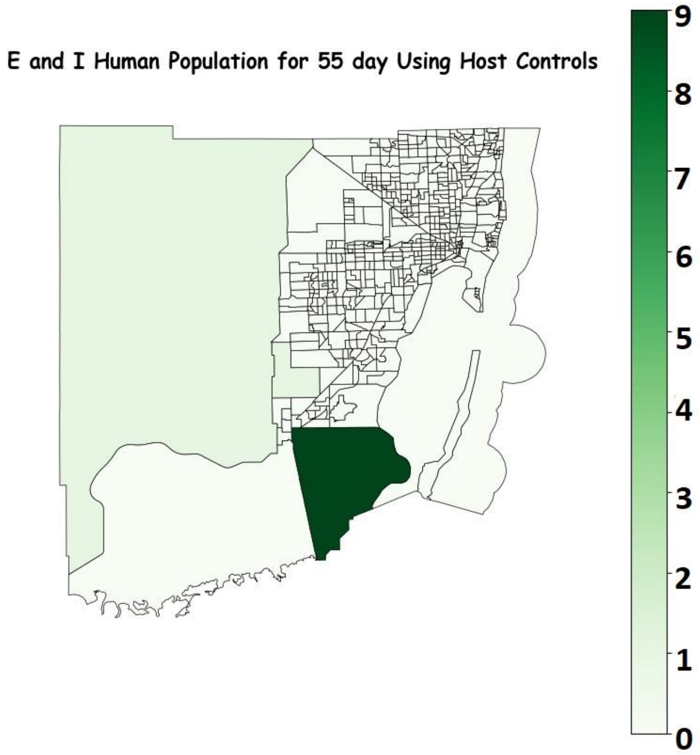
E and I Human Population for 1 day Using Host Controls



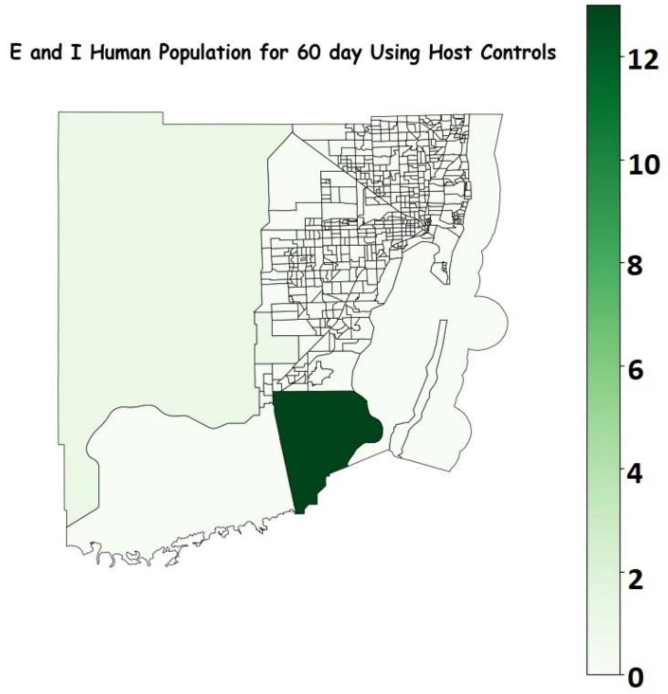
E and I Human Population for 20 day Using Host Controls


