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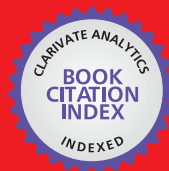
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# Network Formation and Analysis of Dengue Complex Network

*Hafiz Abid Mahmood Malik*

## Abstract

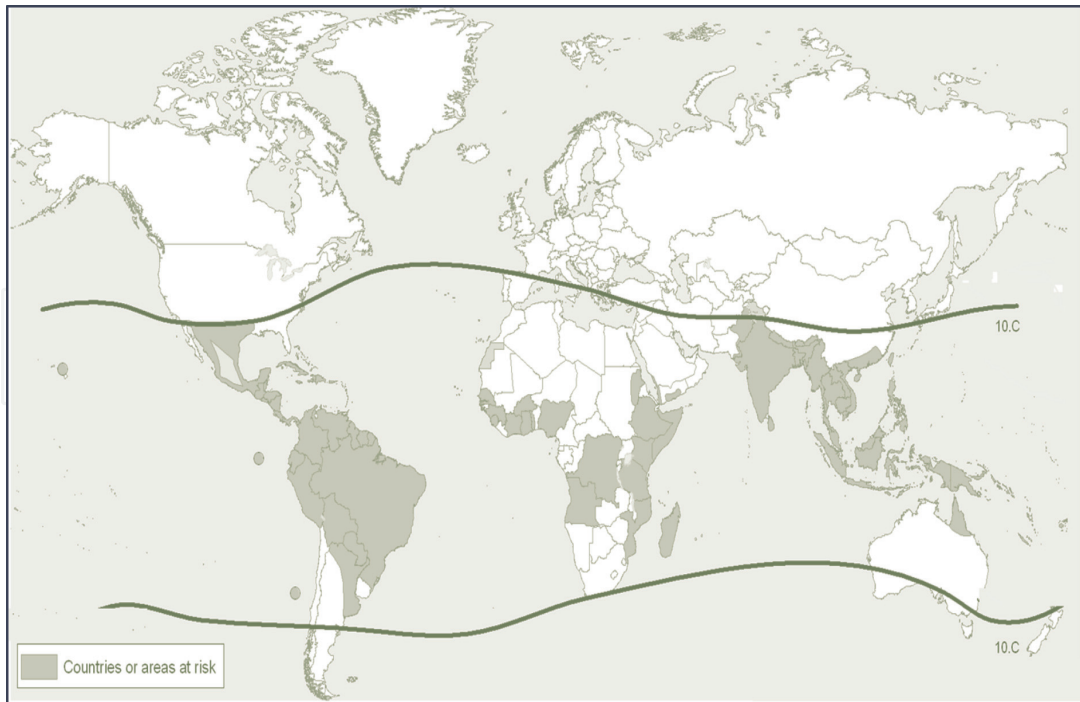
Several efforts have been made and are constantly being made to keep the *Aedes aegypti* virus under control. Numerous scholars are involved in the study of medicine, while others are working in computer science and mathematics to model the spread of this disease. This study will help to comprehend how this epidemic sickness behaves. A complex network has been established from the complex dengue phenomenon. We have evaluated dengue network topology by pondering scale-free network properties. The network's resilience in tracking the dengue epidemic is measured by systematically removing nodes and links. The primary hubs of this network are emphasized, and the vulnerability of the network structure has been examined through an in-depth investigation of the dengue virus's spreading behavior. Understanding the intricate web of dengue outbreaks relies heavily on geographic representation. The applied method on the dengue epidemic network and the results will be added as scientific additions to the literature on complex networks. Different network analysis metrics have been applied (closeness centrality, betweenness centrality, eigenvector centrality, network density), and the network's stability has been evaluated. This network is extremely vulnerable to targeted attacks; results showed that after removing 8% of focal hubs, 34% of the network is destroyed.

**Keywords:** vector-borne disease, robustness, dengue vector, scale-free network, complex network metrics

## 1. Introduction

Most dengue fever cases have been reported in tropical and subtropical areas. However, reports of its spread to numerous other regions, including Europe, have increased significantly during the past decade. There are around 2.5 billion people who could get dengue fever (DF) or dengue hemorrhagic fever (DHF) [1, 2]. In January 2022, the WHO estimated that there might be between 100 and 400 million new dengue cases worldwide yearly. An estimated 3.9 billion people live in these areas where dengue fever arises (**Figure 1**) [1, 2].

The mosquito is the vector for the dengue virus. Bite transmission occurs mostly due to the *A. aegypti* and *Aedes albopictus* species of mosquitoes, both of which are considered the carrier of the disease [2, 3]. *A. aegypti* is a small, dark mosquito with a silvery white pattern of scales on its body and white bands that may be identified on



**Figure 1.**  
World map showing locations with a high risk of dengue fever.

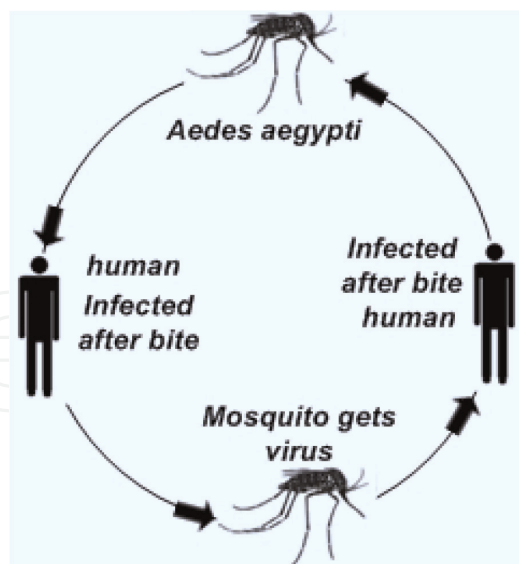


**Figure 2.**  
Dengue vector (*A. aegypti*).

its legs (**Figure 2**). Most people get bitten by this urban mosquito during dawn and evening [4, 5].

### 1.1 Dengue virus outbreak

The *A. aegypti* mosquito can spread the dengue virus to humans through a bite. Mostly female *A. aegypti* mosquitoes have been found to carry the dengue virus, which means that females of this type of mosquito may be the superspreader of the disease [4, 6–8]. Female *A. aegypti* have a lifespan of 12–56 days (mean: 34 days) [9, 10]. In order to produce offspring, female *A. aegypti* mosquitoes mate with males and produce offspring by egg-laying; in this way, a male can carry this virus, too. If *A. aegypti* bites any person and that person acquires the dengue virus (DENV), they also become the source of DENV. **Figure 3** [11] depicts the transmission of DENV from an infected



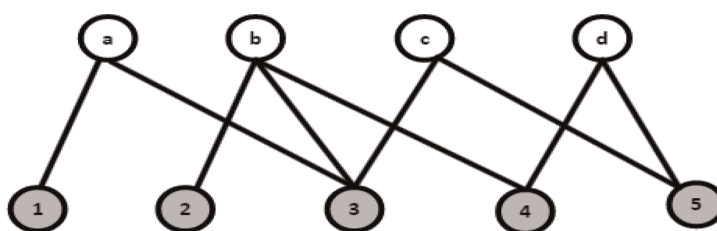
**Figure 3.**  
*Dengue spread.*

individual to another mosquito (not of the *A. aegypti* species) via a mosquito bite [3, 5]. In addition, dengue symptoms often develop 4–14 days after a mosquito bite. Specifically, the dengue virus’s DENV-1, DENV-2, DENV-3, and DENV-4 serotypes have been identified [5, 6, 12]. The infected person’s blood can be tested for any of these dengue serotypes. Any individual infected by one of these serotypes is immune to future infection by the same serotype [3, 6, 13].

## 2. Modeling the dengue epidemic as a two-mode network problem

The structure of some real-world datasets is naturally bipartite. A key characteristic of this sort of network is that it allows for the partitioning of nodes into two groups (primary and secondary) and the creation of linkages exclusively between nodes in the two groups. To define a bipartite graph, we use the triplet  $G = (\mathcal{T}, \perp, E)$ , where  $\mathcal{T}$  is the set of vertices,  $\perp$  is the set of top edges,  $E$  is the list of bottom edges, and  $E \subseteq \mathcal{T} \times \perp$ . Whereas in traditional graphs, links usually go from one group of nodes to another, in this case, the nodes are in two separate but intersecting sets. If two nodes (of  $\perp$ ) in  $G$  have at least one neighbor (in  $\mathcal{T}$ ), then they are connected in the  $\perp$  – projection, which is the graph  $G_{\perp} = (\perp, E, \perp)$ . In **Figure 4**, a–d depict the primary set of nodes in the two-mode network, whereas 1–5 represent the secondary set [14].

This study uses a dataset of weekly dengue cases from various nodes (locales) in Selangor, Malaysia, to formalize the epidemic problem as a two-mode network. This



**Figure 4.**  
*Two-mode networks, illustrated with an example.*

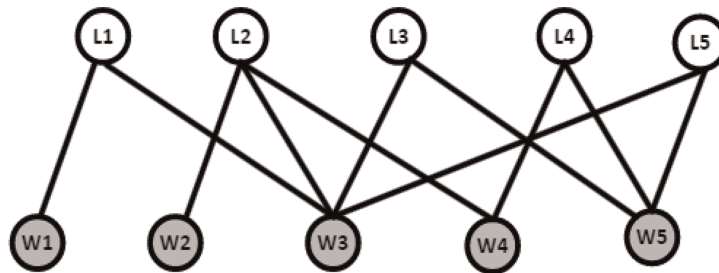
network's primary set of nodes is "localities," whereas the second set is the "number of infected patients in weeks." Two nodes are linked in this network if they have the same number of infected cases within the same week, with the number of cases serving as the link weight. The weighted two-mode network is shown here in **Figure 5**. In Selangor, Malaysia, the weeks are labeled W1, W2, ..., W52, and the locations are denoted by the letters PL1, ..., GL1, ..., and HLL1, ... [14, 15].

