Original Article

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Nature of Complex Network of Dengue Epidemic as a Scale-Free Network

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Objectives: Dengue epidemic is a dynamic and complex phenomenon that has gained considerable attention due to its injurious effects. The focus of this study is to statically analyze the nature of the dengue epidemic network in terms of whether it follows the features of a scale-free network or a random network. **Methods:** A multifarious network of *Aedes aegypti* is addressed keeping the viewpoint of a complex system and modelled as a network. The dengue network has been transformed into a one-mode network from a two-mode network by utilizing projection methods. Furthermore, three network features have been analyzed, the power-law, clustering coefficient, and network visualization. In addition, five methods have been applied to calculate the global clustering coefficient. **Results:** It has been observed that dengue epidemic follows a power-law, with the value of its exponent $\gamma = -2.1$. The value of the clustering coefficient is high for dengue cases, as weight of links. The minimum method showed the highest value among the methods used to calculate the coefficient. Network visualization showed the main areas. Moreover, the dengue situation did not remain the same throughout the observed period. **Conclusions:** The results showed that the network topology exhibits the features of a scale-free network instead of a random network. Focal hubs are highlighted and the critical period is found. Outcomes are important for the researchers, health officials, and policy makers who deal with arbovirus epidemic diseases. *Zika* virus and *Chikungunya* virus can also be modelled and analyzed in this manner.

Keywords: Dengue Virus, Arboviruse, Epidemics, Big Data, Network Meta-Analysis

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I. Introduction

Various kinds of real world complex systems including physical, biological, and social systems can be represented in terms of complex networks. Some important examples are the World Wide Web, electric power grids, scientific collaboration networks, airport networks, the Hajj network, and social networks of friendship [1-4]. In the fields of medicine and biology, the complex networks of diseases such as HIV/AIDS, smallpox, and dengue virus have also been investigated to analyze the spreading phenomenon [5,6]. The dengue virus network includes the mosquito '*Aedes aegypti*'. Dengue is an arbovirus that spreads infections through mosquitoes

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to humans and infected humans to mosquitoes (other than *Aedes* species), constituting a complex network. The network of arbovirus epidemic has become a complex phenomenon. In [7], the robustness of the dengue complex network under targeted versus random attack was observed and it was found that targeted attack gives better outcomes in scale-free networks compared to random networks.

While modeling and analyzing the different complex networks, researchers have observed numerous structural characteristics in different real-world organisms [8]. Specifically, in the last few years the research trend has increasingly moved toward analyzing complex systems by creating networks in the form of nodes and links. This facilitates comprehension of both structural and dynamical features of tangible world complex networks. The research and study of these linkages has played a significant role for immunization in epidemics and network tolerance attacks [9]. The authors observed some scale-free features in the dengue epidemic in Singapore [10]. In addition, they analyzed the dengue spreading situation from the perspective of complex networks and modelled the dataset of dengue affected cases in Selangor as a two-mode network, and then projected it to a one-mode network [5,11]. A dataset of dengue patients has been obtained from the Ministry of Health (MoH) Malaysia, and is provided in Appendix 1. The data are anonymous to protect patients' privacy. The network projection is performed by three methods (weighted Newman, sum, and binary) and the power-law exponent (γ) is calculated, which is an important step to see the deportment of a scale-free network [11].

The existence of a power-law posture is perceived in numerous varieties of complex networks, including metabolic networks, systems of lung inflation, sun motion, and the light from galaxies and the water flow through river [12]. Thus, the power-law has been utilized for discovering complex environments by many researchers in various research areas and contexts.

The power-law is quite different from a bell-shaped normal distribution. A scale-free graph [8] follows a power-law form as given below:

$$\mathbf{P}(k) \sim k^{-\gamma} \tag{1}$$

where *k* represents the degree of a node, the probability of node degree distribution is represented by P(k), and γ (gamma) is a scaling exponent, which is a statistical parameter that is called a connectivity distribution exponent. In reality, γ does not depend on a specific scale of network that is why;

it is called a scale-free parameter. Also, the value of γ has been confirmed in many research studies to approximately range from 2 to 3. R-project has been utilized to find γ and other graphical visualizations in this research.