E and I Human Population for 30 day Using Host Controls
3
2
1
0

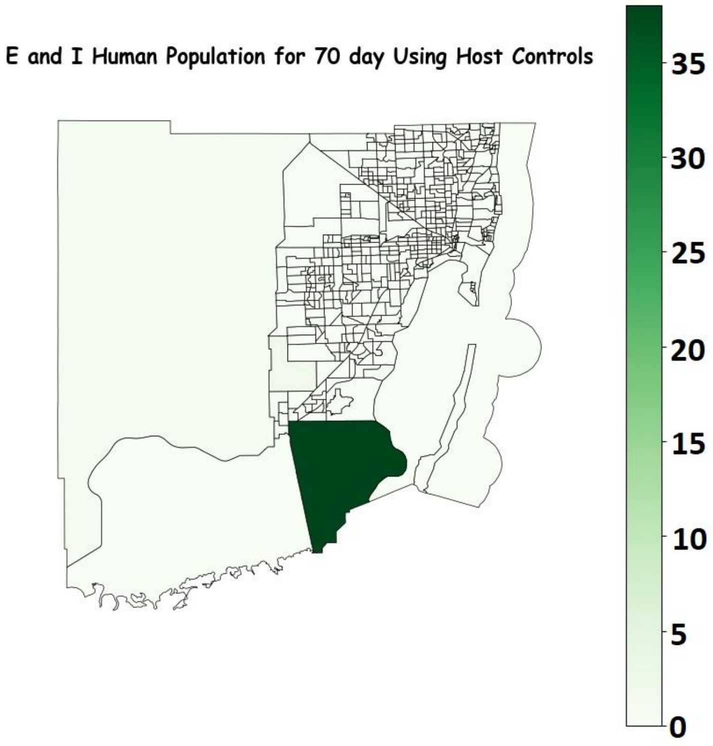

E and I Human Population for 40 day Using Host Controls
10
8
6
4
2
0

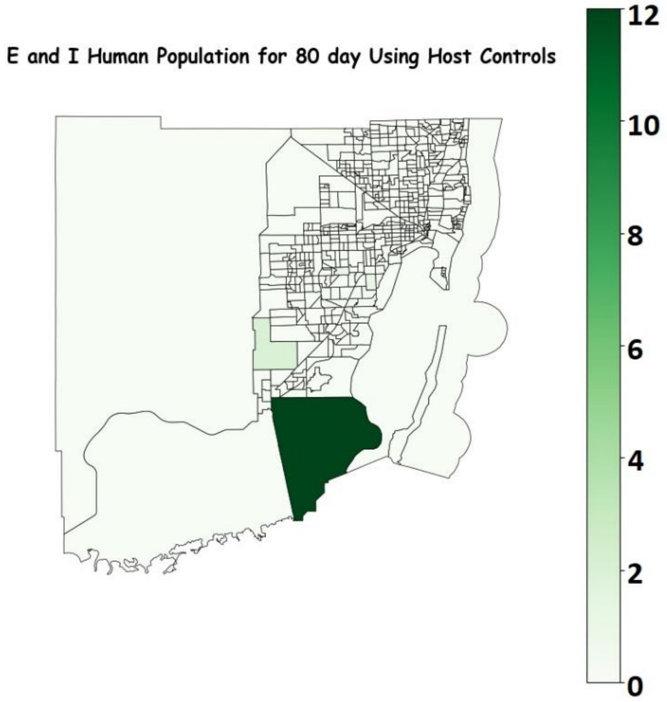


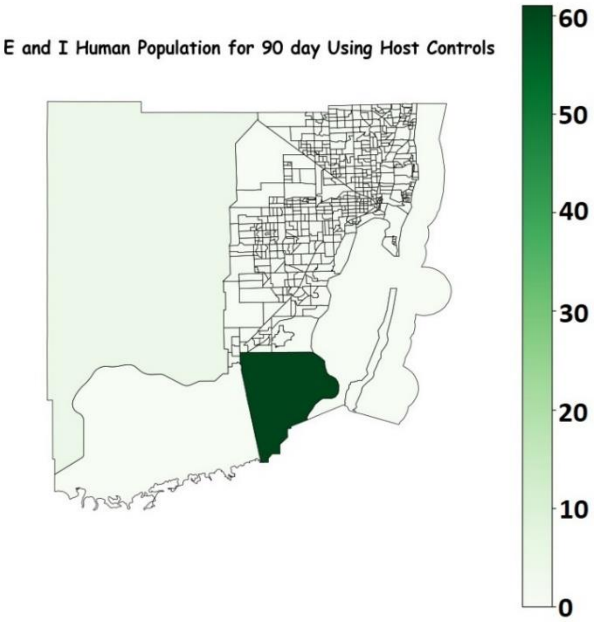
E and I Human Population for 55 day Using Host Controls



