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IDENTIFICATION OF COVID-19 USING VIRTUAL MAP AND SPATIOTEMPORAL ANALYSIS

By

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A DISSERTATION

Presented to the Department of
Computer Science
Program at Selinus University

In fulfillment of the requirements
for the degree of Doctor of Philosophy in
Computer Science

2023

SELINUS UNIVERSITY
OF SCIENCES AND LITERATURE

I do hereby attest that I am the sole author of this Project / Thesis and that its contents are only the result of the readings and research I have done.

Abstract

The purpose of this research was to carry out a spatial analysis of Covid19 in the District 2 of Rizal. The online and mobile GIS (Geographical Information System), mapping dashboards, applications for tracking the virus, and numerical approaches are utilized to model the possibilities of the distribution of the virus on a district size. This article presents and analyses many GIS methodologies, such as buffer and numerical analysis, as well as the presentation of infected areas via a virtual map, with the goal of visualizing and estimating the current pandemic crisis. The program and the dashboards are both receiving data changes in what is referred to as "near real-time." This research also explores several other strategies using GIS that can improve understanding of how to fight against epidemics and disease outbreaks. These techniques can be found toward the end of the publication. This document can be used to highlight significant actions that need to be addressed and implemented in order to successfully offset the impacts of Covid-19. The evaluation of the system yielded a general mean score of 4.60, which is equivalent to the term Strongly Agee. This score indicates that the system is very acceptable to the users.

Keywords:

Covid-19, dashboards, GIS (Geographical information system), spatial analysis

ACKNOWLEDMENT

I am grateful to Almighty God for being so faithful through the duration of this endeavor; and to my wife and my family who supported me all the way, thank you for the love and understanding.

DEDICATION

I dedicate this project / thesis to God Almighty my strong pillar, my creator, my savior, my foundation of encouragement, wisdom, knowledge, and understanding. He has been the basis of my fortress throughout this program and on His wings only have I glided high. I also bestow this work to my family; Dr. Agustin who has cheered and motivated me all the way and whose encouragement have made sure that I give it all it takes to finish that which I have started. To my family and friends who have affected in every way possible by this journey, my source of inspiration and joy. Thank you. My love for you all is immeasurable. God Bless!

Chapter 1

INTRODUCTION

In December 2019, a new virus that causes severe acute respiratory syndrome (also known as the coronavirus disease COVID-19) emerged in Wuhan, which is located in the province of Hubei, China. This virus was initially referred to as "Novel Coronavirus 2019-nCoV," but it was later renamed to SARSCoV-2. This virus rapidly spread to other parts of China as well as other countries around the world, in spite of China's massive efforts to contain the disease within Hubei. The COVID-19 coronavirus spread at an alarmingly rapid rate, especially when contrasted with the 2002–2003 SARS-CoV and the 2012–2014 MERS-CoV (Middle East Respiratory Syndrome-related coronavirus). It took almost two and a half years for MERS to infect 1000 people, and it took approximately four months for SARS to do the same. However, the unique SARS-CoV-2 infected 1000 people in just 48 days.

On January 30, 2020, the World Health Organization (WHO) announced that the new SARS-CoV-2 coronavirus outbreak represents a Public Health Emergency of International Concern. This announcement came as a result of the WHO determining that the outbreak is an international concern (PHEIC). Geographic information systems (GIS) and methods, including, among other application possibilities, online real- or near-real-time mapping of disease cases and of social media reactions to disease spread, predictive risk mapping using population travel data, and tracing and mapping super spreader trajectories and contacts across space and time, are proving indispensable for our timely understanding and response to seasonal influenza outbreaks. This is similar to the original SARS-CoV epidemic that occurred in 2002/2003 [3] and with seasonal influenza in point of fact, specialists in the health care industry have long recognized traditional mapping, and more recently geographic information systems (GIS), as essential instruments in the fight against and tracking of infectious diseases. The first time the relationship between location and health was depicted on a map was in 1694, and it was in the context of the prevention of the plague in Italy.