Limited network analysis metrics can be used for the original, unaltered version of two-mode networks, which is challenging to perform an in-depth analysis [16]. In order to study these kinds of two-way networks, it is common practice first to transform them into a one-mode network.

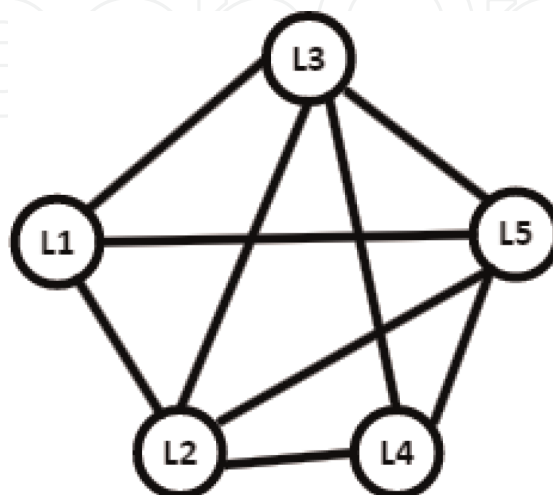
All of the nodes in a two-mode network are linked by the fortuitous occurrence of weeks, thereby converting the network to a single mode. The actual two-mode network is depicted in **Figure 5**, whereas the one-mode projection is shown in **Figure 6**.

A white node represents the locality in Selangor, while a gray node symbolizes the number of weeks; W1 denotes the first week, W2 the second, W3 the third, W4 the fourth, and W5 the fifth.

Projection is commonly used to transform two-mode networks into single-mode ones [16–18]. Here, we use three different projection techniques—Binary, Sum, and Weighted Newman—to turn a two-mode network into a single-mode one. Based on outcomes, it is determined that the Newman technique is better suited to the dataset under consideration.



**Figure 5.**  
A simulation based on an actual dataset.



**Figure 6.**  
The two-mode dengue network is transformed into a one-mode from a geographic perspective, represented in **Figure 5**.

Since many real-world networks have weighted information in their linkages, Newman's approach does not account for this fact adequately. The Weighted Newman technique is a generalization of Newman's approach that Opsahl suggests [17–19]. He claims that the weight can be expressed mathematically as Eq. (1).

$$w_{ij} = \sum_p \frac{w_{ip}}{N_p - 1} \quad (1)$$

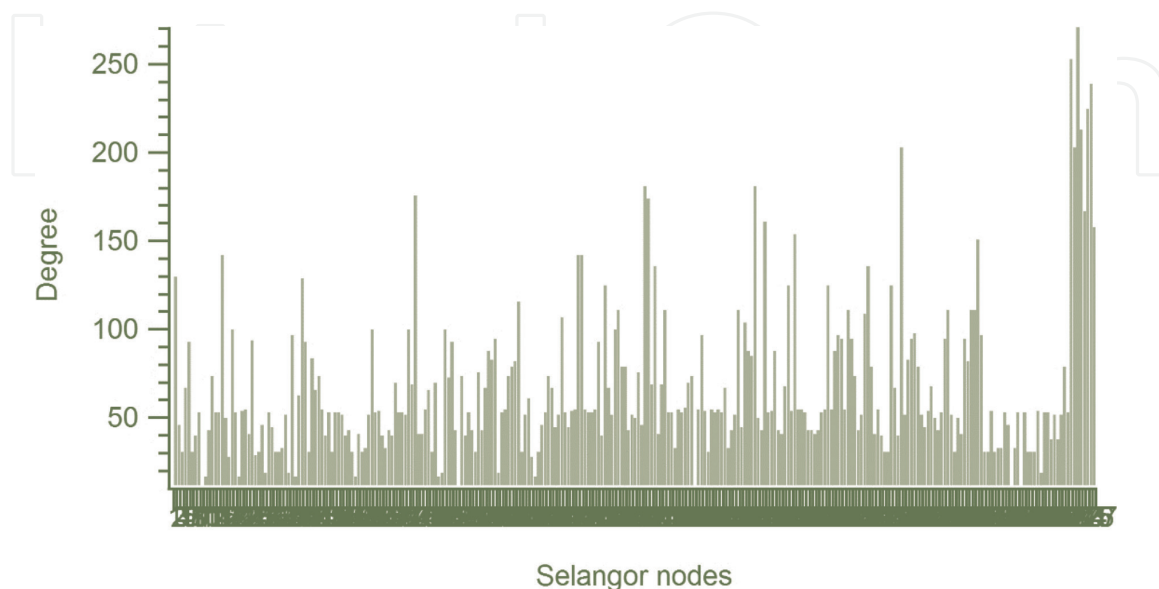
The link from node  $i$  to the co-occurrence has a weight of  $w_{ip}$ , where  $w_{ij}$  is the weight between  $i$  and  $j$ .

## 2.1 Dengue epidemic: A network analysis

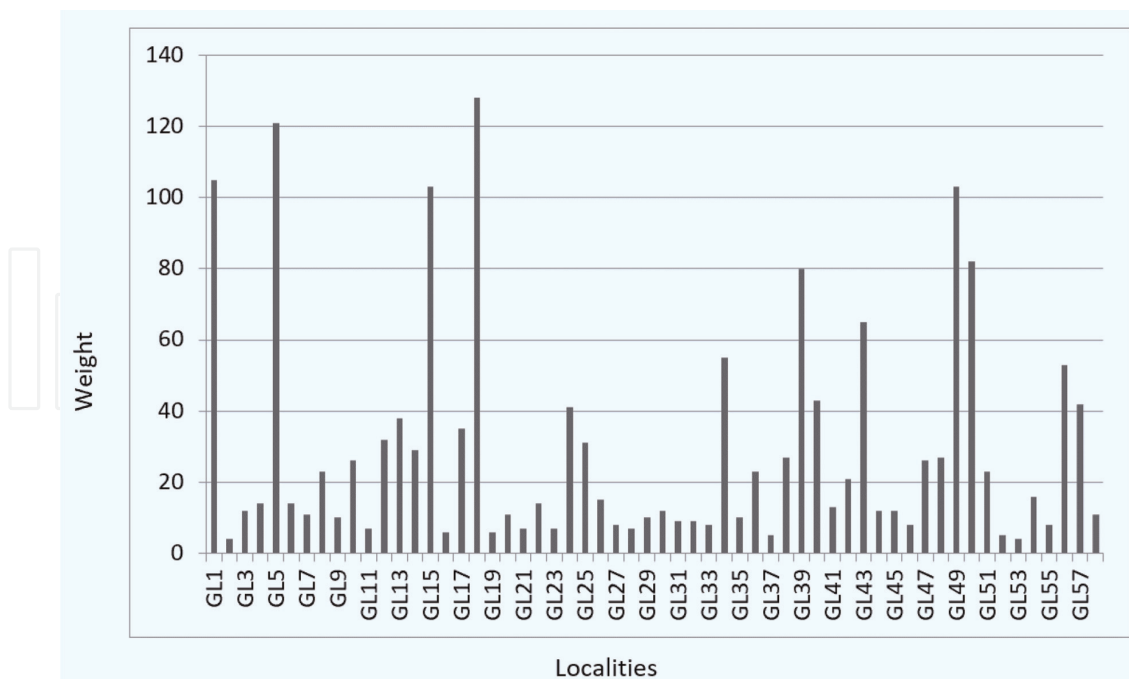
Network visualization and analyses of one and two-mode degrees, weighted degree, density, closeness, betweenness, and eigenvector centrality measures are used in this study to examine the dengue outbreak. Primary nodes in the network analysis are the places, whereas secondary nodes are the weeks. As a means of analyzing the predicted results of weighted Newman algorithms, above mentioned network metrics are used.

**Figure 7** is a graph depicting the degree centrality of all nodes in Selangor, Malaysia. All of Selangor's dengue hotspots are plotted along the x-axis. Weighted Newman projection using the centrality metric has been utilized for this purpose. Selangor dengue network nodes with the highest centrality are PL216, PL31, PL137, PL134, HLL161, PL54, HLL84, HLL117, and HLL115, which indicates they have a lot of ties to other nodes. Here, the granularity of these vertices can be observed [15, 20].

