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BIPARTITE NETWORK MODELLING AND ANALYSIS TO UNDERSTAND THE DYNAMICS OF DENGUE INCIDENCE IN ECUADOR DURING THE 2014-2021 PERIOD

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DEDICATORIA

Llena de orgullo, de amor y esperanza, dedico esta tesis, a cada uno de mis seres queridos, quienes han sido mis pilares para seguir adelante.

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RESUMEN

El dengue es un importante problema de salud pública en los países tropicales, particularmente en América Latina, donde su incidencia es alta. La enfermedad es endémica en la Costa, la Amazonía y en las estribaciones andinas del Ecuador. La prevalencia del dengue está relacionada con varios factores, incluidos los patrones climáticos, las condiciones socioeconómicas, las medidas de control de vectores y la movilidad humana. Si bien se han empleado métodos estadísticos para analizar los patrones de incidencia en Ecuador, estos no consideran la conectividad entre ciudades. Para llenar este vacío, se desarrolló una red bipartita para comprender la concurrencia de casos de dengue entre las ciudades ecuatorianas e identificar los nodos críticos de la enfermedad. La técnica de proyección de Newman ponderada generó una red donde los nodos eran ciudades con casos de dengue notificados. Las métricas de centralidad de redes se aplicaron para identificar nodos focales en la propagación del dengue. Estos nodos claves fueron Guayaquil, Machala, Santo Domingo, Quevedo, Manta, Orellana y Lago Agrio, los cuales juegan un papel crucial como conectores y propagadores de la enfermedad. Los resultados de este estudio se pueden utilizar para centrarse en intervenciones médicas como la limpieza y la inmunización y cómo se puede evitar o controlar el virus del dengue en áreas contiguas. El análisis de red para este estudio se realizó con R y Gephi, pero podría automatizarse completamente en R. Este estudio destaca la importancia de utilizar un enfoque de red para comprender la propagación del dengue, particularmente en regiones con alta movilidad e incidencia. Los hallazgos de este estudio podrían ayudar a los funcionarios de salud pública y a los formuladores de políticas a desarrollar estrategias efectivas para controlar el dengue en Ecuador y otras regiones similares.

Palabras clave: incidencia de dengue, redes bipartitas, nodos control, centralidad de redes, Ecuador.

ABSTRACT

Dengue is a significant public health concern in tropical countries, particularly Latin America, where its incidence is high. The disease is endemic on the Coast, in Amazonia, and in the Andean foothills of Ecuador. Dengue prevalence is closely related to various factors, including climatic patterns, socioeconomic conditions, vector control measures, and human mobility. Although statistical methods have been employed to analyze incidence patterns in Ecuador, they do not consider the connectivity between cities. To fill this gap, we developed a bipartite network to understand the co-occurrence of dengue instances among Ecuadorian cities and pinpoint illness hotspots. The projection-weighted Newman technique generated a network where nodes were cities with reported dengue cases. The centrality metrics of networks were applied to identify focal nodes in the spread of dengue. These key nodes were Guayaquil, Machala, Santo Domingo, Quevedo, Manta, Orellana, and Lago Agrio, which play a crucial role as connectors and propagators of the disease. The results of this study can be used to focus on medical interventions such as cleanliness and immunization and how the dengue virus can be avoided or controlled in contiguous areas. The network analysis for this study was performed using R and Gephi, but it could be fully automated in R. This study highlights the importance of using a network approach to understand the spread of dengue, particularly in regions with high mobility and incidence. The findings of this study could aid public health officials and policymakers in developing effective strategies for controlling dengue fever in Ecuador and other similar regions.

Keywords: dengue incidence, bipartite networks, control nodes, network centrality, Ecuador.

Bipartite network modelling and analysis to understand the dynamics of dengue incidence in Ecuador during the 2014-2021 period

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Abstract

Background: Dengue fever is one of the predominant vector-borne diseases in tropical and subtropical zones. In the Neotropics, *Aedes aegypti* is the primary incriminated vector of this disease. Dengue is endemic to all urbanized settlements in the Coast, Amazonia and the western and eastern foothills of the Andes. The typical approach to analysing its incidence is the temporal and spatial strategy. Another novel method for studying the transmission of infectious diseases is network analysis, specifically a bipartite network. To understand how synchronized cases are among cantons, we model and analyze the spread dynamic of dengue in Ecuador during 2014-2021 using the social network analysis method.

Material and methods: The annual hospital discharges in Ecuador from 2014-2021 were used in this study. At first, the incidence rate and trend patterns of dengue were analyzed. Then, the construction of the unipartite network involved three steps: the structure of the bipartite network, transformation through the weighted Newman method, and the illustration of the net in Gephi. Then, we evaluated the nodes of networks by centrality metrics to determine control nodes. At the same time, we assessed the robustness of regional networks (Amazonia and Coast) in a targeted attack.

Results: The exploration of data showed that the years 2015, 2020 and 2021 had higher incidence values. Both, for the Coast and the Amazon, the incidence has a similar main pattern and year seasonality; but the peaks of cases are in April-May for Coast and January-February in Amazonia. The network analysis model revealed that the global measurement of annual networks indicated how dengue proliferated between cantons. In addition, the Guayaquil, Machala, Santo Domingo, Quevedo, and Manta control cantons were determined by betweenness and closeness centralities. Finally, the network of Coastal provinces is more robust than the Amazonia net.

Discussion: Dengue is sensitive to social features and changes in climate conditions. On the one hand, the increase in the incidence of dengue in 2015 and 2020-2021 was possibly caused by ENSO, and the COVID-19 pandemic, respectively. Some contributions affirm that dengue has a seasonal pattern, and high level occurs during the rainy season. On the other hand, the global attributes of the network allows the understanding of dengue transmission in past years. Still, the centralities allows to identify connector and propagator nodes that are important for deciding public health interventions. Finally, despite those networks being scale-free, the Coast net is more robust than Amazonia due to the difference in the number of nodes and edges.