Over the next 225 years, the utility of maps as a communication tool grew in the service of understanding and tracking infectious diseases such as yellow fever, cholera, and the influenza pandemic that occurred in 1918. This was accomplished through the use of maps. When computerized geographic information systems were first developed in the 1960s, the possibilities for analyzing, visualizing, and spotting patterns of disease experienced a significant uptick. These capabilities continue to expand to this day. According to the findings of a literature study conducted on health GIS in 2014, 248 out of 865 included papers, or 28.7%, concentrated on infectious disease mapping. Since then, we have witnessed a revolution in the field of applied health geography brought about by instruments based on the Internet. Now, as we use these tools to protect human lives, we are able to ingest huge data from its sources and display the outcomes in dashboards that are interactive and as close to real-time as possible. In the course of the COVID-19 epidemic, these internet dashboards have emerged as an essential source of information. This document provides pointers to a variety of useful online and mobile GIS and mapping dashboards and applications and describes them. These dashboards and applications can be used to keep track of the coronavirus outbreak and accompanying events as they occur all over the world. One of these dashboards and applications is meant for individual users in China to check if the app user has had any close contact with a person confirmed or suspected to have been infected with SARS-CoV-2 in the recent past. Some of these dashboards and applications are receiving data updates in near-real-time (at the time of writing), and others are receiving data updates on a more delayed basis. In addition, we provide a brief overview of some additional ways that GIS can assist in the fight against the emergence and spread of infectious diseases.

Coronavirus COVID-19 (COVID-19) had a negative impact on people's lives and was a contributing factor in the slowdown of economies in a number of countries. A significant number of people who had previously been unwell or witnessed the deaths of others were impacted by this pandemic. People who were infected with this coronavirus experienced a wide range of symptoms, including a cold, fever, difficulty breathing, and bone pain, which ultimately led to the development of pneumonia. Since there were no vaccines available at the time of the outbreak, the initial spread of the virus turned into a significant problem.

As a result, it is essential to take extensive precautions, like donning masks, socially isolating oneself, adhering to an exhaustive hygiene protocol (including avoiding direct contact and regularly washing one's hands, among other things), and so on. The virus moves throughout each location at an alarmingly rapid rate. In an effort to stem the spread of the disease and slow down the exponential curve, some nations have instituted bans on human crowds. The people in an increasing number of countries are being confined, and severe quarantines are being imposed, in order to keep an eye on the spread of the highly contagious disease. The COVID-19 outbreak has immediately had an impact on our day-to-day lives as well as our enterprises, which has hampered worldwide trade and commerce. Because the virus may move so rapidly from one individual to the next, it is essential that the illness be identified as early as possible so that it can be contained. The manufacture of vaccines has been slowed down in the majority of countries. (Haleem, A., Javaid, M., & Vaishya, R., 2020).

According to a poll that was carried out in the Philippines, 37 percent of respondents thought that the COVID-19 coronavirus outbreak had an effect on their day-to-day lives as well as the lives of their families.

(Statistica, 2021). First, it would appear that the economic model of the Philippines itself makes the country more susceptible to the outbreak of disease. It is predicated on the movement of people; yet, sectors such as services, tourism, and growth that is supported by remittances are all susceptible to closures caused by pandemics as well as a drop in consumer confidence. Travel on a global scale drew to a halt, tourism was impacted severely, and on a domestic level, the retail, restaurant, and hotel industries were severely hampered by closures and movement restrictions. Thankfully, the country's business process outsourcing (BPO) sector is shown some signs of resilience; nonetheless, its core markets were severely impacted by the pandemic, which is forcing the sector to rapidly retrain and adapt to new challenges in accordance with the new normal. (Mendoza, Ronald U.,2021). In addition, there were 3,668,940 COVID-19 confirmed cases in March 2022, with a mortality count of 57,258; a total of 135,251,295 vaccine doses were administered to the population of the Philippines. (WHO, 2022). It was reported that in order to manage enough doses for each 10% of the population, an average of 717 887 doses are being provided each day or 31 days. (Reuters, 2022).

The majority of the time, the data of the sick people could usually be viewed by looking at the records that were uploaded by WHO and the Department of health. The majority of the reports merely specified the locations and numbers inside a specific location where sick people are located. Additionally, the list and the information could be located on a variety of dashboards. The data that is displayed on the website and in the dashboard do not reveal clearly how many individuals are sick and how many deaths have occurred in each region; as a result, people's thoughts about the situation are quite restricted. Because of this constraint, the people's lack of knowledge about the sickness could put them at risk of contracting it, which would turn their innocence into a potentially terrible experience.

