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Correlation Networks and Hot Spot Detection of Dengue Morbidity in Cebu City, Philippines

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ABSTRACT

Dengue is considered to be the fastest re-emerging disease in the world (WHO, 2012). Currently, it is one of the most prevalent diseases in the Central Visayas Region, Philippines particularly in Cebu City (Gubler and Clark, 1995). Each year, large number of dengue outbreaks continues to occur causing tremendous burden not only to health but to the economy as well. Thus, to address the increasing concern about the threat posed by Dengue Incidence, a clearer picture of epidemiology and important risk factors is needed. In this study, the weekly data on Dengue morbidity for each barangay in Cebu City from year 2011- 2015 were obtained from the Department of Health (DOH) region 7. A network is created per week based on the number of incidence occurring in each barangay. A hotspot or hub was then produced after running the network analysis for five (5) years. Results showed that there is a statistically significant cluster present in Cebu City and that its geographical distribution has expanded over the years. This finding provides data to inform program planning for possible Dengue Incidence control in the locality.

Keywords: *Correlation, Networks, Dengue hotspot, Dengue morbidity*

INTRODUCTION

Dengue is a tropical disease of viral origin transmitted through *Aedes aegypti* mosquito (WHO, 2012). It is responsible for approximately 2.5 billion infections worldwide (Gubler and Clark, 1995). Presently, it is one of the most widespread diseases in the Central Visayas Region, Philippines particularly in Cebu City. Because of this, it is considered as one of the most serious public health problems among reemerging diseases (Gubler, 2002). Thus, it is important to clearly define the control objectives and preventive measures. Despite the impact of this disease, still it left us with unanswered questions such as its importance of the means of transport about the Dengue's spreading dynamics and the network of disease across barangays (brgys.) and municipalities. In the previous works, several attempts have been made in studying and analyzing dengue network and the interaction of its elements such as two-mode complex network (Malik et al., n.d.), SIR- network model model (Stolerman et al., 2015), probabilistic effective distance network pattern (Brockmann and Helbing, 2013), and scale-free cluster of network (Eduardo et al., 2008). However, in this paper, the Static Aggregated Network to determine the mechanism for the spread of Dengue across brgys. in Cebu City is utilized. Specifically, it determined the: (1) the Dengue network for a five year data of dengue morbidity on a weekly basis, and

(2) the hotspot or hub from the network analysis from the 5-year period data.

In the next sections, we create a single network each week and aggregate the whole network for a total of 52 weeks from the gathered data of dengue incidence in Cebu City from 2011 - 2015. Then, hotspots or hubs are then identified from the generated network.

Methodology: Dengue network and hotspot detection

The Department of Health Region VII provided the data set used in this work. It included the number of incidences recorded weekly for 88 brgys. in Cebu. There are 52 weeks in a year and the data set covered a total of 5 years (2011-2015).

In this paper, we treated the data through network analysis method[8] in developing a better understanding of the dynamics and structural geometry of the complex web of interdependencies at work in the onset, incidence, and spreading of dengue.

The network was constructed by connecting the brgys. whenever a dengue incidence was recorded therein within the same week. This is interpreted as the co-incidence of dengue between two brgys. whenever a certain brgy. has reported an incidence. Simply put, when there is a dengue incidence in one brgy., it is correlated to the incidence of another if they occur in the same week. The number of incidences is not taken into consideration. This same procedure of constructing a weekly network is repeated for all the weeks in the data set. We make use of the concept of Static Aggregated Networks (SAN) to form the network of 5 years from the network that is constructed in a weekly basis. If the same link between any two pairs of nodes is repeated for the networks generated weekly, then the total weight of the link is equal to the summation of the recurrences of that link. The larger the weight, the stronger is the level of co-incidence between two barangays and their shared occurrence can therefore no longer be considered random and must take root from a common source.

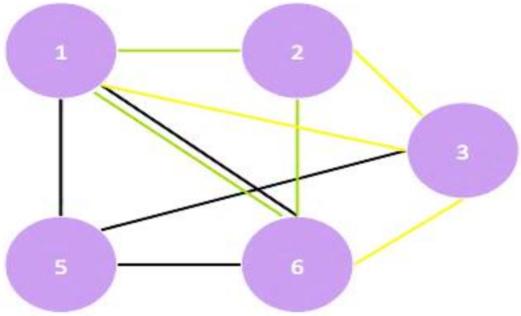

Figure 1. Connection diagram of the dengue network. Nodes represent barangay locations; the links represent a co-incidence between two barangays within a week. The color of the links represents the week at which they were generated. In the example above, the network is an aggregated network worth 3 weeks for 6 barangays. Repetition of a link between node pairs would increase the weight of the link. The link between nodes 1 and 6 has a weight of 2.

One of the objectives of this work is to find dengue hotspots based on the network structure. To do this, we look into the weight of the links. Since the network is undirected, we cannot distinguish which among a given node pair is the source or the target and can therefore not assign the value of the weight. We deal with this by assigning the weight to both of the connected components. A node receives the accumulated weight from all the connections it has made. This accumulated value is the node's strength and is taken as the influence of that barangay to the dengue incidences of its connected members, since it is the representative of inter-barangay correlations.