Keywords: dengue incidence; bipartite networks; control nodes; network centrality; Ecuador

Introduction

Dengue fever is a viral infectious disease caused by dengue virus (DENV), which belongs to the genus Flavivirus, family Flaviviridae, with four distinct serotypes (DENV-1, DENV-2, DENV-3, DENV-4) [1]. The virus is transmitted to humans mainly by the bite of *Aedes aegypti* female mosquitoes infected with DENV. The mosquito has diurnal habits; it can feed on the blood of multiple hosts quickly and overlaid its eggs in any containers that store water [2]. Climate change, biodiversity reduction, and growing urbanization have been demonstrated to favour the proliferation of DENV vector mosquitoes [3]. Although, it is not contagious; nevertheless, the virus can be spread to uninfected mosquitoes through the ingestion of blood when a virus carrier is bitten [4].

Network analysis diagrams are used in public health to understand the spread of disease and make prevention and treatment decisions. In the networks, everything is connected in various ways, and when we are connected to infected people or areas, knowing how to describe these interconnections using graphs theory provides an understanding of how diseases can spread [5]. During the last decade, many complex systems have been modelled and analyzed using graphs theory and complex networks; this has allowed the research about epidemic diseases, their interactions, and their modelling [6].

According to the World Health Organization (WHO), the number of reported dengue cases has increased eight times in the last 20 years. In 2000, there were 505430 cases, while in 2019, there were 5.2 million cases. Furthermore, the deaths notified between 2000 and 2015 went from 960 to 4032 [7, 8]. Thus, dengue has become a public health problem affecting most of the countries of Asia, Latin America and Africa and is one of the causes of hospitalization and mortality in children and adults [9]. In Ecuador, the four dengue serotypes show an endemic-epidemic behaviour, being a priority public health problem that threatens the tropical and subtropical zones of the country. Due to the Ministerio de Salud Pública (MSP) has proposed vector control in epidemiological zones, epidemiological surveillance, and entomological studies, together with monitoring of the distribution and *Aedes aegypti* density [10]. However, based on the Official Vector Gazettes, in 2020, there were 16570 confirmed dengue cases with a fatality rate of 0.036%, whereas, in 2021, there were reported 20592 and a fatality rate of 0.92%. While during 2022 until epidemiological week 41, 14636 confirmed dengue cases were reported [11]. This indicates that in the last three years, the number of dengue cases has increased, despite the preventive measures of the MSP.

Several mathematical models have been formulated to describe the transmission of the dengue virus in Baguio City, Philippines. [12, 13, 14]. In Ecuador, the previous studies of dengue evaluate the prevalence, identify the serotype of the dengue virus, or the influence of social and ecological factors on epidemic outbreaks in a specific place and time [15, 16]. However, no study about the spatial or cantonal relation shows dengue disease distribution analysis. Therefore, this study provides modelling based on the graph theory and complex networks, which allows the identification of nodes (cantons) with high centrality potentially of interest for epidemiological control.

Nevertheless, although network analysis has focused on studying unipartite networks (single node), the bipartite networks or two-mode/node network enables

a deeper study of epidemiological variables by classifying individuals by gender, location, infectious agent, or comorbidities. The bipartite networks can model vector-borne diseases and the spread of diseases in which the primary set nodes belong to geographic locations where the epidemic occurred, and the second set consists of infected cases [17]. Two-mode networks are often transformed into single-node networks by projection methods for analysis [18].

A bipartite network was applied to formalize the phenomenon of dengue propagation in Gombak, Malaysia. The primary set nodes were localities of Gombak; on the contrary, the secondary set nodes were epidemiological weeks, and the number of dengue cases in that place and time gave the bond between them. The bipartite network was projected using different methods (Sum, Binary, Newman, and weighted Newman), so the locations connected through links that were established by the co-occurrence of the week were obtained [18, 19, 20]. This study showed that the weighted Newman projection method is more accurate and allows us to determine the focus nodes which facilitate the spread of dengue and have a more significant influence on the transfer of the virus. These focus nodes are a crucial point for control and treatment since they reduce the interconnectivity of the network [6].

On the other hand, in the Philippines, two-node network modelling (bipartite network) was used to analyze dengue incidence data from 2010 to 2018 in Baguio City. The data set used for this research was the location, where the smallest political unit was *barangays*, time in months, and patient age. As a result, generated different bipartite networks, for example, time-location, time and location-age. These networks were projected through Newman and weighted Newman method, which preserves connectivity information of the net. Finally, both projection methods were compared by applying network measurements to the one-mode and two-mode networks. This allowed us to identify control points with more concentrated dengue activity, the months corresponding to a peak dengue season, and the most common dengue age group [21].

In this paper, we model and analyze the diffusion dynamic of dengue in Ecuador during 2014-2021 using the social network analysis method. Using an actual data set of dengue cases in Ecuador, we construct bipartite networks and project them into unipartite networks using the Weighted Newman projection method. The social network analysis finds the qualities of graphs and the centrality of each canton. The results allow knowing how cantons interact and identify control cantons that may be super-spreaders in a cluster. The approach analyzes dengue distribution in Ecuador cantons, identifies areas that require special attention for medical intervention and provides more details about the distributions of dengue infection than previous studies.

Methodology

Information collection (Data)

In 2013, the Sistema de Información de Vigilancia Epidemiológica from MSP implemented a standardized system for case records of diseases caused by vectors. However, complete records have been available since 2014 [11]. A proportion of infected people requires hospitalization; these data are reported by the MSP to

the Instituto Nacional de Estadística y Censos (INEC) [22]. In this study, we used publicly accessible data at INEC webpage for hospitalized dengue cases in continental Ecuador during the period 2014 to 2021. That entity is responsible for hospitalization records in Ecuador through annual hospital discharges. From now on, the dengue instances that have required hospitalization will be described as "cases". For each dengue case, the date attributes incorporated the epidemiological week, year, canton, province and region. This pre-treatment was performed using R 4.2.2 [23].

Exploratory analysis and generalization of the bipartite network structure

Initially, the annual incidence of dengue cases for every 100000 people was determined at the county level. The population data were obtained from INEC population projections 2010-2025 [22]. The data on dengue cases was employed to analyze the trend and seasonal patterns at the country and regional levels. For the average dengue incidence used the total Ecuadorian cantons (223) as the denominator, but for the average dengue instances only the number of cantons with active cases was counted. Additionally, cantons level yearly maps were generated to visualize temporal patterns. Both analyses were carried out in R 4.2.2 [23], using libraries raster, sf, dplyr, tidyr, RColorBrewer, geodata, forecast, tseries, and ggplot2.