E and I Human Population for 60 day Using Host Controls


E and I Human Population for 70 day Using Host Controls
35
30
25
20
15
10
5
0


E and I Human Population for 80 day Using Host Controls
12
10
8
6
4
2
0



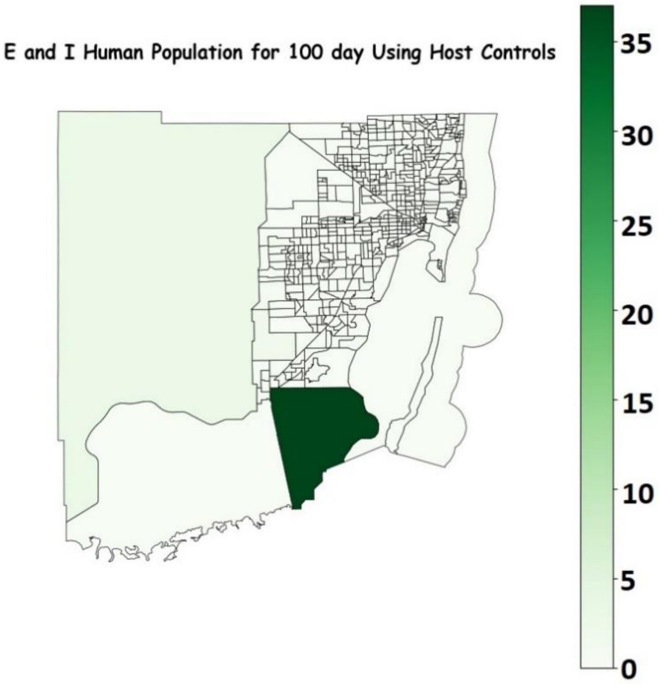
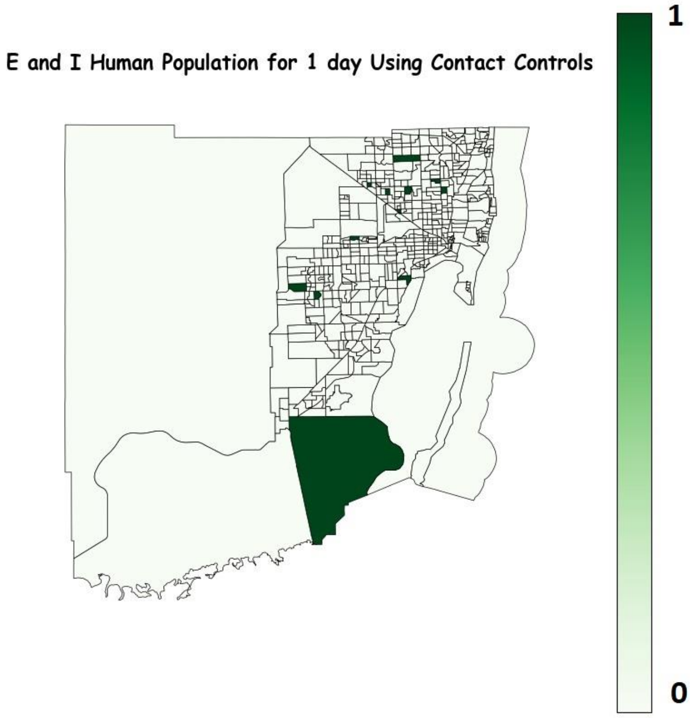
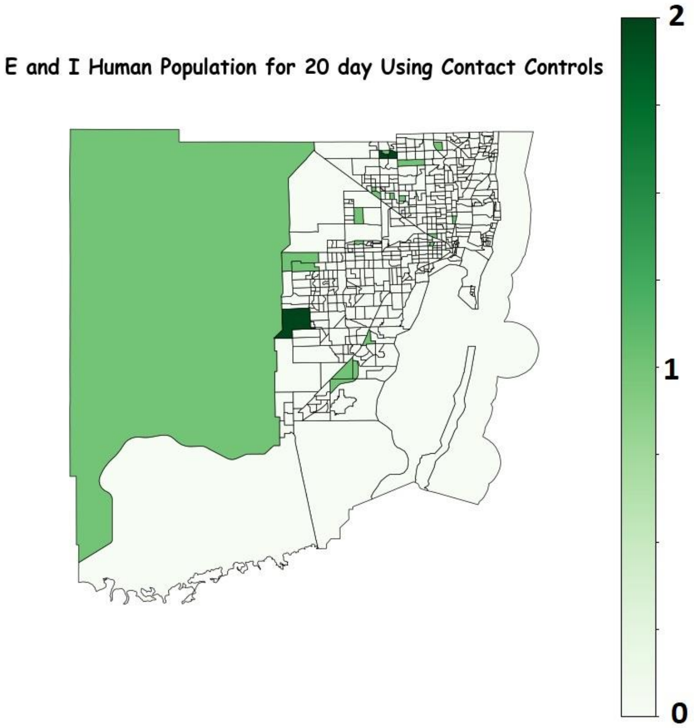
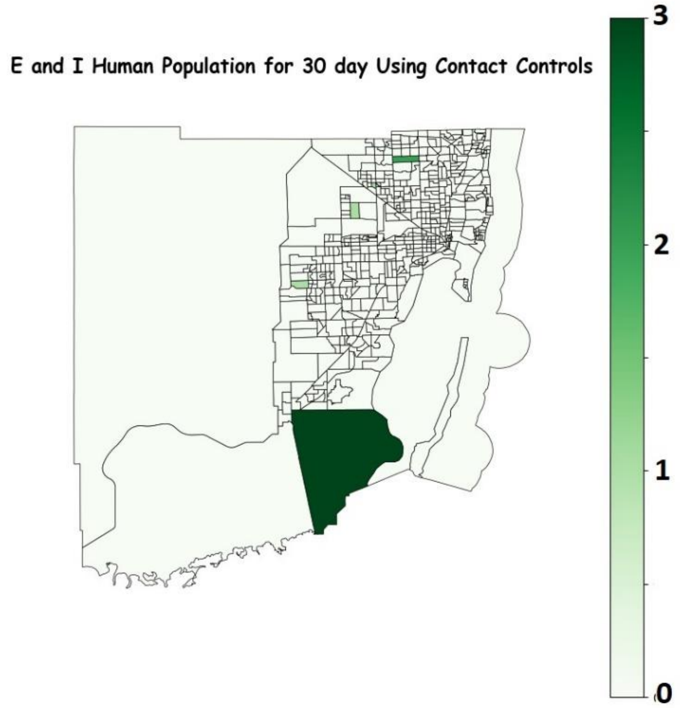
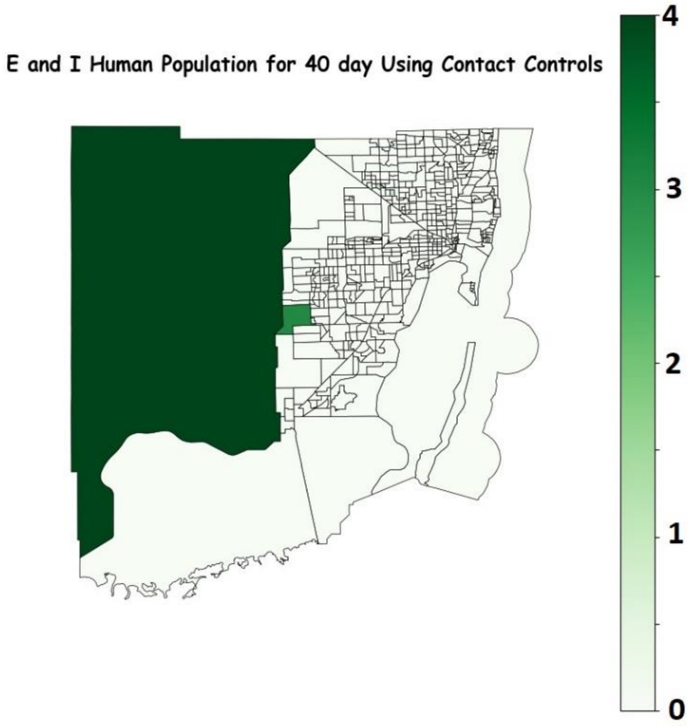