From the perspective of degree analysis, the simple degree measure has less relevance in this network and is the crude measure. The binary method does not produce satisfactory outcomes when considering the strength of nodes (weighted degree). With the binary approach, it's clear that the degree and strength of a single mode are identical. The weighted Newman technique (**Figure 8**) produced the out-strength of nodes, which may be read as the overall number of dengue cases



**Figure 7.**  
The weighted Newman degree of nodes.



**Figure 8.** Gombak network node strengths calculated with the weighted Newman approach.

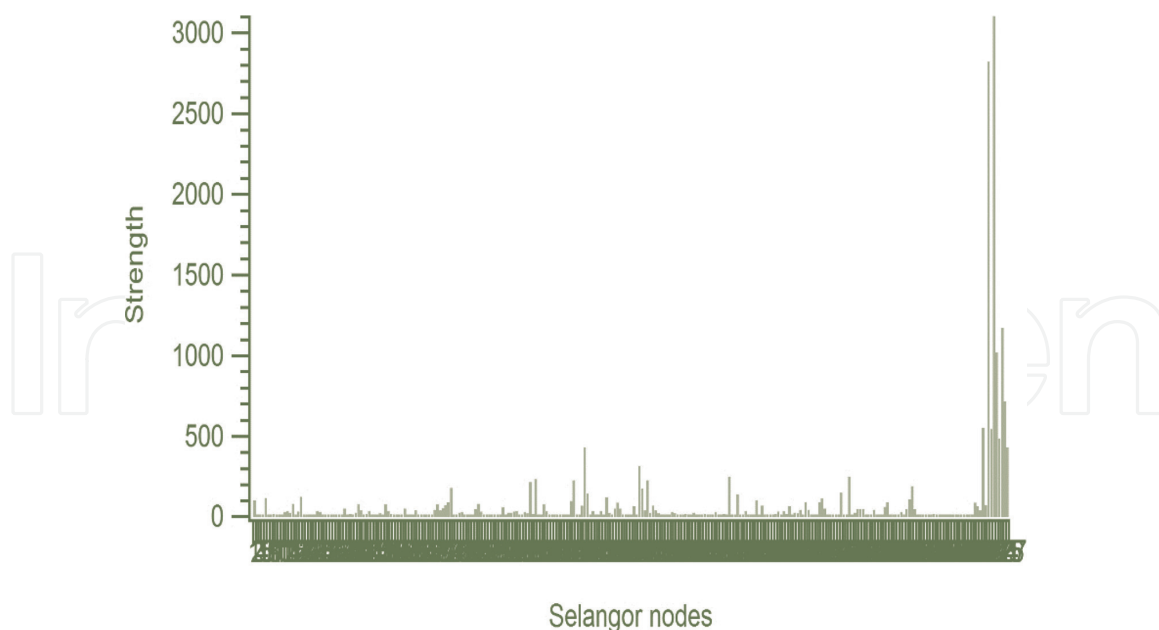
reported in certain nodes [21]. On the x-axis, 58 dengue-affected nodes in the Gombak district are illustrated, while the y-axis depicts the strength of these nodes. The strongest network strength was seen at node GL18, corresponding to the highest reported node total of dengue cases (128 cases).

Dengue fever cases were also the second most numerous in GL5, with a total of 121 being reported within the specified time frame. There were four confirmed dengue infections in GL2 and none in GL53. The strength of the two-mode projection and one-mode weighted Newman projection method is the same, suggesting that weighted Newman projection generated more suitable outcomes than Sum and Binary projections.

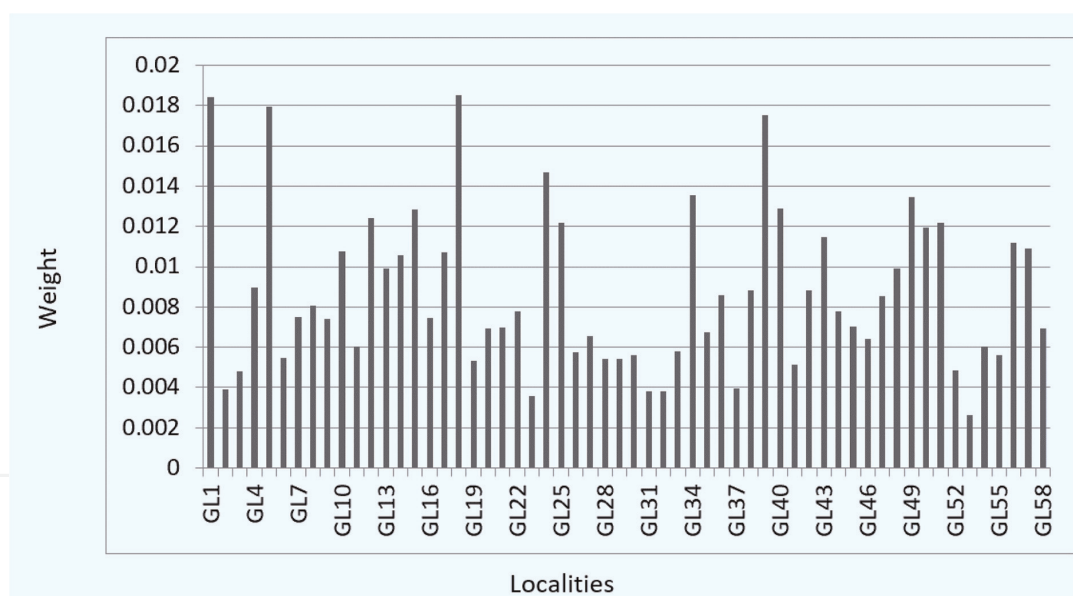
**Figure 9** is a graph displaying the measured strength of all Selangor nodes. The x-axis shows the total number of dengue hotspots in Selangor (across six districts), while the y-axis displays their relative strength. The weighted Newman projection method was utilized to evaluate the node strength. The Selangor dengue network's strongest nodes are PL120, PL25, PL128, PL121, HLL130, PL31, and HLL64. These hubs are deeply rooted in the dengue epidemic's underlying network.

### 3. Centralization approaches considered for the dengue network

The weighted Newman approach is utilized to calculate closeness centrality, which is displayed in **Figure 10** [15, 22, 23]. Eq. (2) is applied in the closeness centrality. As  $\alpha$  is set to 0, the shortest path measure is used to determine a node's centrality. Alternatively, if  $\alpha=1$ , the distance is determined using the link weights. Weighted Newman method results show that GL18, GL1, and GL5 are the three closest values. In other words, these hubs serve as the most direct routes for the dengue virus to spread. Based on the number of reported dengue cases, GL18 is the most important node in the network, whereas GL1, GL5, and GL39 are the most connected. It's proof that there are a lot of dengue virus cases in those areas.



**Figure 9.**  
 The weighted Newman method's analysis of the Selangor network's node strengths.



**Figure 10.**  
 The Gombak network's weighted Newman centrality in terms of closeness.

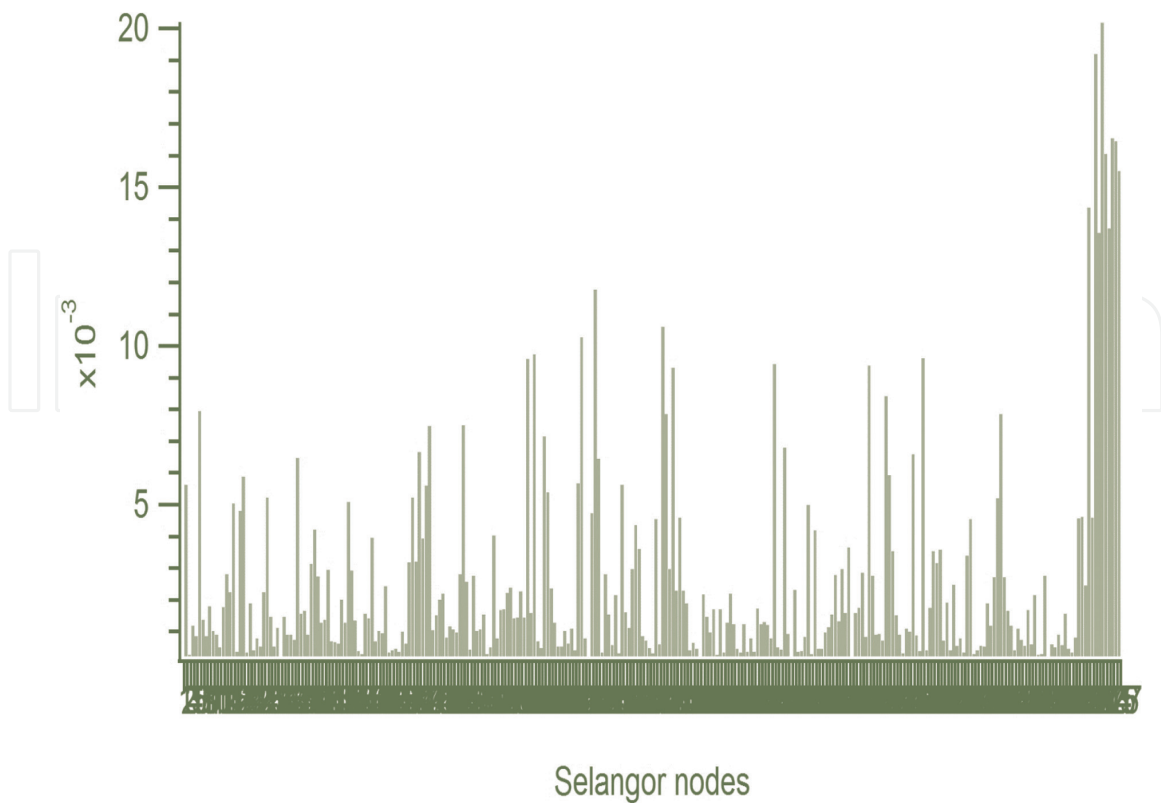
Researchers [17, 24–26] calculated a weighted closeness centrality, provided in Eq. (2).

$$C_C^{W\alpha}(i) = \left[ \sum_j^N d^{w\alpha}(i,j) \right] \quad (2)$$

$C_C^{W\alpha}(i)$  is the weighted closeness centrality of node  $i$ , and  $\alpha$  is the tuning parameter. However,  $d^{w\alpha}(i,j)$  is the weighted distance between nodes  $i$  and  $j$ .