A bipartite network was generated using cantons, epidemiological weeks, and the number of cases. The bipartite network has two different sets of nodes; the primary set corresponds to the "location/canton" (source), and the secondary nodes to the "epidemiological weeks" (target). The links which connect both sets were the number of reported cases, so the network is a weighted one Fig. 1, Bipartite Network.

Projection to a unipartite network

Bipartite network analysis is complex in its original form, so it is regularly converted to unipartite networks by tnet package of R-project [23] and then analyzed. The network transformation was performed using the Weighted Newman projection method [19] given by Eq. 1, which has shown accurate results compared to the Binary, and Sum methods [6, 21]. This method was proposed by Opsahl, where the link weight is formalized as follows:

$$w_{ij} = \Sigma p \frac{w_{ip}}{N_p - 1} \tag{1}$$

where w_{ij} is the weight between node i and j, w_{ip} is the link weight of node i with the co-occurrence, and N_p is the number of nodes linked to node p or co-occurrence.

In the projection, the connected locations/cantons were obtained through direct links set by the number of reported cases and the epidemiological week. The cantons were linked if they presented claims in the same epidemiological week; see Fig. 1, Projection to a unipartite network for each year.

Network parameters to identify critical nodes

The projected networks were plotted in Gephi 0.9.5 [24]. For each network, the global metrics (average degree, average strength, diameter, density, average path

Figure 1: **Projection of network.** Projection of a bipartite network to a unipartite network through the Weighted Newman projection method using locations with dengue cases by epidemiological weeks. Colours represent geographical regions within the country. Orange for Coast, blue for Amazonia, and green for Interandean region
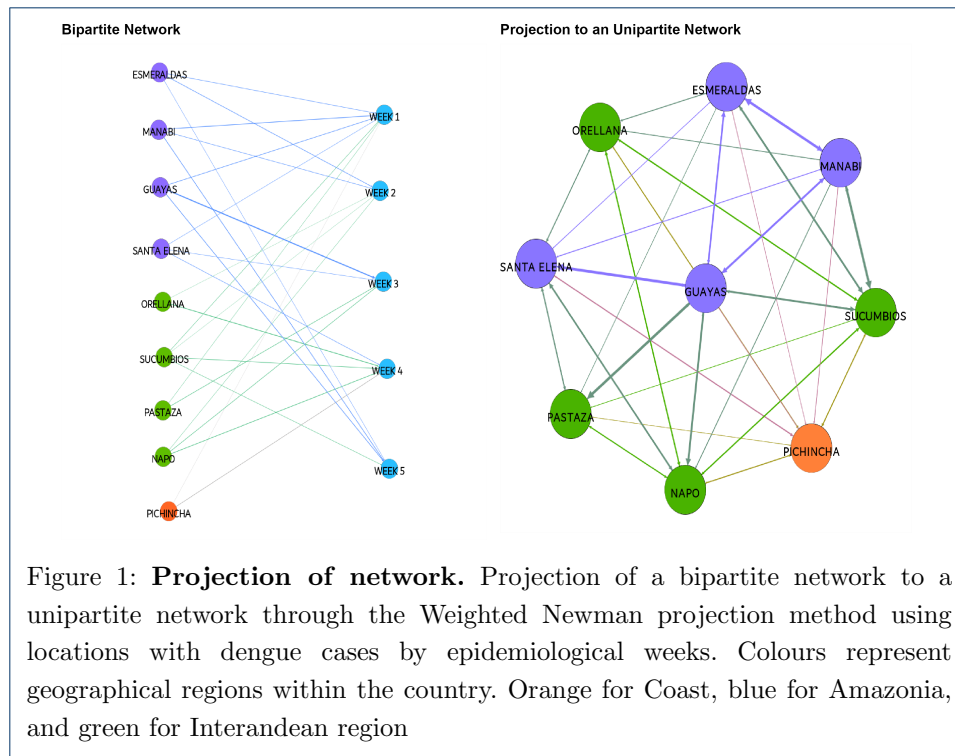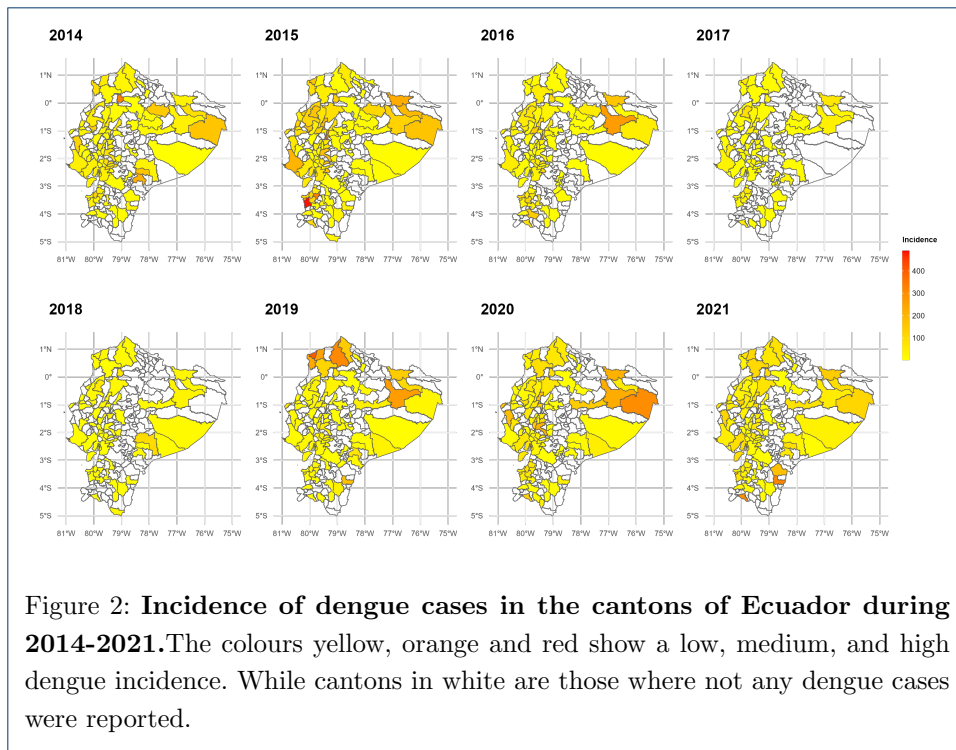
length and modularity) and local properties for each node (Degree, Closeness and Betweenness centralities) were determined. Additionally, those centrality ratings can reveal information about cantons that have a significant impact on establishing a network in specific settings.