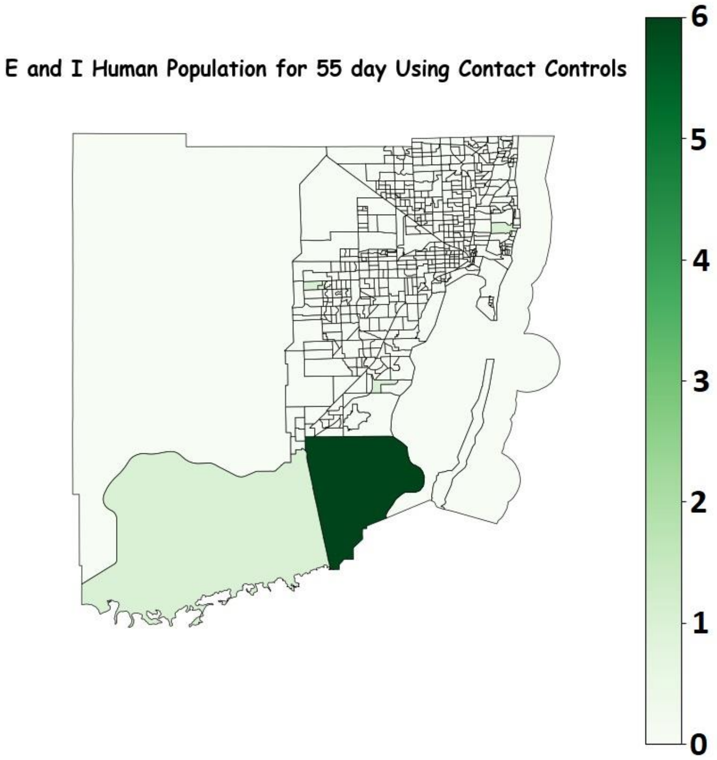
Figure S2. The Day 1, Day 20, Day 30, Day 40, Day 55, Day 60, Day 70, Day 80, Day 90 and Day 100 scenario results for the host-based controls. The color represents the accumulated cases of Zika infection predicted in the host control scenario.