**Figure 10** displays the closeness centrality of just the Gombak nodes, while **Figure 11** depicts the closeness centrality of the entire Selangor dengue network.





**Figure 11.**  
The weighted Newman method of determining the closeness centrality of the Selangor network.

The x-axis depicts all of the Selangor locations where dengue fever has been confirmed. The closeness centrality measure has been calculated using the weighted Newman projection technique. The nodes with the highest closeness centrality scores in the entire Selangor dengue network are located at PL126, PL31, PL134, PL137, PL127, PL200, SL5, PL28, PL54, and HLL64. This demonstrates that the dengue virus is more likely to propagate from these specific nodes to the rest of the network. As a result, reducing the size of the dengue outbreak requires a concentrated effort at these hubs.

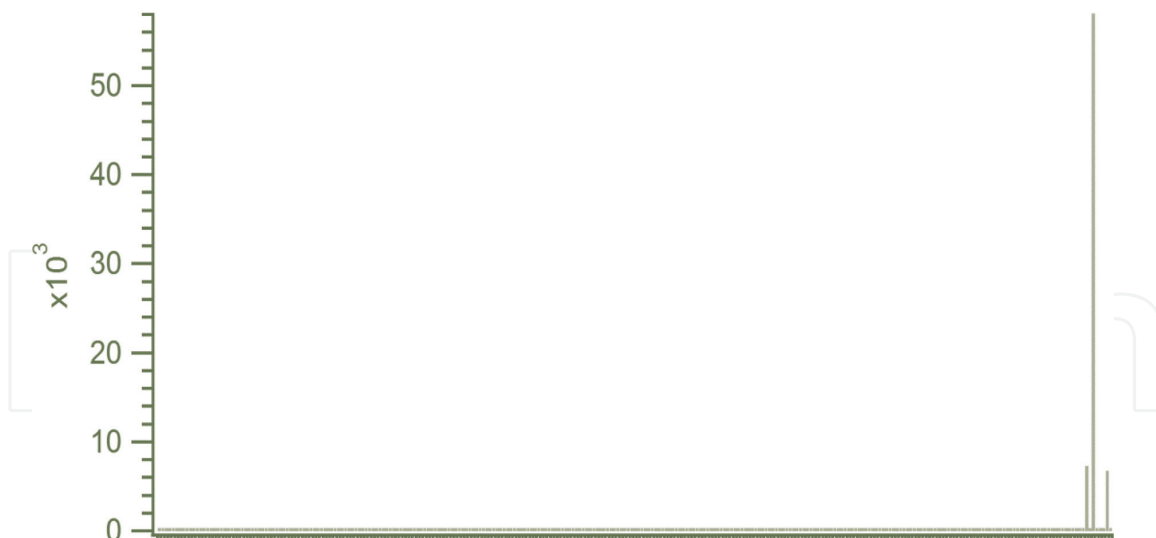
While using the Newman approach, the three closest values are GL18, GL1, and GL5, whereas when using the Sum technique, the top three closest values are GL5, GL18, and GL1. The sum approach of calculating the shortest path has given more weight than the weighted Newman method.

The entire dengue network in Selangor is depicted in **Figure 12** as a betweenness centrality. Weighted Newman analysis was used, with the x-axis representing all dengue-infected nodes in Selangor. The nodes PL126, PL31, and PL137 here have the highest betweenness centrality in the entire Selangor dengue network. This suggests that these three nodes have been crucial in boosting the spread of the epidemic virus across the network.

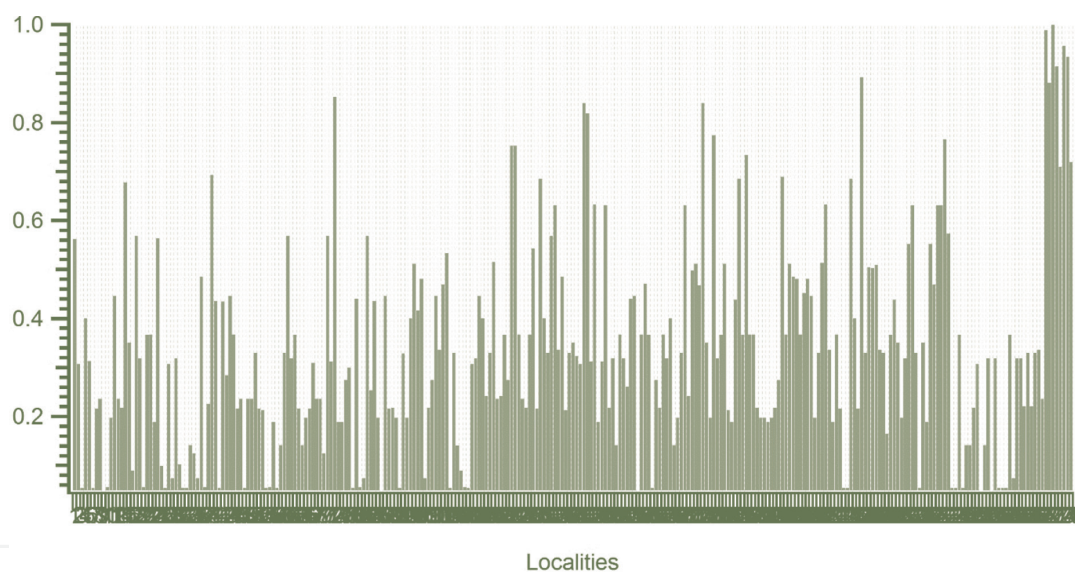
The generic version of weighted betweenness is Eq. (3) [17–19]:

$$C_B^{w\alpha} = \sum_j^N \sum_k^N \frac{g_{jk}^{w\alpha}(i)}{g_{jk}^{w\alpha}} \quad j \neq k \quad (3)$$

$g_{jk}^{w\alpha}(i)$  depicts the total number of the weighted shortest paths between two nodes, while  $g_{jk}^{w\alpha}(i)$  represents the number of those paths that pass by node  $i$ .



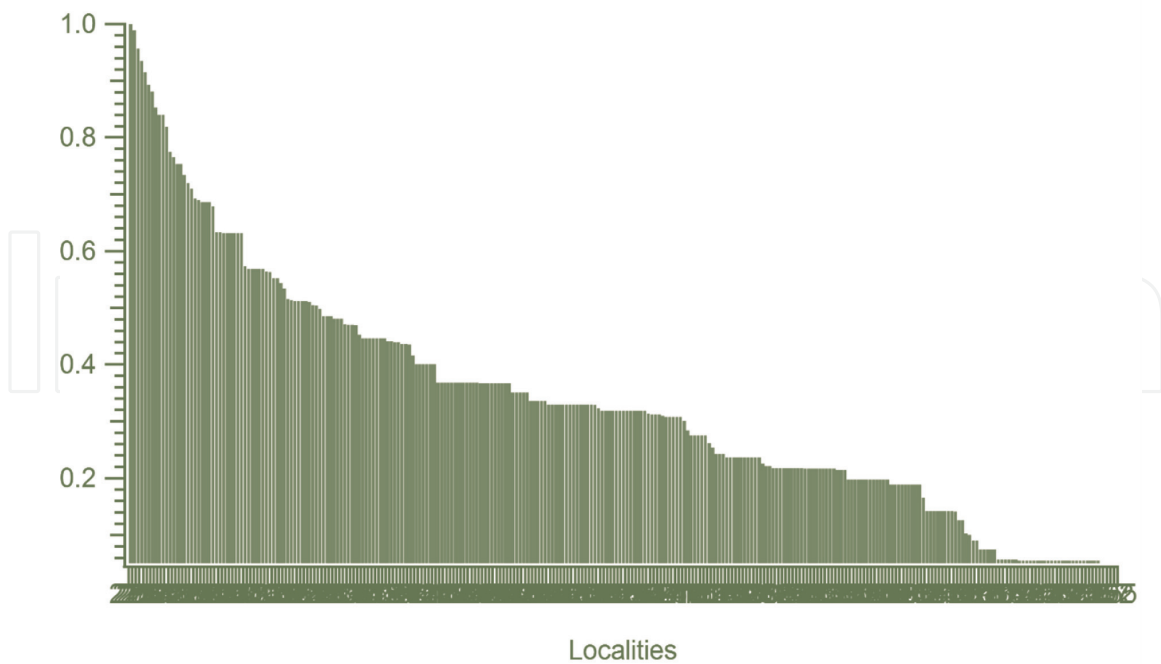
**Figure 12.**  
 The weighted Newman betweenness centrality measure applied to the Selangor network.