A ranking of the first twenty nodes with high closeness and Betweenness centralities of each annual network was generated. All the top-ranked cantons were considered highly connected, but those cantons that were all year were the primary control nodes. In comparison, the robustness of Coast and Amazonia networks was analyzed by percolation theory.
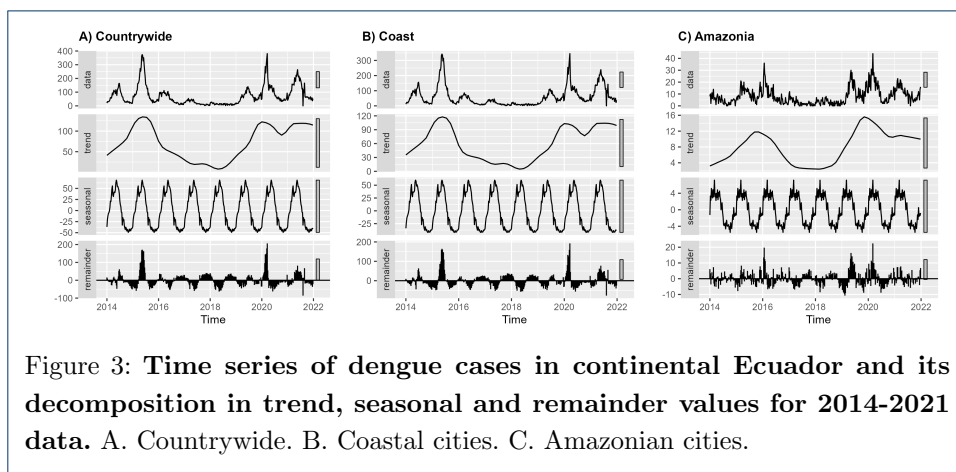
Results

Fig. 2 shows that during 2014-2021, 39 of 221 cantons of Ecuador presented an incidence lower than 200 cases per 100000 inhabitants. The number of cantons affected in each region was 35 from Coast, seven from Amazonia, and seven from the Interandean, particularly those that have a tropical or subtropical climate or are lowlands. Furthermore, there were 111 counties with no cases during 2014-2021. Those are mainly from the Interandean region. Also, the high incidence levels in Lago Agrio, Tena and Orellana are repetitive. But, 2015 had the highest incidence values, with an average of 29.91 dengue cases for every 100000 Ecuadorians, where Arenillas canton showed an incidence rate of 485.50. On the contrary, in 2018, the average incidence rate was 3.58.

The dengue cases averages were 40.54, 69.70, 30.63, 15.86, 9.90, 43.34, 66.76, and 74.61 for 2014, 2015, 2016, 2017, 2018, 2019, 2020 and 2021, respectively. It showed that in the years 2015, 2020, and 2021 there were more amount cases; 6691, 5808, 6193. For that reason, in Fig. 3 (A), the years 2015, 2020, and 2021 are the endemic

Figure 2: **Incidence of dengue cases in the cantons of Ecuador during 2014-2021.**The colours yellow, orange and red show a low, medium, and high dengue incidence. While cantons in white are those where not any dengue cases were reported.

year that showed peaks in the data and trend section, whereas the low levels of dengue occurred in the years 2017 and 2018.

The seasonal sections countrywide exhibited periodic annual patterns, which indicates that there are specific weeks in which the number of dengue cases increases and in others decreases. In the first semester of the year, there is growth in several instances, while in the last semester, they decline; see Fig. 3 (A, B). The trend and seasonality are more uniform on the Coast (B), and in the Amazonia (C), it is random. Nevertheless, the seasonality peak in Amazonia starts a few weeks before the end of the year, while on Coast, it begins weeks after the beginning of the year.

Figure 3: **Time series of dengue cases in continental Ecuador and its decomposition in trend, seasonal and remainder values for 2014-2021 data.** A. Countrywide. B. Coastal cities. C. Amazonian cities.

According to Table 1, and Fig. 4, 2015 had the highest number of dengue cases. This is demonstrated by the 93 existent nodes or cantons and the 6840 edges

generated by projection. Based on the 73.548 average degree value in 2015, it is estimated that a canton affected had a relationship with 73 other cantons. Moreover, the strength is the relationship in the number of dengue cases, which is ≈ 71 cases between two different nodes in the year 2015. The average path length, which had a value of 1.201, represents the distance of the number of dengue cases and counties, suggesting that the places affected are in close proximity. The network diameter value was 2, which also supports this. This smaller value indicates that the maximum distance between cantons in the year 2015 is shorter than the others years. The density of the year 2015 was 0.799. This value is high because the graph 2015 in Fig. 4 is overly dense due to so many nodes and edges.