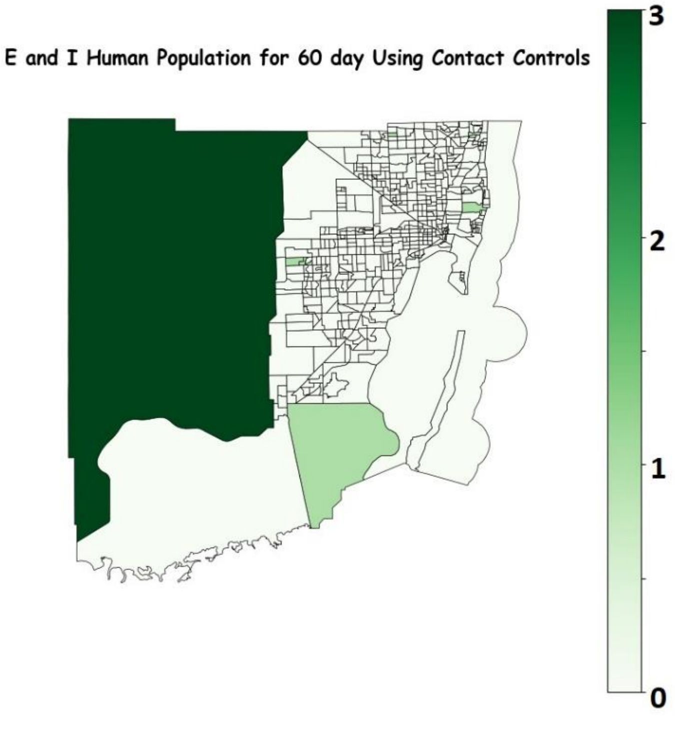

E and I Human Population for 1 day Using Contact Controls
1
0

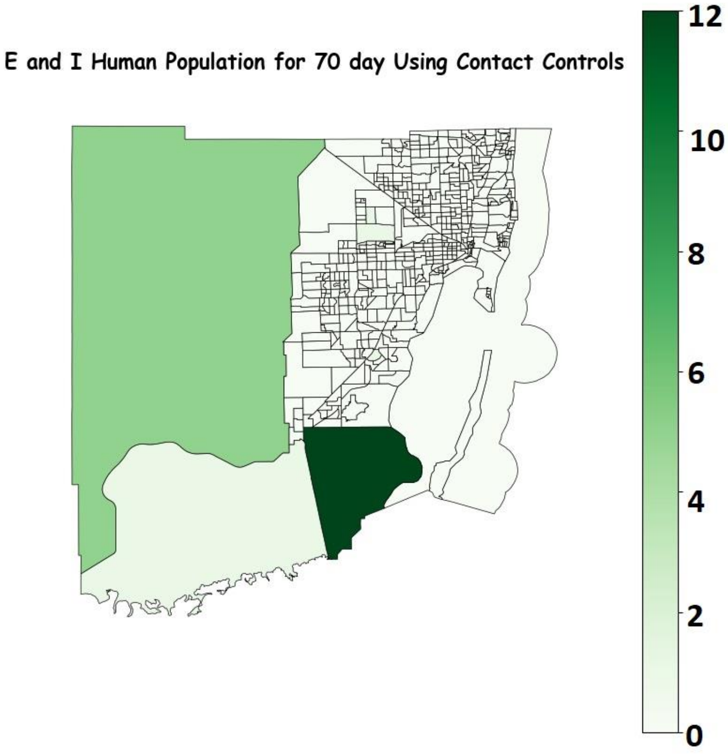

E and I Human Population for 20 day Using Contact Controls
2
1
0

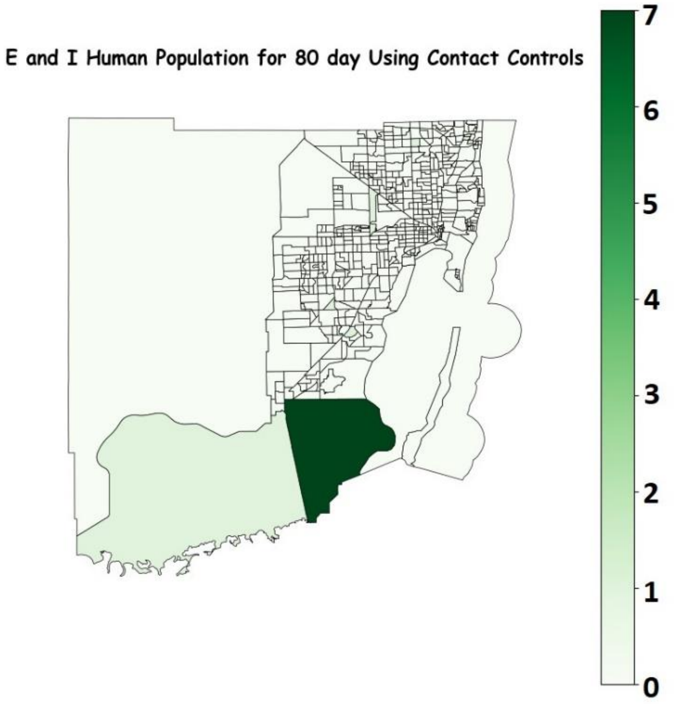

E and I Human Population for 30 day Using Contact Controls
3
2
1
0

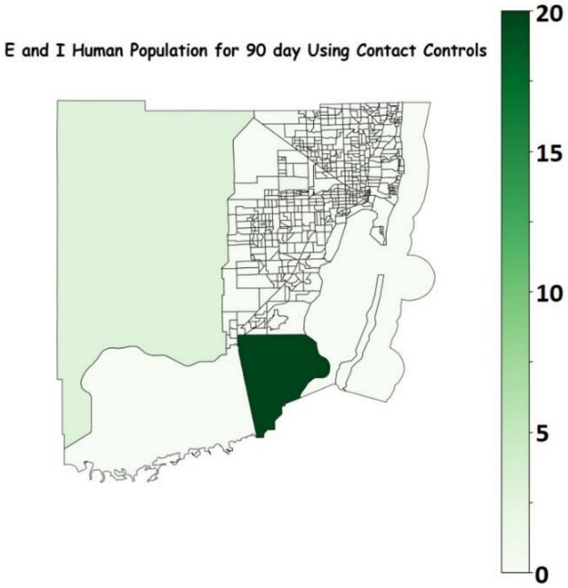

E and I Human Population for 40 day Using Contact Controls
4
3
2
1
0


E and I Human Population for 55 day Using Contact Controls
6
5
4
3
2
1
0