Scale-free network comprises two main characteristics based on the Barabási-Albert model: growth and preferential attachment. The remainder of this paper is structured as follows: Section I-1 provides the background of the study. In Sections II and III, the methodology is presented and the results are discussed. Finally, Section IV gives conclusions of this research and directions for future work.

1. Background

Dengue fever is a major disease in tropical regions of the world. Approximately 25 million people are in danger due to mosquito borne dengue fever [13,14]. It is caused by an arbovirus, *Aedes aegypti*, which is the primary vector of dengue virus [14]. DENV-1, DENV-2, DENV-3, and DENV-4 are four serotypes that have been found in this disease [14-18].

1) Dengue in Malaysia

MoH Malaysia published a report in 2015 noting 107,079 dengue cases with 293 deaths while there were 43,000 dengue cases with 92 deaths in 2013 [19-21]. According to the MoH Malaysia, the presence of dengue has been growing rapidly since 2012 [22,23]. The rapid spread of dengue virus has become more harmful and tackling this matter should be considered urgent. Dengue epidemic is an important field of research and many researchers are investigating this phenomenon from different viewpoints [18,24,25]. In light of the importance of this issue and with the aim of working toward a remedy, the authors have modelled the dengue problem in Malaysia by utilizing the two-mode network technique [11].

2) Modeling of dengue epidemic network

Researchers have been utilizing the two-mode network technique in many fields, such as collaborative work and movieactor networks [26-28]. The authors of this paper have utilized the two-mode network technique in the dengue mosquito network [11]. In this network primary nodes are represented by L1, L2, L3, and L4 and secondary set of nodes are represented by W1, W2, W3, and W4. A two-mode network is usually converted into a one-mode network by projection for better analysis [28]. The current work is an enhanced form and continuation of our previous work [11]. Analysis of the network is based on the power-law behavior, clustering coefficient, and network visualization, and most importantly we observed the characteristics of the *Aedes aegypti* network from the viewpoint of a scale-free network and random network. In general, there are various types of networks and different ways to destroy those networks. It is very important that before attacking any network, the topology of the network should be understood. Similarly, to break down the dengue network, it must be clarified whether it should be treated as a scale-free network or a random network

II. Methods

1. Network Analysis

This section presents an analysis of the weighted two-mode dengue network, which has been performed from the perspective of dengue cases that appeared in different locations in Selangor. After utilizing the projection ways (binary, sum, and weighted Newman) and on the basis of their outcomes, the weighted Newman method has been observed to provide the best fit for this dataset. By this method, the dataset lost the minimum weighted information [11]. From the given dataset, the power-law exponent (γ) is calculated and the results showed the trend towards a power-law. It should be noted that a scale-free network follows a power-law [8]. In this research, the results show the characteristics of a scale-free network and particularly the topology of this complex dengue network is in a power-law form.

To see the graphical trends of the power-law, graphs are formed utilizing the dataset (bipartite) of Gombak, Hulu Langat, and Petaling, where numbers of dengue cases are shown in effected localities, respectively. Furthermore, the clustering coefficient is calculated to observe the deviation of the network.

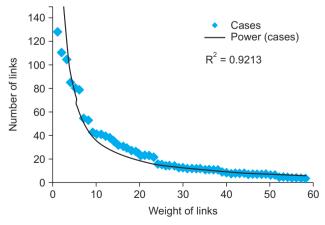


Figure 1. Dengue cases in Gombak, Selangor (2013-2014).

III. Results

1. Power-Law Behavior

In Figure 1, the x-axis shows the weight of links and the yaxis shows the number of links. Dengue cases in different localities of Gombak that occurred during the observed years are represented on a linear scale. The figure displays powerlaw behavior. It clearly indicates that the human populations in a few localities were highly affected by the dengue virus in Selangor, Malaysia, during the given period.

There are 58 localities in Gombak that recorded 1487 dengue cases in total in the given period. The highest number of dengue cases (=128) was registered in location no. 18 whereas only four cases were observed in location no. 2. In Figure 2, Hulu Langat, 185 localities were affected compared to Petaling, where 243 dengue affected localities were registered. It is interesting that in these three areas only a few localities were attacked repeatedly by Aedes aegypti, whereas in other localities this mosquito attacked once or twice in a year. This showed the dengue has effected within this particular area. Similarly, there are a few areas that were highly affected by the dengue virus. In very few places the dengue appearance is high whereas the majority of localities have a small number of dengue cases. There is consequently a need to place greater focus on these few areas to control this disease. On the other side, identification of focal nodes in a complex networks is an important issue for researchers and scientists. Specifically, if the central node is identified, it will potentially make it possible to control the flow of other nodes. Moreover, via that node, other nodes can be captured very quickly. Hence, targeting the areas in which dengue virus is appearing repeatedly and affecting large populations may be a more helpful means to find and control the central node.