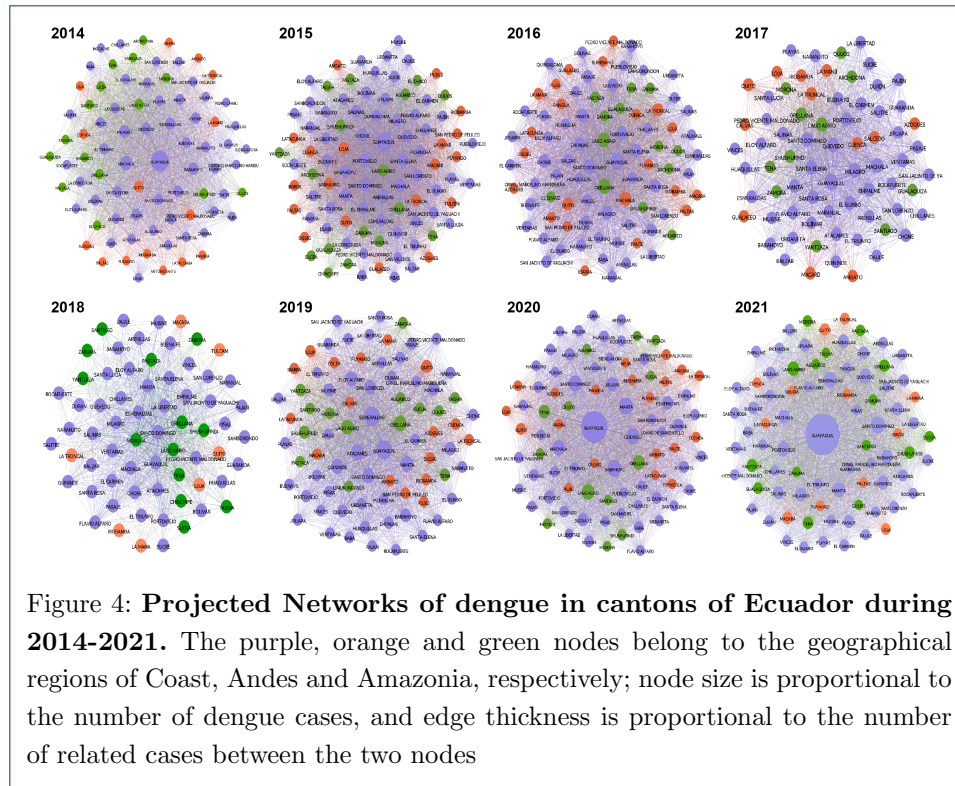Table 1: Attributes of the annual graphs formed by dengue cases.

Year	Nodes	Edges	Average Degree	Average Strength	Diameter	Density	Average Path Length
2014	80	4622	57.8	41.2	2	0.731	1.269
2015	93	6840	73.5	70.8	2	0.799	1.201
2016	87	5028	57.8	30.9	2	0.672	1.328
2017	71	2958	41.7	16.0	2	0.595	1.405
2018	66	1888	28.6	10.1	2	0.440	1.560
2019	80	4222	52.8	43.8	2	0.668	1.332
2020	86	5408	62.9	66.8	2	0.740	1.260
2021	80	5230	65.4	76.6	2	0.828	1.172

Table 1 shows that the network diameter and average path length are reducing, which indicates that the cantons are more united among them, which implies an increase in the transmission rate.

The annual networks there were formed mainly by cantons of the Coast, which showed the most significant number of cases. Guayaquil was on size top with 1527, 1758 and 2494 number dengue cases in 2015, 2020, and 2021 years. Nonetheless, the size of the nodes that are part of the network of 2018 was small, indicating that the number of dengue cases declined notably for this year in all cantons, see Fig. 4.

Fig. 5 shows the cantons with the twenty higher values of the Betweenness and Closeness centralities; those were not the same yearly. However, 12 of them were presented for only one year. Others like Portoviejo, Lago Agrio and Orellana in the Betweenness centrality; Portoviejo, Milagro and Lago Agrio in the Closeness centrality were manifested up to seven times, and control nodes may be possible, see Fig. 6. In comparison, five cantons were in the rankings during all years, such as Guayaquil, Machala, Santo Domingo, Quevedo, and Manta, considered primary control nodes for spreading the dengue virus and had a considerable influence on the transmission of the virus, possibly due to human mobility. Further, these nodes are focused on the treatment of the dengue disease due to they can reduce the interconnectivity of the dengue network, see Fig. 7. This suggests that the rate of disease transmission in these six areas continues for eight years, in comparison to other cantons, where their Betweennees and Closeness centralities are intermittent, such Flavio Alfaro, Morona, Yantzaza, Loja, Muisne, Naranjto, El Guabo, San Lorenzo, Ventanas, Salinas, and others. This could be information for the MSP about the highest priority needs for preventive, therapeutic, or eradication efforts.

Based on this, Fig. 6 shows the frequency of the cantons like central control nodes. The blue colour intensifies when the nodes have been at the top of the ranking for years, for example, Guayaquil, Machala, Santo Domingo, Quevedo, and Manta in the

Figure 4: **Projected Networks of dengue in cantons of Ecuador during 2014-2021.** The purple, orange and green nodes belong to the geographical regions of Coast, Andes and Amazonia, respectively; node size is proportional to the number of dengue cases, and edge thickness is proportional to the number of related cases between the two nodes

Coast, and Orellana and Lago Agrio in the Amazonia. Furthermore, the intensity of the colour decreases for the cantons that were in the ranking only one time, that are those that had dengue cases but are not considered as control nodes with significant influence for the diffusion of the dengue virus. While the counties that do not present dengue cases are white.

The critical points to affect the integrity of the Amazonia network were approximately ≈ 0.75 and Coast was ≈ 1, so the Coast networks have greater robustness. The robustness quality depends on the number of nodes, edges and type of network. Generally, a scale-free network does not fall apart after removing a finite fraction of nodes, and it is necessary to remove almost all nodes ($f \approx 1$) to fragment these networks. For example, the size of the Coast net decrease gradually, only when the fraction of nodes removed $f \approx 1$ it is completely broken. However, the difference is in the shape of the two curves. Indeed, the removal of an f fraction of nodes in the Amazonia network leaves us with a network with less number of nodes than the removal of the same fraction of nodes in the Coast network. Hence, removing an equal f fraction of nodes as 0.50, in both networks causes more damage in the Amazonia than in the Coast network. For this reason, the Coast network had greater robustness than the Amazonia network, see Fig. 7.