As a result of this, the researcher had the bright idea to use spatial analysis to plot on a map the location of the infected persons and the area where the deaths had taken place. In addition, the researcher produced a study that was concentrated on the use of a spatial analysis algorithm to the detection of covid-19 in a virtual map, notably in Rizal.

1.2 Purpose and Description of the Project

The objective of the study is to devise a method for quickly determining the locations of those who perished as a result of the COVID-19 virus in District 2 of Rizal. This will be accomplished by developing a system that is capable of locating the impacted areas where infected people live. It is absolutely necessary to maintain a record of the locations of the areas in Rizal that have the highest infection rates. After the pandemic has passed, these exceptional actions need to be brought to a conclusion and someone needs to be held accountable for them.

To do this, data on those afflicted with the disease and records of deaths kept by the Department of Health and the World Health Organization that were centred on District 2 of Rizal were collected and encoded into the system that was constructed. Following the collection of data from the system, a map will be shown, on which the specifics of the number of people impacted and other information will be presented on the ones of the region that have been marked out. In addition, this served as a hint to indicate that the region had been contaminated by the virus. In addition to that, a Global Information System was utilized so that the map could be navigated. Because of its capacity to store information about demographic factors and disease incidence against a geographic backdrop and because of its capabilities to perform spatial analysis, GIS technology is ideally suited for disease detection and control. This is due to its combination of these two features. The data may be mapped using GIS, which provides decision-makers with a better understanding of trends, possibilities, and relationships.

1.3 General Objective:

By using a spatial analysis algorithm, the study's primary goal is to create and develop a virtual map identification of covid-19.

1.3.1 Specific Objectives:

Specifically, this study aimed to:

- create a virtual map that will allow the 2nd District of Rizal's COVID-19 casualties to be recorded.
- Identify and map the locations of the Covid-19 persons who have been proven to have died and/or been exposed using spatial analysis.
- utilize the ISO 25010:2011 standard to assess the system's acceptance and operation.

1.4.1 Conceptual Framework:

With the difficulties and remedies mentioned in the earlier Chapters, the researcher developed the conceptual framework below:

INPUT	**PROCESS**	**OUTPUT**
Requirements: Data - Related Literature - Related Studies - Interview / Survey - Covid-19 Records Hardware - Arduino Nano - Server - Network Infrastructure - Raspberry Pi Software: - PHP - Arduino IDE - Python - MySQL People - Developer - Testers	Plan Analyse Design Implement Maintain ISO Standard	**IDENTIFICATION OF COVID-19 USING VIRTUAL MAP AND Spatiotemporal Analysis**

Fig. 1. Conceptual Framework

Figure 1. The Input-Process-Output (IPO) procedure for establishing how COVID-19 is being mapped in Rizal is shown in this diagram. The emphasis of the requirements is on employees, data, hardware, and software. The World Health Organization and the Department of Health contributed the majority of the data sets. Some of the input data

are derived from research and relevant publications. In order to guarantee the system's compatibility, hardware and software are supplied. This prevents issues with connecting the server to other devices. Peopleware is a representation of the system's users. The management and upkeep of the system depend on the users. By doing this, the system is guaranteed to carry out the intended functions. The Systems Development Life Cycle was used to create the system (SDLC). The requirements analysis was the first step in the development process, during which the appropriate data for the system's design was gathered, examined, and identified. Here, careful preparation is necessary to produce the ideal system design. The analysis comes next to make sure that the problem can be solved using the information gathered. Tools and techniques for the system's flow direction were also used in the layout design process. To accomplish the goals of the study, the program was coded. Functionality and dependability tests were run on the system. Although the implementation was completed, adjustments were made as a result of errors found during the system's overall testing.

Chapter 2

AN ANALYSIS OF THE RELEVANT RESEARCH AND LITERATURE

After an outbreak of the sickness in the city of Wuhan in China, a number of researchers started looking into the coronavirus in order to investigate, comprehend, and even anticipate the behavior of the illness and the progression of cases. This research could serve as a blueprint for government agencies to follow in order to improve the population's health as well as their quality of life while pandemics are occurring.

