A web-based geospatial toolkit for the monitoring of dengue fever

CrossMark

Eric M. Delmelle [a, c, *], Hongmei Zhu [b, e], Wenwu Tang [a, c], Irene Casas [d]

[a] Department of Geography and Earth Sciences, University of North Carolina at Charlotte, 9201 University Boulevard, Charlotte, NC 28223, USA
[b] Clark Labs, Clark University, 950 Main Street, Worcester, MA 01610, USA
[c] Center for Applied Geographic Information Science, University of North Carolina at Charlotte, 9201 University Boulevard, Charlotte, NC 28223, USA
[d] Department of Social Sciences, Louisiana Tech University, Ruston, LA 71272, USA
[e] Department of Geography, University of Connecticut, Storrs, CT 06269, USA

ABSTRACT

Keywords:
Dengue fever
Accelerated kernel density estimation
Space-time query
Spatial point patterns
Web GIS

The rapid propagation of vector-borne diseases, such as dengue fever, poses a threat to vulnerable populations, especially those in tropical regions. Prompt space-time analyses are critical elements for accurate outbreak detection and mitigation purposes. Open access web-based geospatial tools are particularly critical in developing countries lacking GIS software and expertise. Currently, online geo-spatial tools for the monitoring of surveillance data are confined to the mapping of aggregated data. In this paper, we present a web-based geospatial toolkit with a user-friendly interactive interface for the monitoring of dengue fever outbreaks, in space and time. Our geospatial toolkit is designed around the integration of (1) a spatial data management module in which epidemiologists upload spatio-temporal explicit data, (2) an analytical module running an accelerated Kernel Density Estimation (KDE) to map the outbreaks of dengue fever, (3) a spatial database module to extract pairs of disease events close in space and time and (4) a GIS mapping module to visualize space-time linkages of pairs of disease events. We illustrate our approach on a set of dengue fever cases which occurred in Cali (659 geocoded cases), an urban environment in Colombia. Results indicate that dengue fever cases are significantly clustered, but the degree of intensity varies across the city. The design and implementation of the on-line toolkit underscores the benefits of the approach to monitor vector-borne disease outbreaks in a timely manner and at different scales, facilitating the appropriate allocation of resources. The toolkit is designed collaboratively with health epidemiologists and is portable for other surveillance data at the individual level such as crime or traffic accidents.

Published by Elsevier Ltd.

Introduction

The rapid propagation of vector-borne diseases, such as dengue fever, poses a threat to vulnerable populations, especially in tropical regions (Bhatt et al. 2013; Gubler & Clark, 1995; Gubler & Trent, 1993; San Martín et al. 2010). Urban and suburban environments are particularly vulnerable due to rapid population movement and the abundance of potential breeding sites. In Colombia, South America, dengue fever reemerged in the 1970s after being eradicated in the 1950s and 1960s (Ocampo & Wesson, 2004; Romero-Vivas, Leake, & Falconar, 1998). Ever since, the disease has become endemic, presenting periodic outbreaks in 1991, 1994, 1998, 2001, and 2006. In 2010 alone, the city of Cali suffered one of

its most significant outbreaks (11,760 cases), resulting in 16 re-ported deaths (population of Cali for the 2006 Census was close to 2.5 million, (Cali, 2008)). To facilitate the monitoring of vector-borne disease outbreaks in space and time, we develop an inter-active on-line GIS toolkit which was collaboratively designed and enhanced through consultation with spatial epidemiologists in the city of Cali, Colombia.

The contributions of exploratory spatial data analysis, including point pattern and kernel density estimation (KDE), to the moni-toring of vector-borne diseases are well documented in the litera-ture (Cromley & McLafferty, 2011; Delmelle, Delmelle, Casas, & Barto, 2011; Eisen & Eisen, 2011; Kulldorff, 1997). Prompt space-time analyses are critical for accurate outbreak detection and mitigation of vector-borne diseases (Eisen & Eisen, 2011; Kitron, 1998, 2000; Vazquez-Prokopec et al. 2009). Spatial analytical methods can generate disease distribution maps revealing signifi-cant information in terms of direction, intensity of a disease, as well as its likelihood to spread to new regions (Duncombe et al. 2012;

* Corresponding author. Department of Geography and Earth Sciences, University of North Carolina at Charlotte, 9201 University City Boulevard, Charlotte, NC 28223, USA.

E-mail addresses: eric.delmelle@uncc.edu (E.M. Delmelle), HonZhu@clarku.edu (H. Zhu), wenwu.tang@uncc.edu (W. Tang), icasas@latech.edu (I. Casas).

Yoon et al. 2012). However, recent efforts to estimate the space-time signature of vector-borne diseases have primarily been focused at the aggregate level, mainly due to the scale at which data are generally reported (Hsueh, Lee, & Beltz, 2012; Young & Jensen, 2012).

As underscored by Boulos and Wheeler (2007), there is an increasing interest among health communities to disseminate analytical functionality over the internet, partly due to the availability of massive epidemiological datasets (e.g. social network such as twitter, Chunara, Andrews, & Brownstein, 2012). Second, the participation of volunteers in mapping health information has the inherent potential to promote community involvement, ultimately improving public health (Cromley & McLafferty, 2011; Delmelle, Casas, Rojas, & Varela, 2013; Dickin, Schuster-Wallace, & Elliott, 2014; Eisen & Eisen, 2011; Eisen & Lozano-Fuentes, 2009; Skinner & Power, 2011). This latter is critical in developing countries with constrained financial capabilities and where GIS expertise is limited (Duncombe et al. 2012; Fisher & Myers, 2011; Kienberger, Hagenlocher, Delmelle, & Casas, 2013).