Discussion and conclusion

This paper presents the incidences and patterns of dengue cases during 2014-2021 and an approach for identifying the crucial nodes in the dengue spread in Ecuador by network analysis method. Calculation of incidence rate using a constant population can consider a solution when the incidences are small ($<100/100,000$ people), or
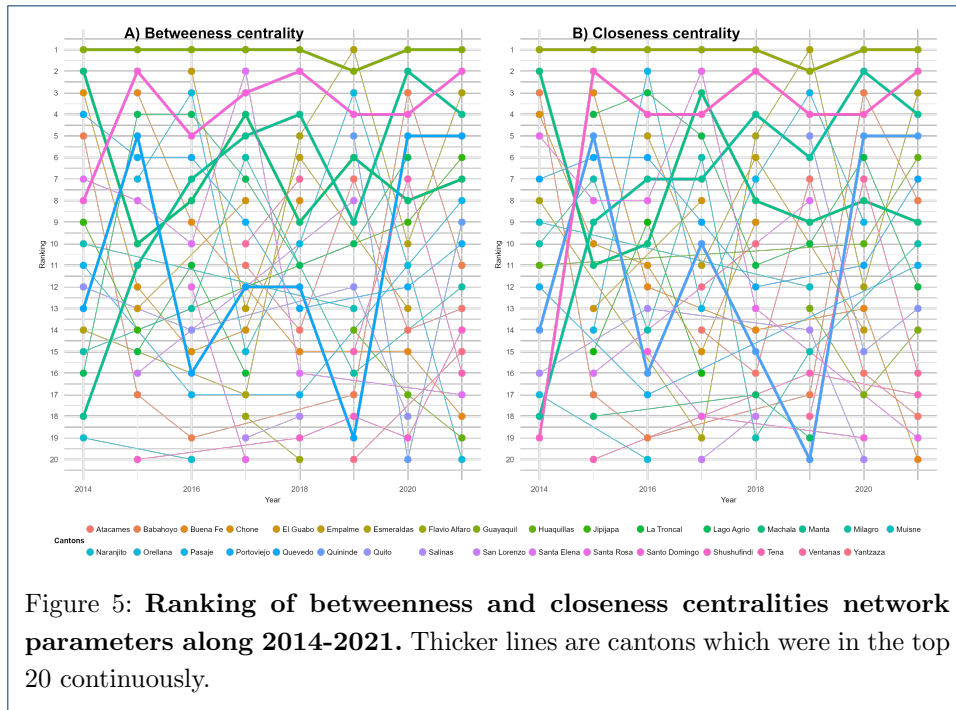
Figure 5: **Ranking of betweenness and closeness centralities network parameters along 2014-2021.** Thicker lines are cantons which were in the top 20 continuously.
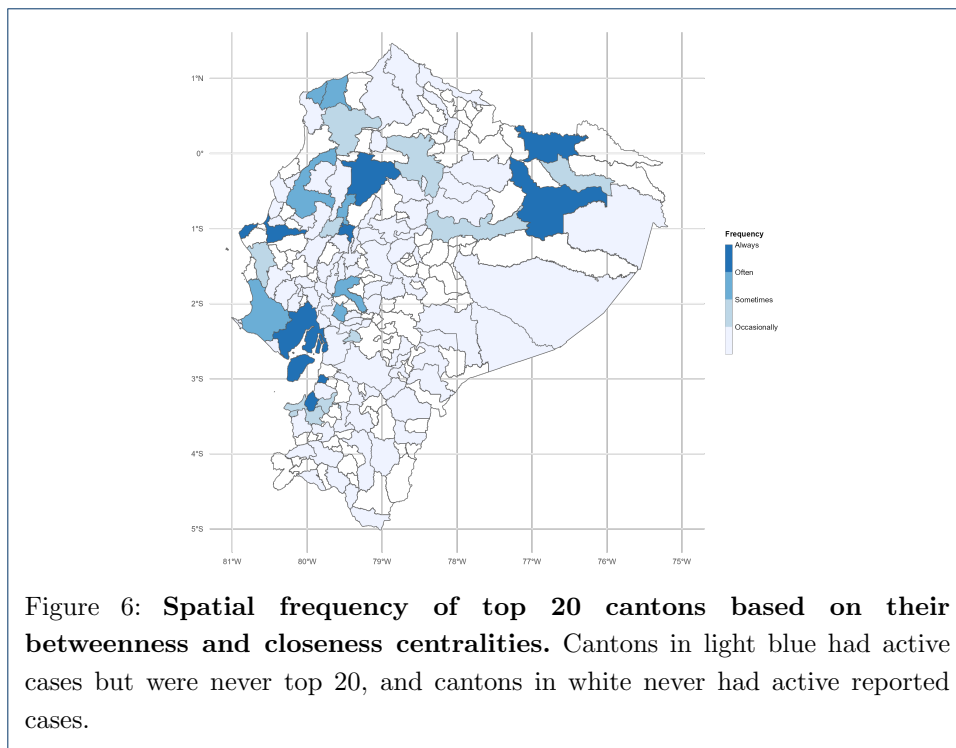

Figure 6: **Spatial frequency of top 20 cantons based on their betweenness and closeness centralities.** Cantons in light blue had active cases but were never top 20, and cantons in white never had active reported cases.

when the population size change is small compared to the estimated effects [25]. In this study, there are medium and high incidences (>100/100,000 people). For that reason, the incidence was calculated with a variable population obtained from INEC population projections [22].
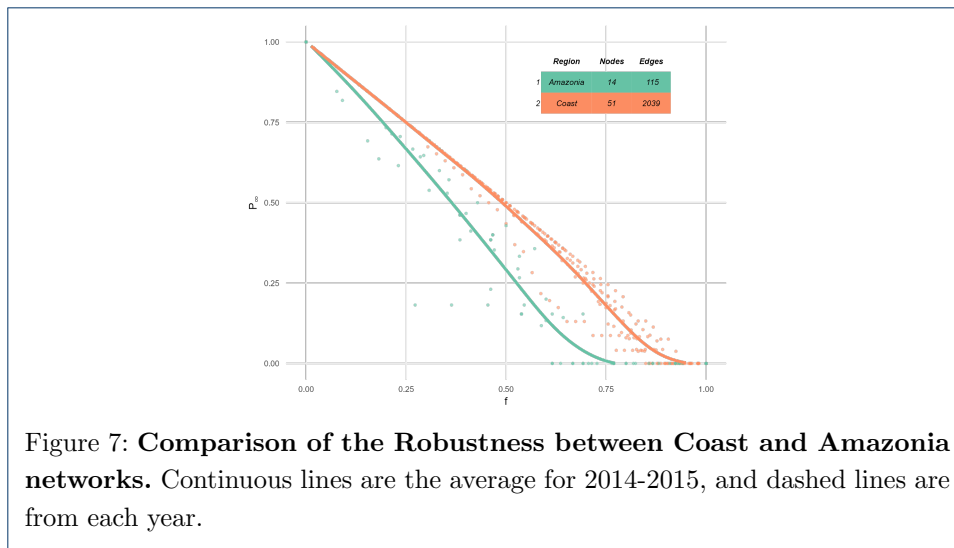
Figure 7: **Comparison of the Robustness between Coast and Amazonia networks.** Continuous lines are the average for 2014-2015, and dashed lines are from each year.