**Figure 13.**  
 Eigenvector centrality measure.

In **Figure 13**, we see the outcome of applying the weighted Newman projection method to the concept of eigenvector centrality. The centrality score was computed using Eq. (4). The eigenvector centrality (EVC) measure determines the most significant nodes in a network. Moreover, EVC explains how not every link is of the same value. Based on this centrality study, the most significant Selangor dengue network nodes are 272, 270, 275, 276, 273, 219, 271, 73, 142, 175, 143, 178, 242, and 122. These hubs are significant (in terms of high dengue cases); hence, it is recommended that they be taken into account while designing more effective treatments to curb the current dengue epidemic in Selangor. Eq. (4) defines EVC [17, 19, 24, 25].

$$x_i = \frac{1}{\lambda} \sum_{j=1}^n A_{ij} x_j \quad (4)$$



**Figure 14.**  
EVC resembled a power-law form.

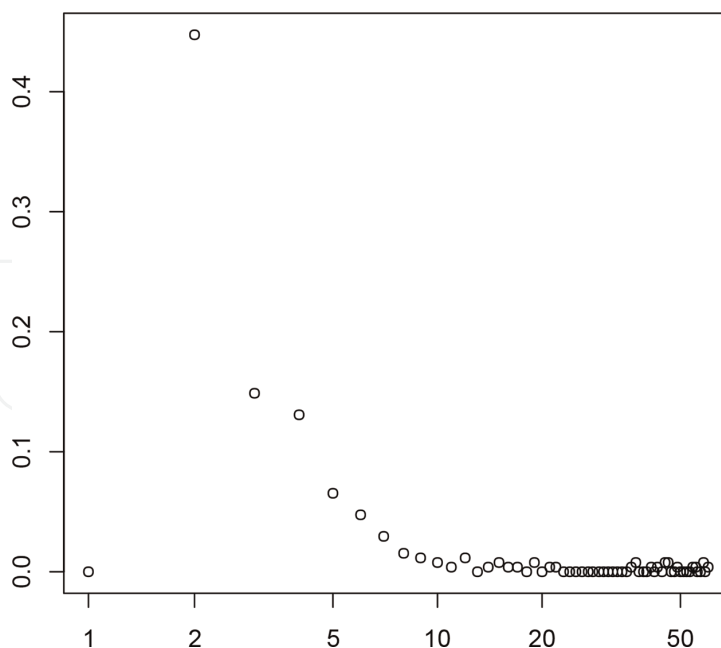
Where  $x_i$  is the eigenvector centrality of  $i$  network,  $\lambda$  is a constant and  $A_{ij}$  is the adjacency matrix ( $A_{ij} = 1$  if links  $i$  and  $k$  exist, and  $0$  otherwise).

This can be shown in **Figure 14** for the network as a whole using eigenvector centrality, where the power-law form can be observed to indicate the small number of nodes with disproportionately high weights (importance) in comparison to the vast majority of nodes with lower weights [27, 28]. Because more dengue cases appeared at these higher weighted nodes, they should be considered while treating the dengue epidemic network.

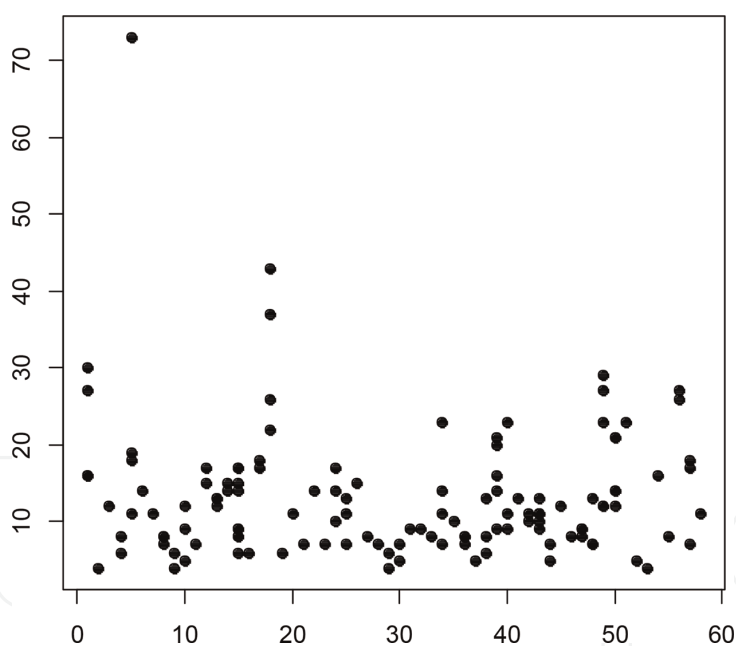
### 3.1 The network density

If we define a potential link as a connection that could exist between two nodes, then the density of a network is the fraction of these potential links that are actually linked. With a density of 0.52 nodes per node, the network is dense. It's clear from this that most of the network's dengue cases are concentrated in a small subset of nodes. **Figure 15** demonstrates the dense nature of the network. For the Gombak dengue network, the y-axis indicates the likelihood of link weights, while the x-axis displays the link weights themselves.

The density of the nodes in the Gombak dengue network is shown graphically in **Figure 16** as a scatter plot, where the x-axis displays the link weight, and the y-axis shows the total number of linkages. As can be seen, the weight of many nodes is low, while the weight of a select few is significant. If this network is partitioned into distinct clusters, as shown in **Figure 17**, then the clusters will be dense. Therefore, treating these clusters effectively is important to disrupt the global dengue transmission system. The y-axis depicts the connection weight in the Selangor dengue network, while the x-axis displays the total number of linkages.



**Figure 15.**  
*The network density.*



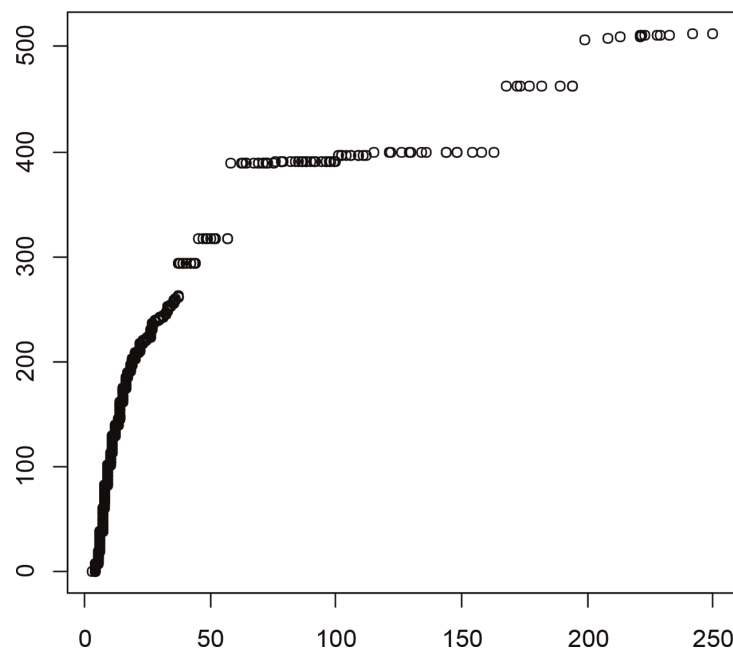
**Figure 16.**  
*The density of nodes.*

#### 4. Dengue network: scale-free aspects

A few instances of scale-free networks (SFNs) with varying values for the power-law exponent are listed in **Table 1**. Observations of the topological structure of complex systems in several areas of biology have been the focus of many recent studies. When Barabasi modeled the World Wide Web and its hypertext links, he introduced the concept of a spectral family network (SFN) with power-law exponents  $\gamma_{in} = 2.1$  and  $\gamma_{out} = 2.7$ . Here,  $\gamma_{in}$  and  $\gamma_{out}$  represent the in-degree and out-degree of the

Network examples	Power-law exponent ( $\gamma$ )
Food web	1.1
Co-occurrence	1.8
Cellular	2.2
Movie actor	2.3
www	2.1