In Figures 1–3, R^2 is the coefficient of determination. This

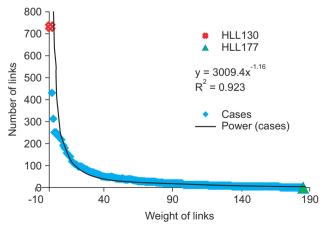


Figure 2. Dengue cases in Hulu Langat, Selangor (2013-2014).

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statistical measure shows how good the regression line estimates the real data points. R^2 provides information on the goodness of fit of a model. Here, $R^2 = 0.9213$, 0.923, and 0.9102 specify that the regression line perfectly fits the data, respectively.

The coefficient of determination is calculated as:

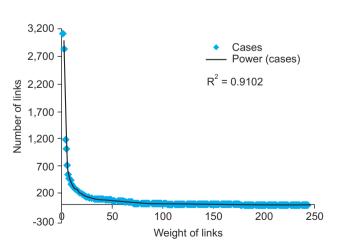
$$R^2 = 1 - \frac{SS_{res}}{SS_{tot}}$$
(2)

where SS_{tot} represents the total sum of squares and SS_{res} is the residual sum of squares.

In Figure 2, the x-axis shows the weight of links and the yaxis shows the number of links. The number of dengue cases in different localities of Hulu Langat that were included in this network during the given period. The weight of links as dengue cases in different localities is shown on a linear scale. Out of 185 dengue affected localities, 7,854 dengue cases were registered. The highest number of cases (= 729) was recorded in the location HL130, whereas the smallest number of cases (= 4) was recorded in location HL177.

In Figure 3, the x-axis shows the weight of links and the y-axis shows the number of links. The numbers of dengue cases in different localities of Petaling are displayed on a linear scale during the period 2013–2014. It can be grasped that there are few localities that registered an extraordinary number of cases. Out of 243 affected localities of Petaling, 15,261 dengue cases were recorded throughout the given period. The highest number of dengue cases (= 3,107) was registered in Petaling (location no. 126). The smallest number, four cases, was observed in Petaling (location no. 240 and 243).

In the literature, some examples of scale-free network are presented, where the power-law exponent has different values. Researchers considered these networks to be scalefree [1,8]. Investigations of the topology of complex systems





from different domains of life have shown interesting results. For example, Barabasi and Bonabeau [8] modelled World Wide Web pages and their hyper-links and brought the idea of scale-free network with power-law exponents $\gamma_{in} = 2.1$ and γ_{out} = 2.7, where γ_{in} and γ_{out} are in-degree and out-degree, respectively. In 2001, Liljeros et al. [29] modelled and investigated human sexual connections as a network. Researchers found this societal occurrence to be scale-free and showed that it follows the power-law form (where $\gamma_f = 2.54$ for females and $\gamma_m = 2.31$ for males). Newman formed a scientific association network as a two-mode network, where he modelled nodes as scientists and their collaborated papers. Two scientists are linked if they worked on a joint article as primary nodes. He observed the degree distribution of this network in the case of a high energy physics databank, which follows a power-law with the exponent $\gamma = 1.2$ [1].

Figure 4 shows the probability distribution of node strength (number of dengue cases in different areas of Selangor) on a log scale, for cases recorded in a given period. R-project has been utilized to calculate the power-law exponent (γ) . The broken line is the slope of the declining curve and it represents that this network is geographically structured as a scale-free network. γ is close to the lower bound of its limit. Here, $\gamma = -2.1$, which indicates a decreasing slope of the distribution. This probability distribution indicates that the distribution follows a power-law; it has geographically organized itself during the given period. The power-law is an important indicator of scale-free network. Moreover, important links are few in number and should be focused on as they have huge weight compared to other links. A scale-free network is very important in solving the epidemic issue. Epidemic diseases can be better controlled by this type of net-

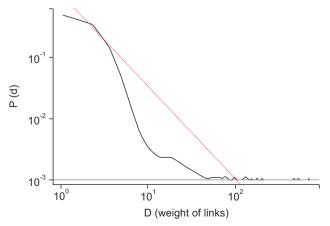


Figure 4. Probability distribution of node strength distribution on log scale in Selangor (2013–2014). The x-axis shows the strength of links and the y-axis shows the probability distribution of links strength.

work topology by focusing on main hubs (nodes), compared to a random distribution.