The cantons with high dengue incidences are in the Coast and Amazonia regions. It is consistent whit [26] that showed the morbidity rates by the vector-borne disease are minor in the Interandean region than in the Coast and Amazonia. The difference in dengue incidence in each canton can be a result of socioeconomic and population features, along with vector presence and its relation with climate and El Niño-Southern Oscillation (ENSO) [27].

Ae. aegypti prefers to imbibe on human blood multiple times as an energy source for egg development, thus generating great proximity with humans [28]. Despite, it feeding on the blood of multiple host species, it prefers human blood; because of low-isoleucine and high-triglycerides (lipids) concentrations in human blood, which help the mosquito accumulate more energy reserves, for that reason included at least one human host in its diet [29]. In addition, the nearness between infected and susceptible individuals is more frequent in densely populated urban areas than in smaller communities in rural areas [30]. For that reason, the mosquito population and diffusion rate of dengue increase in densely populated places [31]. The populated places are crowded areas that experience higher human movement fluxes than less dense settlements [32]. According to the road connectivity analysis in Ecuador report , there are seven clusters connected to various populated centres, five of which could be related to dengue dispersion. In a minimum travel time of two hours, the vital clusters connect central-Occident, north-Occident, and south-Occident zones on the Coast, and north-Orient and south-Orient in the Amazonia [29, 33]. It indicate that in Ecuador the main areas of agglomeration by population density and human mobility are Guayaquil, Santo Domingo, Portoviejo, Manta, Machala, Lago Agrio, Coca, and zones from Morona Santiago y Zamora Chinchipe [22]. The great connectivity of these areas can result in that dengue cases being related in each cluster, due to there being a higher probability of their inhabitants commuting to infected areas or receiving infected visitors. The infected person can travel between active areas and disease-free areas driven by the geographical spread of infectious pathogens [30].

In the Coast region, the elevations do not exceed 800 m.a.s.l; and the ideal altitude for mosquitoes in the tropics is below 1200 m.a.s.l [34]. Therefore the lowlands

from Coast can be the most suitable habitat for the mosquito, and areas with high elevation can act as biogeographic barriers [31]. Nevertheless, a mosquito was found at 2302 m.a.s.l in Colombia's Andean area with characteristics similar to the Interandean zone in Ecuador [35]. In the Interandean region of Ecuador, 1680 m.a.s.l was the maximum altitude where *Aedes aedypti* was reported [28].

The temperature affected the different phases of the vector development cycle, including maturation, survival, and population density [36, 37]. The ideal temperature for the development of dengue mosquitoes is between 22°C and 26°C [38] like in the Coastal or Amazonian cantons. However, *Ae. aegypti* can survive in a temperature range of 21.6- 32.9°C [39] while *Ae. albopictus* between 16.2- 31.6°C [40]. Part of the territories of some Andean cantons are located in the eastern or western foothills and have troipical or subtropical climate. Is why cantons (parishes) like Tulcán (Tobar Donoso, El Chical, and Maldonado), Ibarra (Lita and La Carolina), Pedro Vicente Maldonado, Quito (Nanegal, Nanegalito, Pacto, and Gualea), La Maná, Pangua, Colta (San Miguel, Chaumala, Gatazo Grande, La Alegria), La Troncal, Cuenca (Molleturo, Chaucha), Santa Isabel (Santa Isabel, Abdón Calderón), Paute (Paute), Puyango, Paltas, Macará, Loja, Calvas (Sanguillin, El Lucero), Espindola (El Ingenio, 27 de Abril) reported dengue cases, because they have an average annual temperature of 22°C, therefore an optimal climate for vector development and disease spread [41]. This information was verified in the Plan de Desarrollo y Ordenamiento Territorial newsletters of each canton.

In Amazonia, the forest area and natural ecosystem can be favourable to the mosquito population and dengue fever [42, 36, 3]. But, the zones continuously affected are in the north of the region, in cantons such as Tena, Orellana, Lago Agrio, and Shushufindi that belong to the Sucumbios, Napo and Orellana provinces. The differences between the zones can be a result of spatial differences, lack of health services, disease vector abundance, and household population.

Therefore, the dengue risk is associated with environmental and societal features. For example, population growth and high population density, human mobilization, rural to urban migration, and growing and disorganized urbanization driver the outbreaks, proliferation and rising dengue incidence [37, 43, 44, 36, 3]. The climatic conditions have a direct and indirect in the mosquito population [45, 37, 46, 47]. The elevation, temperature, humidity, precipitation, and sunlight are linked to mosquito density and dengue transmission [45, 48, 49, 50], can affect larval growth, adult biting rates, gonotrophic development, and extrinsic incubation period of the virus in the mosquito [27].

The increase of cases in 2015 had been implicated to ENSO, a global climate phenomenon which affects human infectious diseases and the misreporting of chikungunya cases like dengue, while in 2020 and 2021 years as a result of the pandemic caused by COVID-19. The inter annual dynamics of ENSO are related to climate anomalies and dengue incidence in South American countries [51, 27]. The study assessed ENSO development during 2015, their findings showed a high possibility that there were drought conditions in northeast Ecuador and high rainfall and flooding in coastal Ecuador. This event possibly can be associated with high dengue transmission in 2015. Because the dry conditions can increase the habitat for juvenile mosquitoes and reduce the incubation period, and wet conditions promote

Aedes spp. breeding, both conditions favour mosquito breeding [52, 27, 53, 54]. The annual climatological bulletin 2015 by Instituto Nacional de Meteorología e Hidrológica [55] displayed that the yearly rainfall presented increases/decreases in the Coast region and exceeded annual climatology values in Amazonia [56]. This year was warm for Ecuador, with positive anomalies up to 2.4°C. It indicates that in 2015 there were climatic changes that could affect the dengue occurrences. However, there were cases that were clinically diagnosed as dengue, but were chikungunya infections, and these individuals were registered as dengue in the MSP [57].