The disease is contextualized through social characteristics using a set of ordinary differential equations in order to gain an understanding of how the spread occurs, how it is feasible to control epidemics that have an effect on society, and how this might lead to the development of preventive measures. Examples of this type of model include the modified SEIR models that were proposed by Yang et al., as well as the SEIR (Susceptible, Exposed, Infectious, Recovered) model with age-structured quarantine class that was used to analyze the effects of policy control for the coronavirus epidemic in Brazil, and the SEIRQ (Susceptible, Exposed, Infectious, Recovered, Quarantine) model with age structure that was proposed by Gondim and Mach This model's objective is to conduct an analysis of the most effective quarantine measures in order to assist health managers in making decisions.

The studies of Dong et al. provide insight into a number of initiatives designed to facilitate Covid-19 screening and monitoring. An online interactive panel was developed by Dong et al. for the purpose of visualizing Covid-19 infected cases and deaths in real time. This effort provides researchers, health authorities, and the general public with a tool to track cases as the disease progresses. Because of the rapid spread of the coronavirus, it became increasingly important to categorize infected patients and determine which groups of people were more likely to be severely affected by the disease. Because of this, Xie and colleagues suggested a model of clinical prediction for patient mortality based on multivariable logistic regression in order to improve the utilization of limited healthcare resources and quantify the patient's chance of survival. In addition, in order to assist with the diagnosis, Feng et al. developed the online calculator S-COVID-19-P based on Lasso regression. This calculator is for the early detection of suspected cases of Covid-19 pneumonia in adult patients who are admitted to the hospital with a fever. A system that is based on deep learning has been proposed by Jin et al. for the rapid diagnosis of Covid-19 with precision that is comparable to experienced radiologists. This system is also capable of accurately classifying pneumonia, CAP (Community-Acquired Pneumonia), influenza A and B, and Covid-19. They used LASSO to determine the 12 features that were most useful in distinguishing Covid-19 from other pneumonias, and they found those qualities. By analyzing chest X-ray images, Gomes et al. presented a system that would enable the diagnosis of Covid-19. This system would be able to distinguish Covid-19 from bacterial and viral pneumonias using employing texture-based image representation and classification by Random Forests. Gomes et al. avoided deep learning-based solutions and adopted texture and shape features to provide users with a low-cost computational web-based computational environment that is able to deal with several simultaneous users without overcharging network resources. This is in contrast to other more complex Covid-19 x-ray feature extraction approaches.

Calculating the likelihood of infection based on the results of straightforward and uncomplicated laboratory tests was the goal of Meng et alcreation .'s of the Covid-19 Diagnostic Aid APP. The researchers were looking for an innovative approach to the early, effective, and accurate control and screening of individuals thought to be infected with the Covid-19 virus. The diagnostic procedure may be improved and medical resources could be saved if a large number of suspicious persons were investigated. Barbosa et al. took into consideration the fact that, in many parts of the world, RNA testing is not always available due to the scarcity of inputs. As a result, they developed HegIA, an intelligent system that is based on Bayes Networks and Random Forests to assist in the diagnosis of Covid-19 based on blood tests from a total of 24 blood tests. In symptomatic persons, the performance is comparable to that of RT-PCR (Reverse Transcription Polymerase Chain Reaction), despite the fact that coronavirus RNA is not searched for. HegIA is a fully working system that may be used without expense and is designed to give speedy testing at a minimal cost.

In terms of statistical epidemiological models, Sarkar et al. propose a mathematical model to monitor the dynamics of six compartments, which they refer to as Susceptible (S), Asymptomatic (A), Recovered (R), Infected (I), Isolated Infected (Iq), and Quarantined Susceptible (Sq). This model is collectively referred to as SARIIqSq. The authors tested their hypothesis using actual data on the COVID-19 pandemic that was occurring in India. In order to investigate the dynamics of the SARS-CoV-2 disease, the authors simulated the SARIIqSq model for 260 days, beginning with the date of the first COVID-19 case that was reported in India. This was done for each state and for the entire country. They used statistical analysis to demonstrate that a reduction in the contact rate between uninfected and infected persons, achieved by isolating susceptible individuals in a quarantine setting, can successfully lower the basic reproduction number. They also demonstrate that it is possible to put an end to the ongoing SARS-CoV-2 pandemic by combining the tight social separation with the contact tracing. However, the authors also underline the uncertainty of accessible legitimate data. This is especially relevant to the exact baseline number of infected patients due to sub-notifications, which may lead to equivocal outcomes and inaccurate projections by orders of size.