E and I Human Population for 60 day Using Contact Controls
3
2
1
0


E and I Human Population for 70 day Using Contact Controls
12
10
8
6
4
2
0


E and I Human Population for 80 day Using Contact Controls
7
6
5
4
3
2
1
0



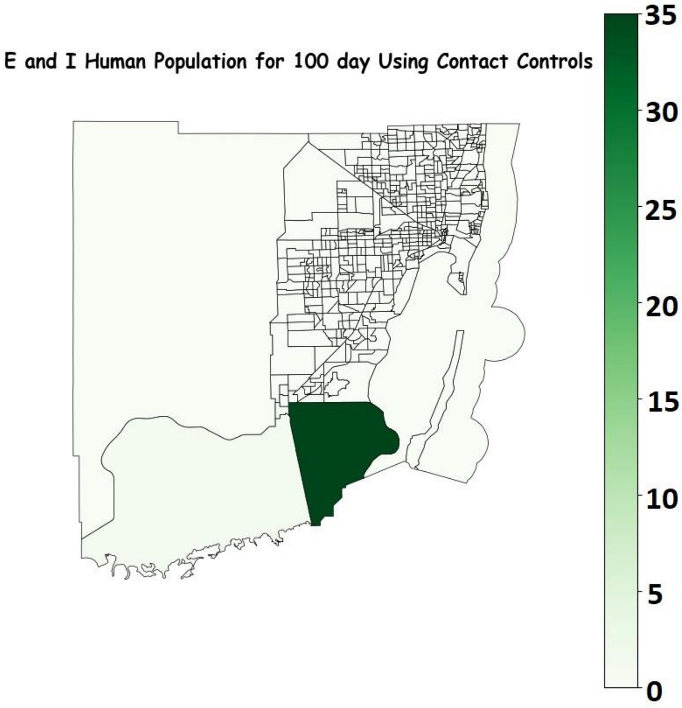


Figure S3. The Day 1, Day 20, Day 30, Day 40, Day 55, Day 60, Day 70, Day 80, Day 90 and Day 100 scenario results for the contact-based controls. The color represents the accumulated cases of Zika infection predicted in the contact control scenario.