Link's density is shown in Figure 5, where the x-axis represents the number of links and the y-axis shows the weight of links on a linear scale. It specifies that some links in this two-mode network highly affect the whole network. The majority of nodes have weight below 200, whereas a minority of nodes has high weight in terms of dengue cases that appeared in these nodes.

In Figure 6, a weekly comparison is shown among 6 dengue affected districts in Selangor. This graph indicates the most crucial time period when the attack of *Aedes aegypti* was at its peak. It can be observed from the graph that Petaling is the most affected area followed by Hulu Langat. The human populations of Gombak, Sepang, Hulu Selangor, and Klang have also been victims of *Aedes aegypti*. The dataset showed the peak activity was from December 2013 till the end of February 2014. These twelve weeks were the most critical in these two highly affected districts. These districts had high infection rates in these 9 weeks compared to the other 3 weeks

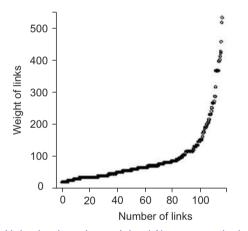


Figure 5. Links density using weighted Newman method of projection.

in the year. For the remaining four districts, the time series suggests activity without a clear, sustained epidemic burst between October 20, 2013 and October 18, 2014. Sepang, for instance, appears to have higher activity from October 2013 to the end of December 2013, without any significant activity in 2014. Gombak represented an isolated peak in the 25th week of 2014 and Hulu Selangor showed slightly elevated activity by the end of 2014 (41st week onwards). It is observed that out of 12 months, these 3 months showed the highest rate of dengue infections. It can be concluded that, apart from the importance of focal nodes, time duration is also important, as 3 months showed the highest rate, and also showed power-law resemblance. This feature also indicates a scale-free network.

2. Clustering Coefficient

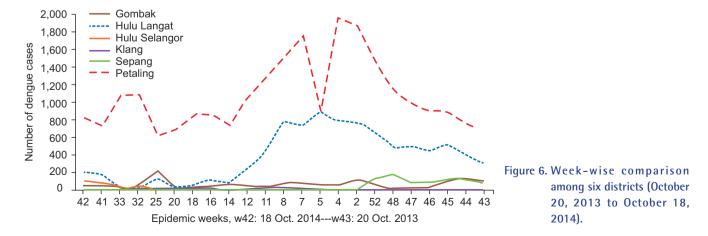
The global clustering coefficient has been generalized to weighted two-mode networks with weighted links [28]. The value can be constructed on the weights of links, and can be defined utilizing the four methods as a one-mode weighted clustering coefficient [27]. For the weighted two-mode network, global clustering coefficient is defined as follows:

$$C^{*w} = \frac{\text{(Total value of closed 4-paths)}}{\text{(Total values of 4-paths)}} = \frac{\Sigma \tau^* \Delta w}{\Sigma \tau^* w}$$
(3)

where $\tau^* w$ represents the values of 4-paths and $\tau^* \Delta w$ shows the value of these 4-paths that are closed by being part of at least one 6-cycle (i.e., a loop of six links with five nodes).

Here, the global clustering coefficient is computed for the weighted two-mode network using five methods, i.e. binary (Bi), arithmetic mean (AM), geometric mean (GM), maximum (Max) and minimum (Min).