RESULTS AND DISCUSSION

Co-incidence is the number of times a dengue incidence between two barangays is repeated. As the limit is increased, connections break and weakly linked nodes are dismissed as random coincidences and only strong links are retained.

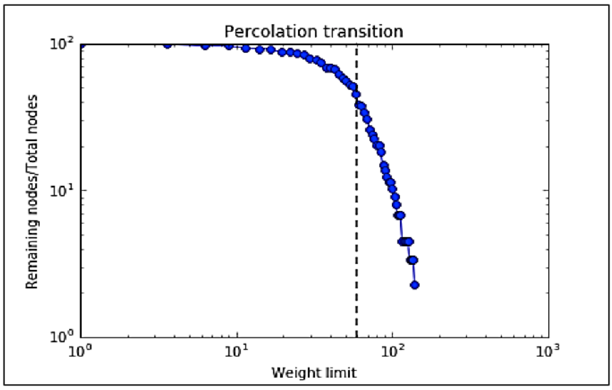

Figure 2. Network breakdown as co-incidence rate is increased. The y-axis shows the percent of nodes retained as a function of the limit. A slow and steady decrease is observed up until 60. At this point rapid decreases of the nodes occur.

Probably the most important aspect in this paper is the weight of the links of connected elements. The link weight distribution as reflected in figure 2 shows two downward sloping regions. One is for the weak links that persists up until 30 and another for the stronger links, characterized by a steeper downward trend. This behavior suggests that dengue co-incidences are dominated by random, simultaneous but uncorrelated incidences. The same behavior was also observed as discussed in the paper of Hugo, Saba, et al. (2014), wherein the result of the distribution between weight and nodes reflected a similar steeper downward trend. Above a certain weight limit, the population of the weights becomes more varied, and the emergence of few but highly correlated pairs emerge.

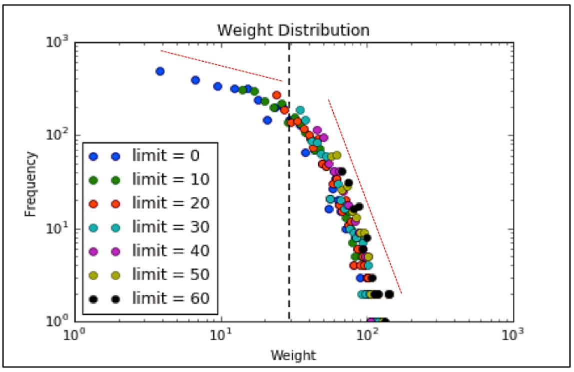

Figure 3. Weight distribution of connected components at different thresholds. The distribution indicates that most dengue incidences are dominated by random coincidences than highly correlated ones.

K nearest neighbors or the network assortativity is the measure of the average degree that a node of a certain degree is connected to. As shown in figure 3, nodes with medium to low degree connect to nodes with the same average degrees, seen as a zero sloping region. High degree nodes most likely connect to nodes with low degree. This can be interpreted as the mode of infection of dengue in the barangay level. Large degree barangays become the source of dengue carriers to low incidence barangays. This claim is also supported in the study of Chia-Hsien Lin and Tzai-Hung Wen in Taiwan. They reported a high correlation between human densities and dengue incidence rates. This high correlation was expected since higher human density may lead to higher vector-host contact rates (Lin and Wen, 2011). Similar studies conducted in Florida and Puerto Rico also revealed the same conclusion about the spatial pattern between human population and the number of dengue incidence (Morrison et al., 1998).

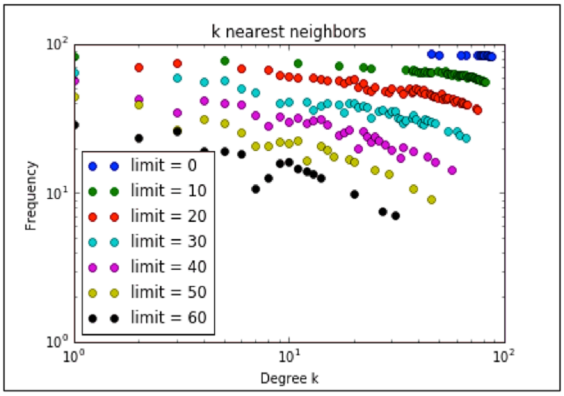

Figure 4. Distribution of k nearest neighbors. Increasing the weight limit produces a more downward sloping trend.

Moreover in this paper, we wanknow how far correlated barangays are apart. Knowing this, we get a picture of the probable causes of the shared incidences and verify geographically if connected pairs can be logically connected. From the distribution shown in figure 4, we find that most separation distances are less than 10 km regardless of the weight limit.