**Table 1.**  
 *$\gamma$  for certain representative network systems.*

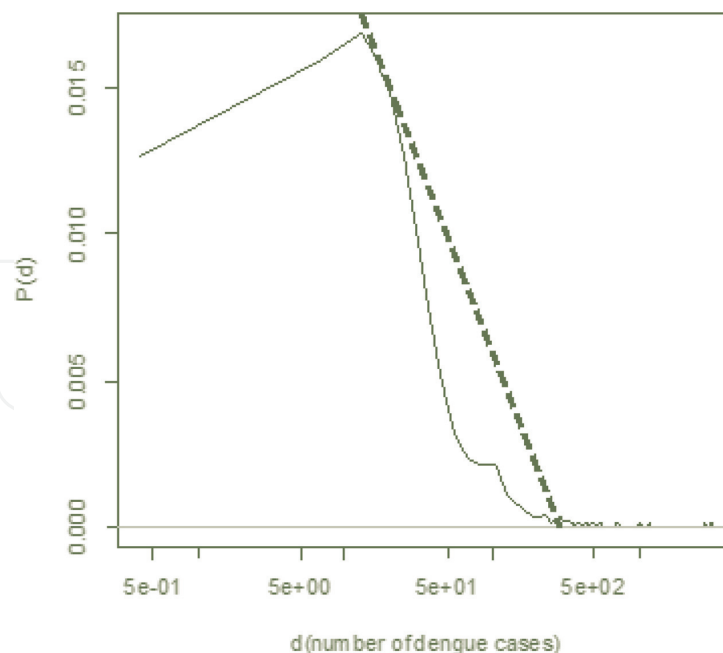


**Figure 17.**  
*The density of clusters.*

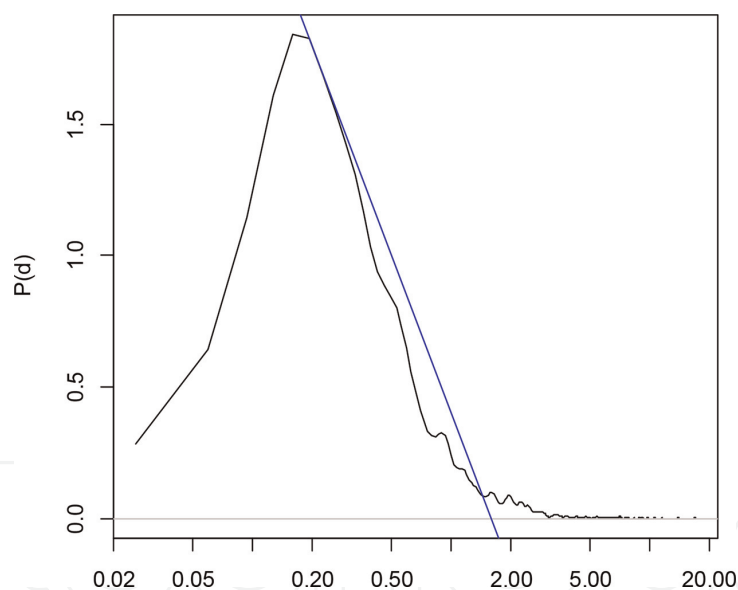
network, respectively [28, 29]. Scale-free power-law distributions were discovered for this social phenomenon, with  $\gamma_f = 3.4$  for females and  $\gamma_m = 3.3$  for males. Newman modeled scientists as nodes and their scholarly articles as edges in a defined two-mode scientific collaboration network [24, 25]. In this network, the major ties between the two scientists are articles they have co-authored. In the instance of the high-energy physics database, he discovered that the degree distribution of this network follows a power law with the exponent  $\gamma = 1$ .

In **Figure 18**, we see a log–log scale depicting the probability distribution of node strength (the number of dengue cases in various areas of Selangor). If the exponent is roughly near the lower bound of the power-law exponent limit, as shown by the broken line in **Figure 18**, then the network has spatially arranged itself into a scale-free network [15]. As the distribution has a negative slope, the power-law exponent takes on the value  $-1.9$ . This probability distribution shows power-law organization across time. Important for determining SFN is the presence of a power-law distribution [15, 24, 27–29].

Moreover, a small number of links carry disproportionately heavy weight relative to the rest. SFN is crucial to addressing the problem of epidemic diseases. If the



**Figure 18.**  
 Dengue fever incidence follows a power law distribution  $\gamma = - 1.8$ .



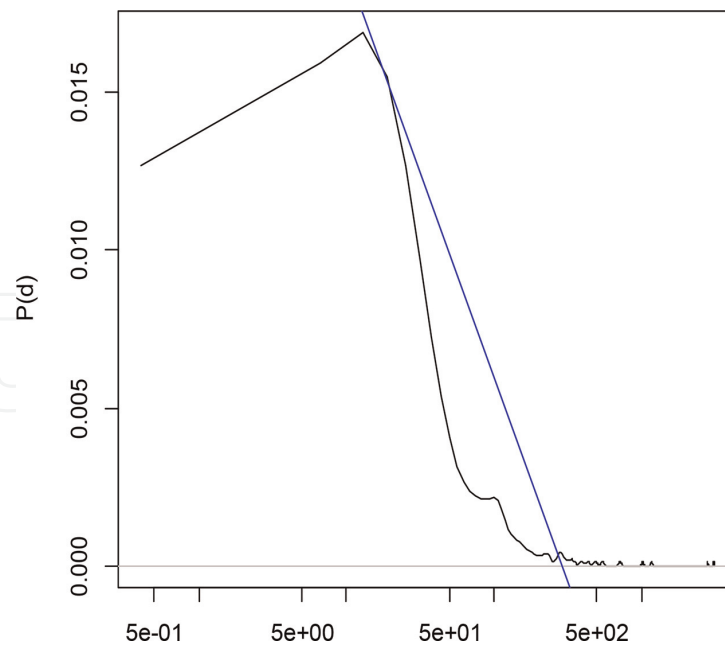
**Figure 19.**  
 Node strength by using Newman projection.

epidemic diseases are SFN, this network topology will be more effective in stopping them. In contrast to the random network, targeted attacks can take out central nodes.

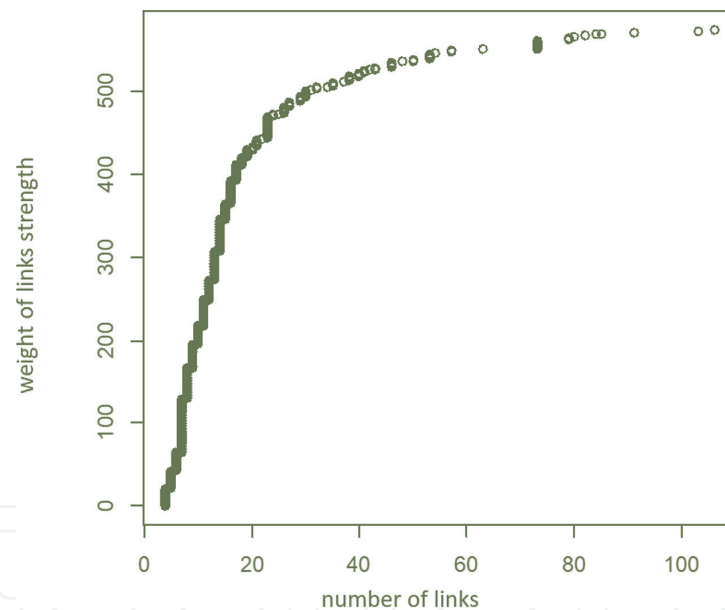
The distribution of node strengths reveals the general behavior of the network's strength, which is the weighted degree of dengue cases at each node.

The node strength of the weighted Newman projection is depicted in **Figure 19**; the x-axis depicts the strength of linkages, while the y-axis shows the probability distribution of link strengths. The network's geographical organization resembles a power-law distribution, as represented by the line on a declining curve.

**Figure 20** shows connection strength and probability distribution on the x- and y-axes, respectively. It's important to note that the logarithmic scale is used here.



**Figure 20.**  
*Node strength of Sum projection.*



**Figure 21.**  
*Weight of links.*

A power-law distribution can be seen in the network's geographic organization, as represented by the trendline on the decreasing curve. As this graph demonstrates, however, the dengue virus particularly hits hard only a small subset of nodes. Heavy tails and right skews were seen in the link weight probability distribution.

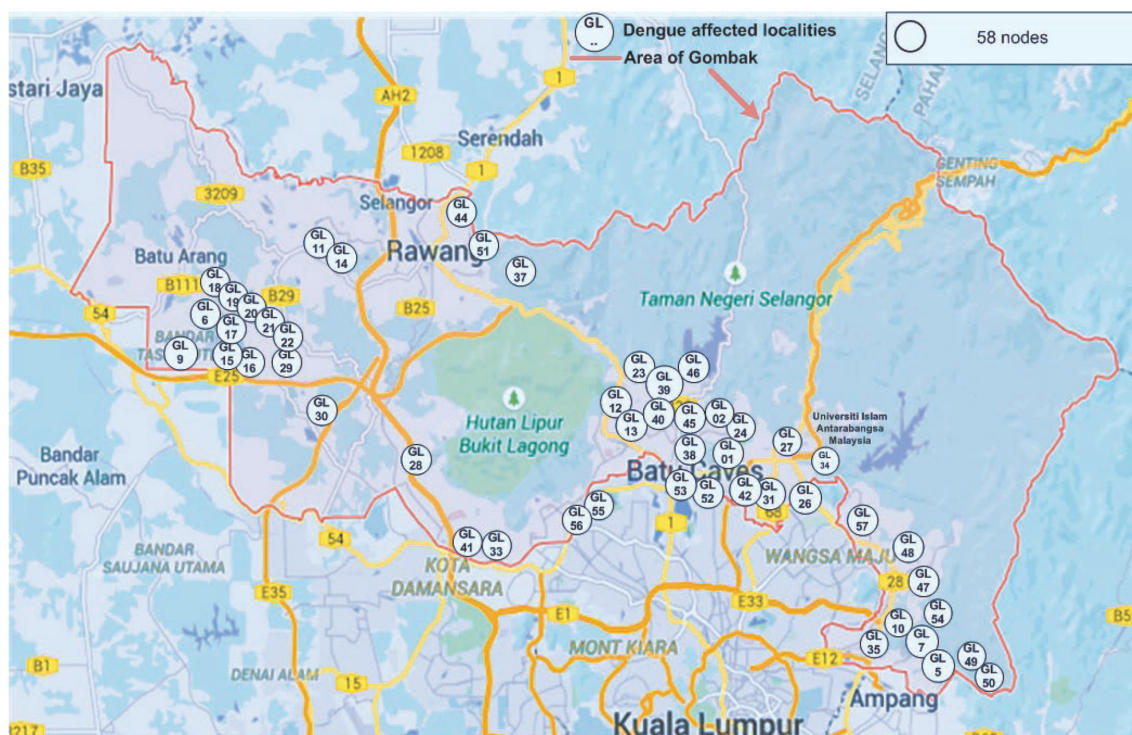
In **Figure 21**, we see a representation of link strength as a linear function of link weight, where the x-axis indicates the total number of links, and the y-axis reflects the strength of individual ties. It shows that a small number of links in this two-way network have disproportionately impacted the entire network. There are only a handful of major hubs where dengue fever has been widely reported.