In Figure 7, the global clustering coefficient is shown in two-mode networks by utilizing the above-mentioned five methods. The results showed that the network of localities is clustered, where dengue cases are considered as the weight of



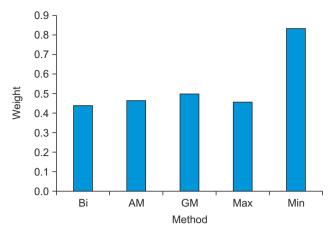


Figure 7. Different methods of global clustering coefficients (comparison) in two-mode network. Bi: binary, AM: arithmetic mean, GM: geometric mean, Max: maximum, Min: minimum.

the links. It can be observed that a few links have very high weight and, because of this, the minimum method showed the highest value (= 0.85), which also showed resemblance to a scale-free network. The results of the binary method do not include the weight of links to complete 4-paths. On the other hand, the maximum method showed a lower value compared to all other weighted methods (excluding binary) because the majority of links have smaller weight. There are few links having high weight in the network, and for this reason the minimum method represented high values of the clustering coefficient compared to the other methods. In addition, AM displayed an average value compared to other methods. GM meanwhile produced higher values than Max and AM because this method also closes the 4-paths based on GM. Therefore, in terms of the global clustering coefficient, the minimum method is the most appropriate for use in this network. The results obtained by this method indicate that the weighted distribution is very inhomogeneous.

3. Network Visualization from Localities Perspective

Figure 8 presents a graphical view of the dengue network that is plotted in igraph package of R-project. The node ID numbers 1, 5, 15, 30, 36, 38, 39, and 40 are very significant and should be focused on for treatment. This is due to their degree and their role as bridges between different clusters of nodes. This graphic visualization showed that localities are not properly associated in Gombak with each other by the co-occurrence of weeks [11], also gave the output that not all localities were affected in the observed time frame. Further, few nodes (localities) were working as main hubs. An actual map of Gombak is shown in Figure 9. This provides a geographical representation of dengue affected nodes (localities)

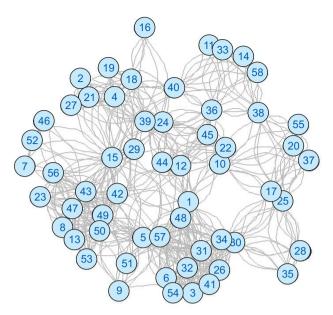


Figure 8. Graphical view of dengue network in Gombak.

in Gombak, Malaysia [11]. It has been observed that there were different clusters, such as Batu Caves, where people suffered greatly due to dengue disease. Grey color nodes represent the critical focal nodes that should be treated first. These nodes also lead this network to be scale-free.

IV. Discussion

Complex networks have become a rich field of study. Many real-world phenomena are modelled and analyzed as complex networks. The locale of this study is Selangor, a state of Malaysia. Here, the dengue epidemic issue has been modelled by considering a two-mode network and the given dataset of dengue affected cases was investigated. A power-law exponent (γ) has been calculated and discussed on the basis of output obtained from the projection methods. The results of network metrics, clustering coefficient, and gamma exhibit the topology of the dengue epidemic as a scale-free network. Furthermore, the dengue situation did not remain the same throughout the year, and it was found that a 12-week period was more crucial and showed a power-law form. The global clustering coefficient of localities network revealed that this network is clustered in terms of dengue cases as the weight of the links. The findings of this study showed the overall trend of this network as a scale-free instead of random network. These outcomes can help health official policy makers to deal with the dengue virus by keeping in view its scale-free nature. The outcomes highlight focal hubs that can be inspected in terms of cleanliness, immunization, and how the dengue virus can be avoided or controlled. In the future,

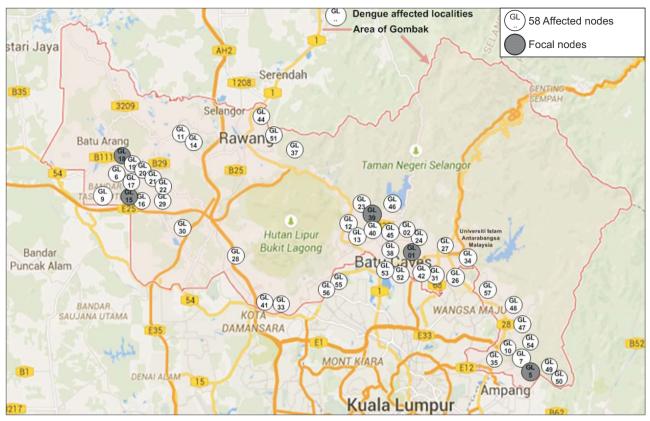


Figure 9. Real map of Gombak, Malaysia. The map showed dengue affected noedes (GL is Gombak, location no. 1 to 58), image captured from Google maps and modified.

the impact of the genetically modified mosquito (GMM) technique can be introduced in focal nodes as an external factor for the treatment of harmful effects of *Aedes Aegypti*. Furthermore, the GMM technique would be less costly and more effective when applied to a scale-free network compared to a random network. The methods and results of this research are also important for researchers and scientists who deal with arbovirus epidemics, such as the *Zika* and *Chikungunya* viruses.