Ndarou et al. present an innovative epidemiological compartment model that accounts for the super-spreading phenomenon that can be caused by some individuals. They are thinking about a fatality compartment, which is associated with death brought on by the virus infection. The constant total population size N is divided into eight epidemiological classes as follows: the susceptible class (S), the exposed class (E), the symptomatic and infectious class (I), the super-spreaders class (P), the infectious but asymptomatic class (A), the hospitalized class (H), the recovering class (R), and the fatality class (F) (F). This model achieved a reasonably decent approximation of the reality of the Wuhan outbreak, anticipating a decline on the daily number of confirmed cases of the disease. The model also has a good correlation with the actual data of daily confirmed deaths. Because the number of patients admitted to hospitals is a crucial factor in determining an estimate of the number of intensive care units (ICUs) required, the model can be regarded applicable for other situations besides Wuhan, China.

The basic reproduction number, often known as R0, is one of the most essential variables in the study of infectious illnesses. R0 is used to determine how contagious an infectious disease is. If R0 is less than 1, it is anticipated that the disease will stop spreading. On the other hand, if R0 is equal to 1, it means that an infected person may, on average, infect only one other person; this indicates that the disease is not spreading. In the event that R0 > 1, the infectious disease has the potential to grow widespread and lead to epidemics.

The transmission dynamics of Covid-19 were difficult to explain, thus Khajanchi and Sarkar came up with a new compartmental model. They used daily data from Covid-19 for the Indian states of Jharkhand, Gujarat, and Andhra Pradesh, as well as for the capital city of Chandigarh, to calibrate their model. They investigated the practicable equilibria of the model that was proposed and the stability of those equilibria with regard to the fundamental reproduction number R0. When the recovery rate of infected persons increases, the disease-free equilibrium becomes stable while the endemic equilibrium becomes unstable. If, on the other hand, the disease transmission rate remains higher, then the endemic equilibrium will always remain stable. The results of the proposed model showed that R0 was greater than 1, indicating that there was a considerable epidemic throughout all of the analyzed Indian states. In addition to this, the model is able to make Covid-19 forecasts for shorter time periods.

Samui et al. presented a model that is able to represent the overall dynamics of SARS-CoV-2 that is deterministic and ordinary differential equation based. In order to formulate the SAIU, they divided the entire human population into four different compartments: susceptible individuals (people who were not infected), asymptomatic individuals (pauci-symptomatic or clinically undetected), reported symptomatic infected individuals (people who were clinically ill but not reported), and unreported symptomatic infected individuals (people who were clinically ill but not reported). This approach is predicated on the supposition that the individuals who have been reported to be infected will no longer associate with the illnesses once they have been isolated and transported to the hospital or intensive care units (ICU). Therefore, only infectious people who are a part of the I(t) or U(t) population can disseminate or transmit the diseases. The authors developed the SAIU model in order to investigate the transmission dynamics of COVID-19 using the data that was readily available for India from January 30, 2020, through April 30, 2020. The time period under research is from January 30, 2020, to April 30, 2020.

The SAIU model determines the fundamental reproduction number R0 and makes predictions regarding the outbreak of COVID-19 based on the estimated data. Given that the basic reproductive number R0 reflects the initial illness transmission and that the sensitivity indices describe the relative importance of various aspects in coronavirus transmission, the authors evaluated the basic reproductive number R0's sensitivity indices. According to the SAIU model, diseases remained present when R0 was greater than 1. For the sake of this investigation, the endemic equilibrium point E* was locally asymptotically stable for R0 > 1.