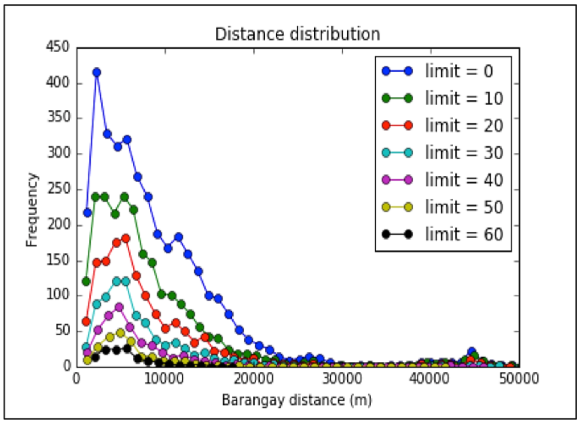

Figure 5. The distance distribution of all connected components. The distribution indicates that most linked barangays are separated by no more than 10 km. Most of the highly correlated barangays are mostly 5 km apart.

According to the WHO, usual flight distances of individual *Aedes aegypti* mosquitos range between 500 to 800 meters on its own energy. Although this might counter-intuitive to the distribution of distances, this can also mean that for some cases, people, rather than mosquitoes in a specific area, rapidly move the virus within and between communities and places.

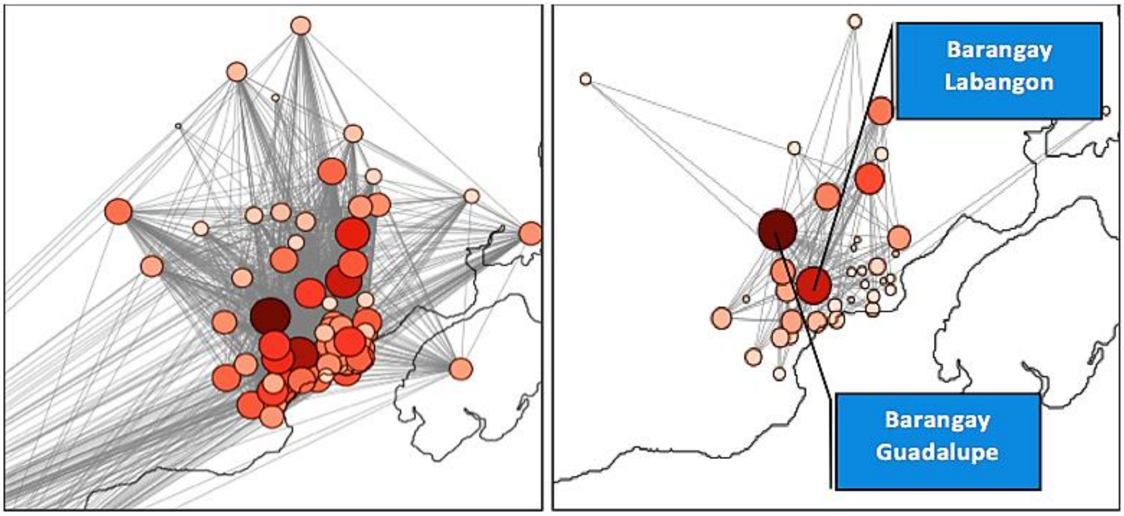

Figure 6. The Cebu Dengue network with correlation limits 10 (left) and 60 (right).

This can also mean that the source may not only be in the barangays itself but on the region in between as is the case when two highly correlated barangays exist without being near to each other. It should also be noted, that the distances calculated here are grave approximations since they are calculated using the coordinates of landmarks within each barangay and not on the center of each area. This can also account for the discrepancy between the possible transmission distance of mosquitoes by themselves and the actual distance measured. Figure 6 shows the constructed dengue network for Cebu for weight limits 10 and 60. Results showed that for the span of 5 years, the dengue incidences in Cebu are influenced by the same factors that caused the Dengue in barangay Guadalupe, which is the most highly correlated node in the Dengue network. The size and color of the node reflects the total correlation of a node.

The total correlation is calculated by taking the summation of coincidences connected to a node. This value reveals how many times a dengue incidence of a node is shared by other nodes. This means that the cause of the incidences in that node is the same cause for the other nodes/barangays. In this case, a lot of the dengue incidences in Cebu are influenced by the same factors that caused the Dengue in the strongest node, which for the total of 5 years is Barangay Guadalupe.

CONCLUSIONS AND RECOMMENDATIONS

In this paper we have shown how to create a network of Dengue incidences using the concept of Static Aggregated Networks generated on a weekly basis. From the network and according to the node strength, the greatest dengue hot spot is within or very near to barangay Guadalupe and the second likely hot spot, which is barangay Labangon. The close proximity of these two barangays supports this conclusion. The methods and results of this work may be utilized to aid in efficiently allocate disease mitigation efforts. This work however suffers from a great deal of inaccuracy, which may be grounds for further improvement. First is the resolution of the data set and the crude definition between co-incidence as the simultaneous incidence of any two barangays in a week. We believe greater resolution in the data set (e.g. data collected daily instead of weekly) would help us create better hotspot detection. Second is the approximation of the specific locations of brgys. leading to errors in the calculation of distances between them.

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