Forecasting the propagation of vector-borne infectious diseases using high resolution mobility patterns and other data

Background

Dengue fever is one of the most common vector-borne infectious diseases in the world. In Sri Lanka, dengue poses a significant health risk with about 47,000 infections being reported in 2014 (Perera, 2015). A variety of factors affect the transmission of this disease, including but not limited to climatic conditions, level of immunity amongst the population, the number of prevalent strains, as well as population movements. The *Aedes aegypti* and *Aedes albopictus* mosquito species are vectors for a number infectious diseases beyond just dengue, including chikungunya, and also zika. The global distribution of occurrences for both species is rapidly increasing (Kraemer, et al., 2015). The lifespan of *Aedes* aegypti, which is the primary vector of dengue has a lifespan of around 2-4 weeks and a limited spatial range of less than 1 km (Heilman, et al., 2014). Human movement drives the transmission of dengue over distances beyond this limited range. Individuals exposed to dengue through a mosquito bite in one region may travel to other regions, passing off the virus to the local mosquito population at a destination when bitten. Therefore high-resolution insights (spatial as well as temporal) of intra and inter-region human mobility can help build better models to forecast dengue propagation.

Recently data from mobile operators have been utilized to derive high-resolution mobility insights to model how infectious diseases such as cholera in Haiti (Bengtsson, et al., 2011), malaria in Kenya (Wesolowski et al., 2012), and dengue in Pakistan (Wesolowski et al., 2015) propagate. LIRNE*asia* and the Computer Science & Engineering Department of the University of Moratuwa have also recently collaborated on a preliminary study to model dengue propagation in Sri Lanka using human mobility insights derived from pseudonymized mobile network call detail records (CDRs).

The state of art in using mobile operator meta-data to model disease propagation

Mobile phone operators generate and store call detail records (CDR) in their normal course of operations for billing purposes. A CDR is generated whenever subscriber uses her mobile phone to make or receive a call, send or receive a message and use the Internet. Each record provides information about the time of activity and the whereabouts of the subscriber during the activity in the form of the cell phone tower that served the subscriber. The spatiotemporal data present in CDRs makes it possible to extract time-varying aggregate mobility patterns at high spatial resolutions usually not possible with traditional methods.

Weslowski, et al. (2015) developed a comprehensive framework for predicting the spatial spread of dengue based on human mobility patterns. The research leveraged a CDR dataset of approximately 40 million Telenor subscribers in Pakistan from 2013. High-resolution mobility estimates were generated from this dataset that were then used to predict the spread of dengue across the country, from regions where the disease is endemic to naïve populations. The model was calibrated with weekly reported dengue counts from different regions.

It is worth noting that this research makes a distinction between regions where dengue is endemic and those that are not. In regions where dengue was endemic (e.g., Karachi) the researchers

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employed a simpler ento-epidemiological model that ignores the effect of mobility. The patterns of human mobility between endemic regions (like Karachi) and naïve regions (like Lahore) formed the basis of the model, and was used to predict the introduction of dengue to naïve regions and the subsequent spread of the disease. Climatic suitability of a region for sustaining a dengue mosquito population during the year combined with predictions of the time of earliest introduction of dengue to naïve regions were used to develop dynamic risk maps that provided location specific insights on future epidemic risk.

The findings of this research study highlight the risk of epidemics faced by non-endemic regions such as Lahore and Mingora as a result of importation of dengue through travel from the distant Karachi, which is the main reservoir of the virus in the country. The study showed that regions close to Karachi but with limited mobility between the region and Karachi faced significantly less epidemic risk, even when the regions in question had favorable climatic conditions for Aedes Aegypti.

Preliminary work in Sri Lanka

Recently LIRNEasia and the Computer Science & Engineering Department of University of Moratuwa co-supervised a student research project that produced a preliminary evaluation of a model developed and calibrated based on historic data from Peru in a Sri Lankan setting (Torre, 2010). Mobility patterns for Sri Lanka were derived using a pseudonymized CDR dataset that represents 50-60% of the Sri Lankan mobile subscriber base. In addition weekly reported counts of Dengue at 322 Ministry of Health regions for 2013 were used for training the model. The preliminary models that were tested did not distinguish between endemic and non-endemic regions. This exercise has been useful in highlighting a number of aspects as well as challenges that need to be addressed in developing a fully-fledged forecasting model in a Sri Lankan context.

The significance of the role human mobility plays in a widespread dengue epidemic depends on the extent which dengue is endemic in the region of analysis. If dengue is endemic throughout Sri Lanka, the local vector population rather than human mobility would drive dengue incidence. However mobility would currently play a significant role in the spread of other mosquito borne infectious diseases like chikungunya and zika in Sri Lanka. While zika has yet to be detected in Sri Lanka, building a prorogation model for the disease would be greatly beneficial for planning purposes, given its current global rise.

Next Steps

Many of the challenges in developing a robust forecasting model for vector borne infectious diseases in Sri Lanka concern the availability of data. Access to accurate digitized geographical boundaries for Ministry of Health regions or any other frame of reference used to aggregate dengue incidence will be critical in producing accurate results. Weather data for Sri Lanka available through the Department of Meteorology are spatially coarse grained and sparse which could potentially affect the resolution and accuracy of the model. Local epidemiologists need to be consulted on population and disease dynamics of the local mosquito populations as well as the prevalence of different strains of the diseases to calibrate the model. As such the way forward would require the collaboration between public health officials and experts, data and network science specialists, as well as meteorologists.

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