Khajanchi et al. refined the classical deterministic susceptible-exposed-infectious-removed (SEIR) compartmental model by introducing contact tracing-hospitalization strategies in order to study the epidemiological properties of Covid-19. This allowed the researchers to extend the classical model's susceptible-exposed-infectious-removed (SEIR) compartment. They determined the fundamental reproduction number for the disease and used that information to calibrate their mathematical model using data from confirmed cases in India. The authors have their own calibrated epidemic model for the short-term forecast of the disease's spread across the four provinces and the Republic of India. In the case of the province Kerala, the model fitting is not as good as it is in the case of other states and India as a whole; however, the simulation of the calibrated model was able to capture the increasing growth patterns for three different provinces, namely Delhi, Maharashtra, and West Bengal, as well as the Republic of India. Covid-19 may have the ability to exhibit oscillatory but manageable dynamics in the near future if social distancing and the efficacy of home isolation and hospitalization are maintained. This is suggested by both the simulation of the model and the prediction made from it. The model that has been proposed predicts that isolating or hospitalizing symptomatic members of the population, while maintaining strict hygienic protections and maintaining a social distance, will be significantly effective. Last but not least, Khajanchi et al. provide evidences that the magnitude of an epidemic and the length of its existence can be significantly altered by the timely implementation of a hospitalization or isolation program.

It is challenging to measure uncertainty using the traditional mathematical models of epidemiological prediction, notwithstanding their usefulness, because these models are deterministic and can only demonstrate the behavior of an epidemic on average. An examination of the spatial structure and dynamics of the transmission of Covid-19 was proposed by Wang et al. They provided a spatio-temporal prediction of the breakout of Covid-19 in the United States as a result of their findings. Kapoor et al. conducted research on large-scale spatio-temporal prediction utilizing neural network graphs and data on human mobility in US counties. This approach, along with information about space and time, teaches the model about the epidemiological dynamics. Tomar and Gupta came up with the idea of employing LSTM (Long Short-Term Memory) neural networks and altering curves to predict chaos as part of their space-time method to controlling and monitoring Covid-19. Researchers Ren et al. gathered epidemiological and socioeconomic data with the help of Ecological Niche Models (ENM). Their goal was to precisely estimate the risk areas for the Covid-19 infection. Yesilkanat conducted research utilizing a space-time technique for each of the 190 countries in the world and then utilized the Random Forest method to make a comparison with the number of actual cases of the disease. In addition to adopting a space-time approach, Pourghasemi et al. utilized regression and machine learning to perform an analysis of the trend, change detection, and risk mapping of the Covid-19 virus's spread in Iran. Roy et al. developed a short-term prediction model for the new Coronavirus using canonical ARIMA (Autoregressive Integrated Moving Average) and disease risk analysis carried out using weighted overlap analysis in geographic information systems. This allowed for accurate predictions to be made about the spread of the virus.

The study of the regional diversity of health outcomes and the link between such variations and potential risk factors is what spatial epidemiology is all about. John Snow, a physician who practiced in London in the 19th century, is credited with being a pioneer in the application of spatial epidemiology. He did this by mapping and identifying the deaths caused by cholera during an outbreak in London in 1854. (Begum, 2016). The snow provided conclusive evidence that the source of the pandemic was contaminated water rather than poor air quality as had been previously hypothesized. He mapped the deaths and discovered that most of the people who passed away resided in the area near the Broad Street water pump where there was a cluster of deaths. He presented the results of his inquiry and persuaded the local authorities about the significance of the findings, which ultimately resulted in the removal of the water pump handle. The map drawn by John Snow can be seen in Figure 1. On the map, Snow utilized bars to depict the number of deaths in a household that could be ascribed to cholera. The cholera map that Snows created was an important tool in the fight to contain the disease. The methods that people use today to diagnose and stop the spread of disease are directly influenced by his work.