Conflict of Interest

No potential conflict of interest relevant to this article was reported.

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Appendix 1. Dataset of dengue patients in Selangor (October 20, 2013 to October 18, 2014)

Ref. code	Cases								
GL18	128	GL27	8	HLL13	76	HLL36	28	HLL168	14
GL5	111	GL57	7	HLL63	74	HLL88	28	HLL52	13
GL1	105	GL28	7	HLL89	73	HLL18	27	HLL103	13
GL15	85	GL23	7	HLL129	71	HLL73	27	HLL148	13
GL39	80	GL21	7	HLL82	70	HLL141	27	HLL16	12
GL49	79	GL11	7	HLL139	70	HLL43	26	HLL28	12
GL34	55	GL19	6	HLL174	66	HLL142	25	HLL116	12
GL56	53	GL16	6	HLL34	60	HLL91	24	HLL132	12
GL40	43	GL52	5	HLL12	59	HLL97	24	HLL149	12
GL43	41	GL37	5	HLL75	54	HLL101	23	HLL167	12
GL24	41	GL10	5	HLL77	54	HLL45	22	HLL35	11
GL50	40	GL9	4	HLL152	53	HLL134	22	HLL110	11
GL13	38	GL53	4	HLL164	52	HLL138	21	HLL156	11
GL17	35	GL29	4	HLL166	52	HLL108	20	HLL172	11
GL12	32	GL2	4	HLL24	51	HLL115	20	HLL56	10
GL25	31	HLL130	729	HLL165	51	HLL21	19	HLL61	10
GL14	29	HLL64	435	HLL182	51	HLL31	19	HLL69	10
GL38	27	HLL84	317	HLL185	50	HLL68	19	HLL79	10
GL47	26	HLL117	251	HLL143	48	HLL74	19	HLL157	10
GL8	23	HLL161	250	HLL146	46	HLL114	19	HLL40	9
GL51	23	HLL46	237	HLL9	45	HLL136	19	HLL54	9
GL36	23	HLL60	231	HLL170	45	HLL17	18	HLL83	9
GL42	21	HLL87	228	HLL11	44	HLL29	18	HLL171	9
GL54	16	HLL44	217	HLL2	43	HLL41	18	HLL178	9
GL26	15	HLL184	194	HLL86	43	HLL55	18	HLL8	8
GL6	14	HLL15	183	HLL90	42	HLL153	18	HLL20	8
GL4	14	HLL85	179	HLL50	41	HLL98	17	HLL48	8
GL22	14	HLL158	159	HLL123	41	HLL1	16	HLL53	8
GL48	13	HLL65	149	HLL137	40	HLL113	16	HLL80	8
GL41	13	HLL120	141	HLL39	39	HLL121	16	HLL94	8
GL45	12	HLL72	122	HLL70	39	HLL133	16	HLL106	8
GL44	12	HLL151	116	HLL67	38	HLL147	16	HLL118	8
GL30	12	HLL183	113	HLL26	36	HLL154	16	HLL131	8
GL3	12	HLL127	110	HLL38	36	HLL181	16	HLL4	7
GL7	11	HLL59	103	HLL135	35	HLL105	15	HLL47	7
GL58	11	HLL145	96	HLL180	34	HLL144	15	HLL58	7
GL20	11	HLL150	96	HLL19	31	HLL7	14	HLL92	7
GL35	10	HLL14	95	HLL42	31	HLL30	14	HLL93	7
GL32	9	HLL175	95	HLL96	31	HLL51	14	HLL99	7
GL31	9	HLL76	90	HLL112	31	HLL57	14	HLL162	7
GL55	8	HLL25	83	HLL104	30	HLL78	14	HLL169	7
GL46	8	HLL10	81	HLL37	29	HLL126	14	HLL179	7