#### 4.1 Vulnerability of nodes shown on actual map

Fifty-eight affected nodes are detected in Gombak, Selangor. The dengue-affected locations are shown on the Google Map, highlighting the Gombak area. In **Figure 22**, the Gombak boundary is shown with a curvy red line spotted with a red arrow, and the dengue-affected areas of Gombak are shown in small circles labeled GL1 (Gombak Locality 1) until GL58. Dengue hotspots are displayed here as distinct groupings on the map. GL15 and GL18 are the primary nodes in this cluster regarding the total number of dengue cases reported. Other clusters include GL19, GL20, GL22, GL29, GL6, GL15, GL16, and GL17 [23]. The nodes GL23, GL39, GL40, GL45, GL01, GL38, GL53, and GL52 form a second cluster, with GL01 and GL39 serving as its primary hubs. GL05 is the central core of this cluster. However, other clusters such as GL49, GL50, GL 7, GL5, GL10, and GL54 are also visible.

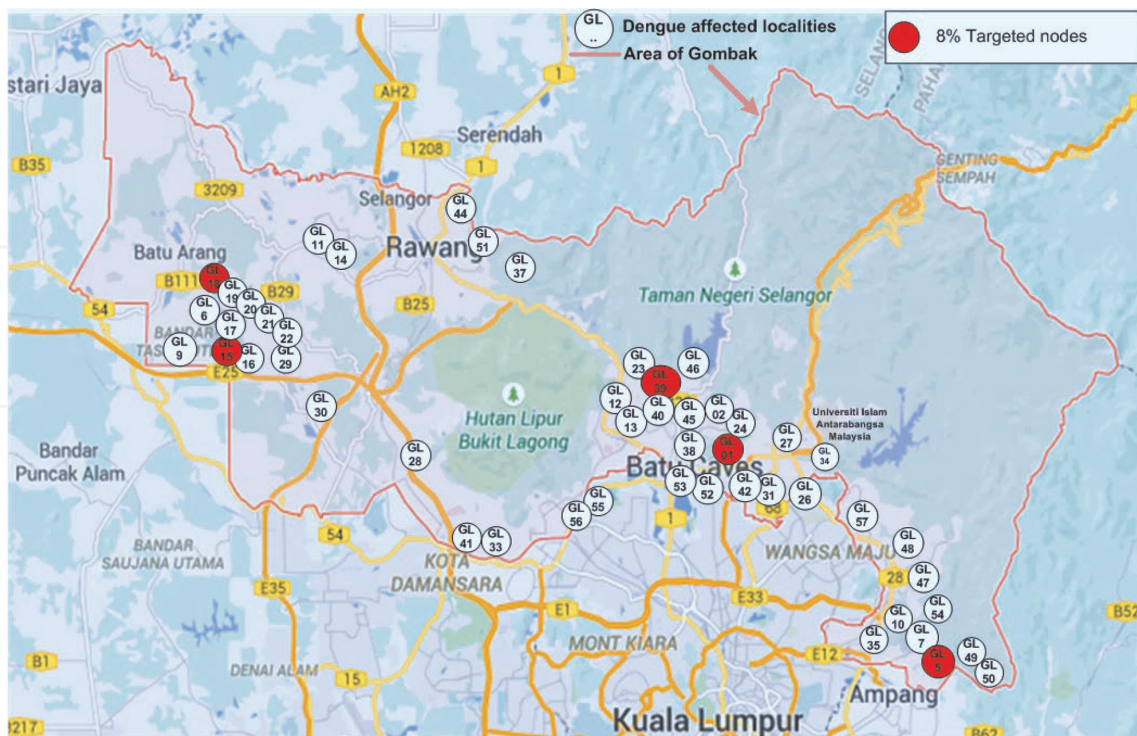
Using a red circle, we have drawn attention to the five major centers (in terms of high dengue-affected cases) in **Figure 23**. These five nodes account for 8% of Gombak's total dengue network. The nodes GL01, GL5, GL15, GL18, and GL39 are colored red. Taking the total number of dengue cases into account, it becomes clear that these are the epicenters that must be addressed to control the spread of the disease. A higher-than-usual number of dengue cases indicate that there are more *A. aegypti* in the area. In addition, these nodes play a crucial role in dismantling clusters, allowing for the elimination of particularly large clusters from the network as a whole.

If this 8% of the network's nodes, symbolized by the green circles in **Figure 24**, are fixed or removed from the network in the future, then this destroys 34% of the dengue network. This is a good illustration of the effectiveness of a targeted attack that is more useful in a scale-free network than a random one.