The incidences before the first reported case of COVID-19 were low compared to 2015. However, dengue cases increased during the COVID-19 pandemic [58]. It is consistent with studies in other countries such as Peru [58], Brazil [59], the Southwest Indian Ocean Islands [60], and Asia [61]. The impediment to leaving home during quarantine probably promotes the reproduction of mosquitoes around the houses [62, 63]. The lockdowns can avoid community participation in mosquito control, and rise the dengue transmission in and around homes [64]. Also, the accumulation of people in one place rises the probability that the mosquito bites everyone, and human blood promotes reproduction. In addition, during the pandemic the vector control measure, preventive campaigns and fumigation were suspended may increase the number of dengue cases [60]. However, some people believe that fumigation can favour COVID-19, so they do not allow to application of this vector control measure, which rises the risk of dengue [65].

The presence of peaks caused by the number of dengue instances perhaps is related to the climatic season. According to, [50], and [38], affirm that the amount of dengue fever patients is higher during the dry season [50, 38]. Since the rainy season can be more suitable for mosquito reproduction, so the spread rate grows [50, 49]. However, these findings contrast with what [58] affirms, in his study area, the number of instances coincides with the rainy season in the Amazonia and the summer on the Coast. A study in Ecuador indicates that the Coast region shows an annual peak of illness during mid-March of each year [66]. Otherwise, from November to April (rainy season), the dengue incidence increases in Peruvian Amazonia [67].

The networks can represent a dengue arbovirus epidemic [68]. The authors have observed scale-free network characteristics in the Singapore dengue epidemic network [69]. In addition, according to the Barabási-Albert model, the growth and preferential attachment are scale-free features [70]. The principal characteristic of the scale-free system is that a few critical links have colossal weight. So a scale-free network is necessary for solving the epidemic issue. Because this type of network topology can control epidemic diseases by focusing on essential nodes [68].

We calculated some graph attributes, such as amount nodes and edges, average degree, average strength, diameter and density network and average path length. The value of nodes is the number of counties affected by active dengue cases. On the contrary, the edges result from the projection bipartite, which indicates the number of times the pair of nodes had active instances in the same week. The average degree is the number of node-to-node links [38]. The greater the average degree value, the stronger the connection between the nodes, and consequently, the network is more robust, i.e., many bonds unite the nodes. The average strength is the sum of the weights of all edges connected to each node [6].

The density corresponds to the proportion of possible ties in the graph; the nodes are more cohesive if the value is closer to 1. The average path length is the distance between one node to another. The lower value shows that there is dengue cases-related so that the distance between the nodes becomes shorter [6]. It is supported by a diameter network with the longest distance between two nodes, so the low values indicate that the nodes are closer [24, 38]. These properties reflect the spread of the virus in an epidemiological network.

Some prominent features include degree centrality, closeness centrality, eigenvector centrality, and betweenness centrality [5, 71, 38]. However, in the Weighted Newman projection, the closeness and betweenness centralities serve for identifying important nodes [6].

On the one hand, the betweenness centrality shows the nodes that connect numerous communities to build a giant net. So the cantons with higher values are network connectors and probably the most influential nodes [38, 5]. Because those facilitate the spread of the dengue virus and significant influence the transfer of the virus [21, 6]. On the other hand, the closeness centrality is a measurement of counties' proximity to all different, so it allows identifying the cantons with the most access to others[38]. Generally, those nodes with higher values have the most connections, but the bonds are weakest [21]. The cantons with higher closeness are spreaders of viruses and are essential nodes in the diffusion of infectious disease.

Those nodes are considered to control nodes due to their role as bridges between different clusters and their proximity to other nodes [68]. In the approach of public health and epidemiology, identifying the connector and propagator nodes is essential for understanding disease transmission and take decisions on medical interventions [5]. Since if the treatment of the dengue disease is focused on control nodes, it could reduce the interconnectivity of the network [6]. Hence, those are significant to trace or prevent the illness propagation [72].

To evaluate the robustness of networks used, the inverse percolation theory is a sub-field of statistical physic and mathematics. The integrity of a network in front of the impact of node failures directly relates to robustness. In the case of a scale-free network under targeted attack, we must remove almost all the nodes to fragment the web. Because, despite dropping the central control nodes, there is still a unique, more considerable giant component. On the contrary, in the regular and random networks, removed nodes generated a division of giant component in clusters [73, 70].

Nevertheless, the kinds of centrality that describe earlier might be a convenient concept to describe the dynamic of disease transmission, and maybe there are other ways to understand and depict disease transmission that has yet to be discovered by social network analysis theorists [5].

One of the main limitations of the study was the available sources of information, the database of the Sistema de Vigilancia Epidemiologica is not freely accessible and the data requirement takes at least three months and although the MSP provides modified information (hospitalization), the reports differ greatly. The incidence is an important marker of risk, but dengue is a multi-factorial disease, for which it is necessary to include the analysis of other variables that influence dengue transmission or the ecology of the vector. In Ecuador there is no system that

unifies information from surveillance systems, entomological information, and vector control and prevention activities; this is despite the fact that the MSP in 2019 claimed to have an integrated system of epidemiological, virological, entomological and environmental surveillance systems.

The dengue propagation has been modelled and analyzed as bipartite networks. This study combines information from health, computer science, and network science. The data set used was the hospitalized dengue cases in continental Ecuador from 2014 to 2021 to understand the diffusion dengue from the perspective of the unipartite network projected through Weighted Newman projection. The exploratory analysis showed that 2015, and 2020-2021 were endemic years caused by ENSO and COVID-19 pandemic. In addition, centralities measure such as betweenness and closeness were used to identify control cantons that are connectors and propagators of the net. The findings allow the focus on medical interventions like cleanliness, immunization, and how the dengue virus can be avoided or controlled in control cantons. Hence, this study has the potential to accomplish the healthcare system goals of the government. The network analysis for this study was performed using R and Gephi but could be fully automated in R. To make this tool available and open source the next step is to develop an R package.

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Additional Files
Additional file 1 — Figure about the rankings Degree centrality in annual networks

Figure 8: **Degree centrality ranking in networks during 2014-2021.** The cities of Guayaquil, Machala, Quevedo, Santo Domingo, Manta and Lago Agrio were within the top 20 each year.