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Appendix 1. Continued 1

Ref. code	Cases								
GL33	8	HLL49	79	HLL163	29	HLL159	14	HLL3	6
HLL5	6	PL158	237	PL208	65	PL10	27	PL49	13
HLL22	6	PL59	227	PL224	65	PL226	27	PL93	13
HLL23	6	PL26	223	PL68	63	PL40	26	PL129	13
HLL27	6	PL171	206	PL111	63	PL166	26	PL144	13
HLL66	6	PL174	192	PL95	61	PL75	24	PL113	12
HLL102	6	PL131	181	PL206	59	PL105	24	PL157	12
HLL107	6	PL79	170	PL3	55	PL27	23	PL183	12
HLL111	6	PL175	166	PL169	55	PL48	23	PL191	12
HLL119	6	PL179	153	PL53	49	PL112	23	PL214	12
HLL173	6	PL69	150	PL57	47	PL156	23	PL227	12
HLL33	5	PL18	145	PL145	46	PL73	22	PL12	11
HLL81	5	PL65	136	PL228	45	PL223	22	PL58	11
HLL100	5	PL87	136	PL118	44	PL6	21	PL155	11
HLL100	5	PL87	136	PL118	44	PL6	21	PL155	11
HLL124	5	PL178	135	PL89	43	PL25	21	PL187	11
HLL125	5	PL44	130	PL130	43	PL72	21	PL15	10
HLL128	5	PL82	90	PL115	20	PL20	8	PL241	5
HLL160	5	PL172	89	PL201	20	PL78	8	PL39	4
HLL176	5	PL193	85	PL203	20	PL81	8	PL164	103
HLL6	4	PL124	83	PL94	19	PL84	8	PL225	102
HLL32	4	PL1	82	PL121	19	PL108	8	PL123	100
HLL62	4	PL80	82	PL125	19	PL149	8	PL236	100
HLL71	4	PL139	80	PL135	19	PL163	8	PL41	98
HLL95	4	PL182	79	PL148	19	PL219	8	PL19	95
HLL109	4	PL66	73	PL216	19	PL220	8	PL192	30
HLL122	4	PL98	72	PL217	19	PL230	8	PL34	29
HLL140	4	PL46	70	PL212	18	PL9	7	PL7	28
HLL155	4	PL238	70	PL64	17	PL119	7	PL61	28
HLL177	4	PL51	65	PL211	17	PL143	7	PL85	21
PL126	3107	PL186	43	PL2	16	PL159	7	PL207	21
PL31	2826	PL52	42	PL104	16	PL160	7	PL154	9
PL134	1174	PL184	42	PL215	16	PL177	7	PL162	9
PL127	1022	PL204	42	PL234	16	PL188	7	PL197	9
PL137	720	PL63	41	PL237	16	PL198	7	PL202	9
PL54	548	PL106	41	PL43	15	PL213	7	PL209	9
PL128	488	PL222	40	PL47	15	PL218	7	PL8	8
PL200	434	PL50	39	PL55	15	PL239	7	PL42	5
PL114	393	PL185	39	PL221	15	PL242	7	PL150	5
PL138	345	PL102	37	PL232	15	PL29	6	PL161	5
PL33	327	PL152	37	PL233	15	PL30	6	PL190	5
PL17	298	PL100	35	PL122	14	PL35	6	PL195	5

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Appendix 1. Continued 2

Ref. code	Cases								
PL173	287	PL99	34	PL146	14	PL56	6	PL210	5
PL132	282	PL14	33	PL77	10	PL62	6	-	-
PL133	275	PL32	33	PL110	10	PL71	6	-	-
PL147	114	PL91	33	PL153	10	PL86	6	-	-
PL141	113	PL97	33	PL194	10	PL90	6	-	-
PL189	113	PL5	32	PL235	10	PL116	6	-	-
PL196	110	PL67	32	PL21	9	PL117	6	-	-
PL22	109	PL120	32	PL38	9	PL142	6	-	-
PL23	109	PL229	32	PL70	9	PL168	6	-	-
PL136	109	PL167	31	PL83	9	PL205	6	-	-
PL92	107	PL37	30	PL103	9	PL231	6	-	-
PL4	104	PL74	30	PL151	9	PL24	5	-	-

Dataset protect patients' privacy, and is also available online [21].