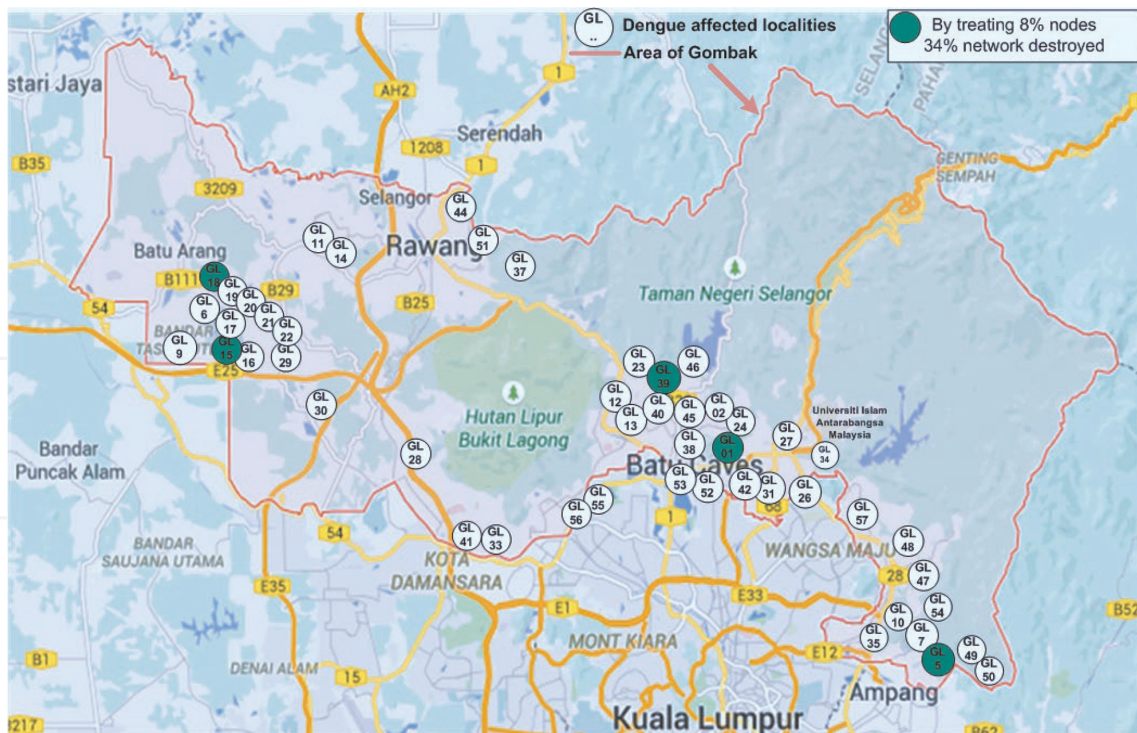


**Figure 22.**  
Gombak dengue map.



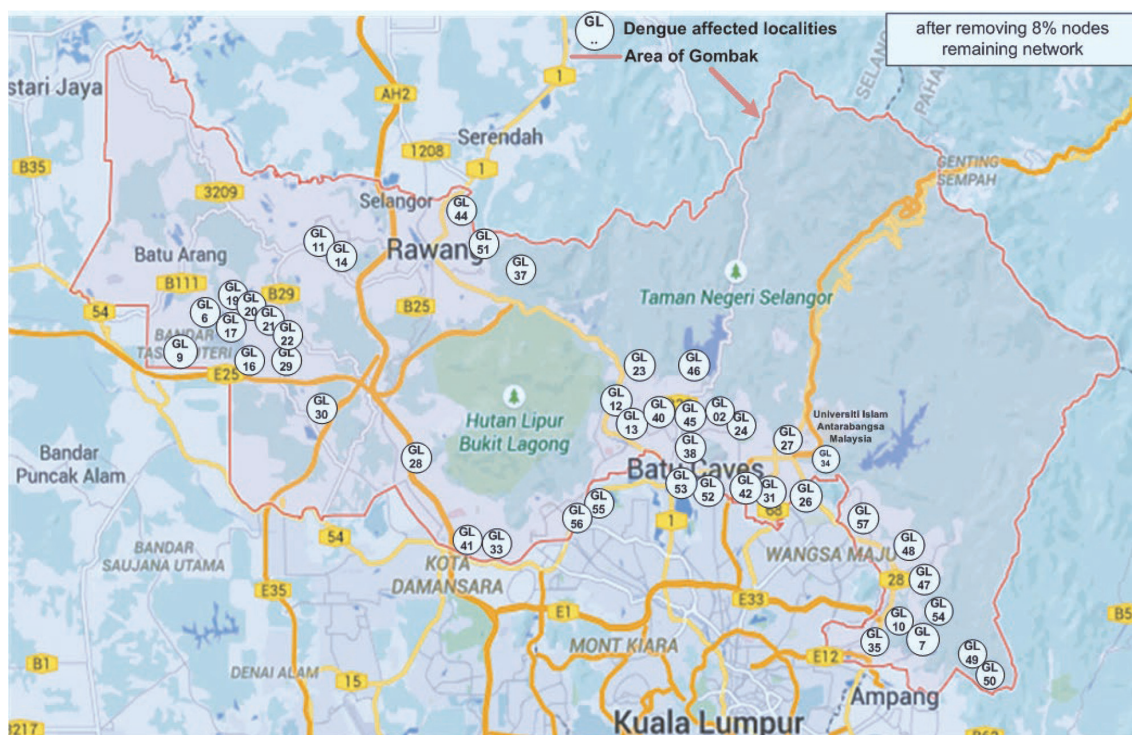


**Figure 23.**  
Targeted 8% nodes (red-colored localities).



**Figure 24.**  
Targeted 8% of nodes are recovered/removed/treated.

After the targeted elimination of 8% of nodes in the dengue epidemic network from **Figure 24**, the remaining 66% of network is shown on the real map in **Figure 25**. Other nodes in the network that serve as focal hubs have also been identified. This strategy can slow or prevent the spread of the dengue virus. It has been analyzed that a



**Figure 25.**  
Remaining 66% of network.

5% targeted approach created equivalent consequences to 65% of random attacks on the network. Accordingly, rather than dismissing this network as random, it should be treated as a targeted attack that is more powerful in the scale-free network.

## 5. Conclusion

Dengue fever poses a significant global burden and new challenge to health policymakers worldwide. Despite the many attempts made to combat *Aedes aegypti* and its detrimental impacts on humans, no definitive victories have been achieved yet, as mentioned in the literature review. We have used empirical methods to describe and evaluate the dengue outbreak as a complex network. The dengue epidemic is established to be a scale-free network using network analysis metrics and robustness under the targeted attacks. The results demonstrated that a dengue epidemic network is vulnerable if they adhere to a scale-free network structure.

Furthermore, the study results indicated that eliminating a small percentage of focal hubs destroyed a big part of the network, demonstrating a feature of scale-free networks. The findings revealed that 8% of network nodes, that is, GL01, GL5, GL15, GL18, and GL39, were removed from the Gombak network, resulting in the destruction of 34% of the total network. Dengue network modeling and proof as a scale-free network will contribute to the body of knowledge on complex networks.

## Conflict of interest

The authors declare no conflict of interest.

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## References

- [1] WHO. Dengue and severe dengue. 2022. Available from: <https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue>
- [2] Eduardo J, Pessanha M. Risk assessment and risk maps using a simple dengue fever model. *Dengue Bulletin*. 2012;**36**:73-86
- [3] Struchiner CJ, Rocklöv J, Wilder-Smith A, Massad E. Increasing dengue incidence in Singapore over the Past 40 Years: Population growth, climate and mobility. *PLoS One*. 2015;**10**(8):1-14. DOI: 10.1371/journal.pone.0136286
- [4] Coelho GE, Burattini MN, Teixeira MDG, Coutinho FAB, Massad E. Dynamics of the 2006/2007 dengue outbreak in Brazil. *Memórias do Instituto Oswaldo Cruz*. 2008;**103**(6): 535-539. DOI: 10.1590/S0074-02762008000600004
- [5] Pessanha JEMP, Caiaffa WT, Almeida MCDM, Brandão ST, Proietti FA. Diffusion pattern and hotspot detection of dengue in Belo Horizonte, Minas Gerais, Brazil. *Journal of Tropical Medicine*. 2012;**2012**:1-11. DOI: 10.1155/2012/760951
- [6] Coutinho FAB, Burattinia MN, Lopeza LF, Massada E. Threshold conditions for a non-autonomous epidemic system describing the population dynamics of dengue. *Bulletin of Mathematical Biology*. 2006;**68**(8): 2263-2282. DOI: 10.1007/s11538-006-9108-6
- [7] Coutinho FAB, Burattini MN, Lopez LF, Massad E. An approximate threshold condition for non-autonomous system: An application to a vector-borne infection. *Mathematics and Computers in Simulation*. 2005;**70**(3):149-158. DOI: 10.1016/j.matcom.2005.06.003
- [8] Derouich M, Boutayeb A. A model of dengue fever biomed. *Engineer Online*. 2003;**2**(4):1-11
- [9] Amaku M, Coutinho FAB, Raimundo SM, Lopez LF, Nascimento Burattini M, Massad E. A comparative analysis of the relative efficacy of vector-control strategies against dengue fever. *Bulletin of Mathematical Biology*. 2014; **76**(3):697-717. DOI: 10.1007/s11538-014-9939-5
- [10] Side S, Noorani S. A SIR model for spread of dengue fever disease (simulation for South). *World Journal of Modelling and Simulation*. 2013;**9**(2):96-105
- [11] Malik HAM, Abid F, Wahiddin MR, Waqas A. Modeling of internal and external factors affecting a complex dengue network. Vol. 144. *Chaos: Solitons & Fractals*. 2021. p. 110694. DOI: 10.1016/j.chaos.2021.110694
- [12] Schapira A et al. Baseline and key container survey for *Aedes aegypti* and *Aedes albopictus* in Albay Province, Philippines. *Dengue Bulletin*. 2012;**36**:182
- [13] Derouich M, Boutayeb A. Dengue fever: Mathematical modelling and computer simulation. *Applied Mathematics and Computation*. 2006; **177**(2):528-544. DOI: 10.1016/j.amc.2005.11.031
- [14] Malik HAM, Mahesar AW, Abid F, Waqas A, Wahiddin MR. Two-mode network modeling and analysis of dengue epidemic behavior in Gombak, Malaysia. *Applied Mathematical Modelling*. 2017;**43**:207-220. DOI: 10.1016/j.apm.2016.10.060
- [15] Malik HAM, Abid F, Mahmood N, Wahiddin MR, Malik A. Nature of

- complex network of dengue epidemic as a scale-free network. *Healthcare Informatics Research*. 2019;**25**(3):182-192. DOI: 10.4258/hir.2019.25.3.182
- [16] Padrón B, Nogales M, Traveset A. Alternative approaches of transforming bimodal into unimodal mutualistic networks. The usefulness of preserving weighted information. *Basic and Applied Ecology*. 2011;**12**(8):713-721. DOI: 10.1016/j.baae.2011.09.004
- [17] Opsahl T, Panzarasa P. Clustering in weighted networks. *Social Networks*. 2009;**31**(2):155-163. DOI: 10.1016/j.socnet.2009.02.002
- [18] Opsahl T. Triadic closure in two-mode networks: Redefining the global and local clustering coefficients. *Social Networks*. 2013;**35**(2):159-167. DOI: 10.1016/j.socnet.2011.07.001
- [19] Opsahl T, Agneessens F, Skvoretz J. Node centrality in weighted networks: Generalizing degree and shortest paths. *Social Networks*. 2010;**32**(3):245-251. DOI: 10.1016/j.socnet.2010.03.006
- [20] Malik W, Abid M. Two-mode complex network modeling of dengue epidemic in Selangor, Malaysia. In: *The 5th International Conference on Information and Communication Technology for The Muslim World Malaysia (ICT4M)*. IEEE; 2014
- [21] Abid MRWH, Malik M, Mahesar AW, Abid F, Waqas A. Two-mode network modeling and analysis of dengue epidemic behavior in Gombak, Malaysia. *Applied Mathematical Modelling*. 2016;**43**:207-220
- [22] Malik HAM, Mahmood N, Usman MH, Rziwan K, Abid F. Analysis of airport network in Pakistan utilizing complex network approach. *International Journal of Advanced Computer Science and Applications*. 2019;**10**(1)
- [23] Malik HAM, Abid F, Wahiddin MR, Bhatti Z. Robustness of dengue complex network under targeted versus random attack. *Complexity*. 2017;**2017**:1-12. DOI: 10.1155/2017/2515928
- [24] Newman MEJ. The structure of scientific collaboration networks. *Proceedings of the National Academy of Sciences of the United States of America*. 2001;**98**(2):404-409. DOI: 10.1073/PNAS.98.2.404
- [25] Clauset A, Shalizi CR, Newman ME. Power-law distributions in empirical data. *SIAM review*. 2009;**51**(4):661-703
- [26] Brandes U. A faster algorithm for betweenness centrality. *Journal of mathematical sociology*. 2001;**25**(2): 163-177
- [27] Solé RV. Linked: The New Science of Networks. 2003:85
- [28] Barabási A-L, Bonabeau E. Scale-free networks. *Scientific American*. 2003;**288**(5):60-69. DOI: 10.1038/scientificamerican0503-60
- [29] Albert R, Barabási AL. Statistical mechanics of complex networks. *Reviews of modern physics*. 2002;**74**(1): 47. DOI: 10.1103/RevModPhys.74.47