The importance of collaboration between health epidemiologists and research institutions has recently been underscored by Robinson, MacEachren, and Roth (2011) and Granell, Fernández, and Díaz (2014). Several agencies such as World Health Organization (WHO); the Center for Disease Control (CDC) and the European Center for Disease Prevention and Control (ECDC) have taken significant steps towards the development of infectious disease surveillance/tracking systems on the web. An example is CDC WONDER which allows individuals to query information of a disease while results are presented through Web browsers in multiple forms (EPI, 2012). DengueNet was developed by the World Health Organization to compare disease burden between countries, but the quality of the underlying data remains a challenge (Duncombe et al. 2012; WHO, 2009). Huang et al. (2012) propose an application that combines datasets on modeled diseases, vector distribution and air network traffic. This application is particularly useful in an educational setting when identifying the risk posed by transportation networks to the spread of an infectious disease.

Web-based GIS applications for the storing, analysis, and visualization of epidemiological data can potentially disseminate spatial analytical concepts (and their results) to virtually anyone (Boulos et al. 2011; Boulos & Wheeler, 2007; Chapman, Darton, & Foster, 2013; Zook, Graham, Shelton, & Gorman, 2010). In spatial epidemiology, Gao, Mioc, Anton, Yi, and Coleman (2008) designed an interoperable service-oriented architecture framework based on Open Geospatial Consortium (OGC) standards to share spatiotemporal disease information. Newton, Deonarine, and Wernisch (2011) developed a web application interacting with an R web–user interface to map disease locations. Highfield, Arthasarnprasit, Ottenweller, and Dasprez (2011) designed Community Health Information System (CHIS), an online mapping system using a Google mapping interface to facilitate the dissemination of health-related geospatial data. Foley et al. (2010) introduced MosquitoMap, a web-based spatial database of mosquito collection records and distribution models, which can integrate geographical data from different sources at various scales. Moncrieff, West, Cosford, Mullan, and Jardine (2013) design and implement an open-source server-side web mapping framework for the analysis of health data, relying on Open Geospatial Consortium (OGC) web map service standard. Their framework, which can handle data query, was applied to the mapping of aggregated population distribution and disease rate.

A common characteristic of these applications is that their spatial analytical capabilities are restricted to the mapping of aggregated data. A notable exception is the work by Dominkovics et al. (2011) who used a commercial geoprocessing service to generate spatial density maps of tuberculosis based on individual observations. Despite these recent technological advances, there remain critical hurdles to the effective development of Web-based GIS applications in the field of spatial epidemiology. First, the functionality that is generally available over the web is restricted to aggregate data since individual-based analysis poses computational challenges. Second, there is a lack of spatial and temporal query capabilities (Boulos, 2003; Thompson, Eagleson, Ghadirian, Rajabifard, 2009). Last, interaction between users and the system is generally passive in that individuals cannot analyze their own data.

In this article, we present an interactive web-based GIS toolkit (OnTAPP: an **O**n-line **T**oolkit for the **A**nalysis of **P**oint **P**atterns), collaboratively designed with epidemiologists from Colombia (South America) with the objective to monitor dengue fever outbreaks over the Internet and conduct spatial analysis in a limited timeframe. Our toolkit allows to 1) analyze epidemiological information at the individual level, 2) conduct temporal and spatial query, 3) generate spatial density distribution maps across a region to better determine the occurrence of hot spots, and 4) visualize space-time connections at a local scale. Our article is structured as follows. The implementation framework is described in Section 2 (Methodology), and modules to conduct space-time query and visualize events close in space and time and density surface are presented. The effectiveness of the toolkit to identify clusters of dengue fever during an outbreak is illustrated in Section 3 (Monitoring Dengue Fever Outbreaks). Section 4 is devoted to conclusions and future developments.

Methodology

OnTAPP (**O**nline **T**oolkit for the **A**nalysis of **P**oint **P**atterns) is a web-based geospatial toolkit, which is designed in a collaborative manner with spatial epidemiologists to assist them in identifying putative sources of the diseases, and facilitate the optimal allocation of resources. The functional features of the toolkit are designed to address the needs of epidemiologists: (1) functionality to upload surveillance information and download results from the analysis, (2) ability to map patterns of raised incidence of disease at large scale (metropolitan level) and at small scale (neighborhood level), (3) identification of space-time disease clusters, and (4) functionality to identify hotspots of disease outbreaks. These functions are organized into four functional modules: geospatial analysis, mapping and visualization, spatial data management, and time and space query.

Modular design

Fig. 1 summarizes the general framework which is adopted for the design of the OnTAPP toolkit and complies with generic Web GIS architecture (Peng & Tsou, 2003). The four modules mentioned above comprise the primary functionality of the server side. On the client side, users which are intended to be health professionals in charge of decision making (public health agency or epidemiologists for instance) send requests to the server side, via a Web-based graphic user interface. The server carries out the corresponding spatial and temporal functionality and conveys the results to the client side for visualization. The framework is scalable and extensible so that additional functions or map layers from external data sources can easily be added to the application, similar to Beyer, Tiwari, and Rushton (2012).

Data management module

Unlike other online GIS which are generally restricted to aggregated mapping and which follows a passive communication, an important feature of OnTAPP is its ability to allow users to