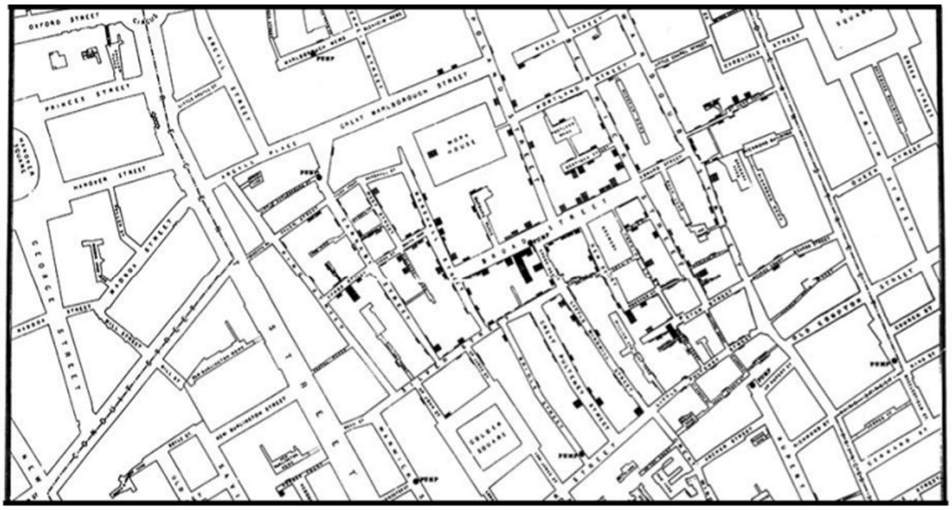


Figure 1. John Snow's map of cholera in Soho, London (Snow, 1854)

According to Elliot and Wartenberg (2004), the field of spatial epidemiology can be broken down into three distinct subfields: (1) disease clustering; (2) disease mapping; and (3) geographic correlation research. They defined illness clustering as the occurrence of an abnormally large number of health-related incidents in a certain time period and geographical location. It reveals concentrations of instances, often known as hot zones. The study of Hodgin's disease that was conducted in several areas of the United Kingdom between 1984 and 1986 is an example of a study that is connected to disease clustering (Alexander et al., 1989). At the level of electoral wards in the United Kingdom, this study discovered some indication of geographical clustering of Hodgin's disease among younger people between the ages of 0 and 34. Disease maps are a visual depiction of the representation of complex geographical information, as defined by Elliot and Wartenberg. These maps can uncover obvious trends in the occurrence of diseases. Disease maps typically make use of standardized incidence ratios (SIR) or standardized mortality ratios (SMR) for determining disease prevalence in geographical areas such as nations, states, counties, and cities (Bivand et al., 2013). In most cases, the SIR or SMR is utilized in order to do disease risk assessments. The SIR or SMR can be calculated by taking the observed number of cases or fatalities and dividing that number by the expected number of cases or fatalities in the region. There is a possibility that an extra source of variability in the map could be introduced by a study that involves mapping of a limited area. For instance, regions with fewer population and nearly no reported cases of disease can have extremely high SIR values, which can generate a significant amount of variation in the estimated disease prevalence rates (Anderson & Ryan, 2017). By utilizing Bayesian methodologies, the estimation of the illness risk in this region can be made more accurate. Bayesian approaches have seen widespread usage in recent years for estimating the relative risk of disease. Martínez-Bello et al. (2017) employed disease mapping approaches for dengue surveillance in Colombia. The researchers attempted to determine the relative risk of dengue fever for each census geographical unit in their investigation. Bayesian areal models were utilized for disease mapping in order to do the estimation of the relative risk. Covariates such as the vegetation index and land surface temperature were incorporated into the models in order to measure the impact that they had on the high risk of dengue. The findings of this study highlighted the significance of employing relative risk maps of dengue in the process of planning for public health. The vegetation index was shown to be connected with a high risk of dengue in Colombia, according to the findings of this study. According to Elliot and Wartenberg, the purpose of geographic correlation studies is to investigate geographic discrepancy across population groups regarding socioeconomic, demographic, lifestyle, and environmental factors to health outcomes, measured on a geographic scale. This can be done in order to better understand the relationship between these factors and health. For instance, Maheswaran et al. (1999) evaluated magnesium's role in drinking water in the association with mortality from acute myocardial infarction at a small area geographical level in northwest England. The study was conducted in this region because of the prevalence of the condition. According to the findings of this study, there is no connection between the amount of magnesium contained in drinking water and the risk of dying from a heart attack. A study that was carried out by Neuberger and colleagues (2009) investigated the effect that exposure to heavy metals at the Tar Creek Superfund site in Ottawa County, Oklahoma, had on the health problems (such as excess mortality, low birth weight, and children's blood lead levels) that were experienced by the people who lived in close proximity to the site. The findings of the study indicated a possible link between exposure to heavy metals and both the health of children and adults as well as chronic disease.

One of the areas of focus that COVID-19 related studies have been interested in is spatial epidemiology. Studies have made use of disease maps in order to investigate the spread of COVID-19 and evaluate the impact of the disease. Disease maps have been created using spatial models in a significant number of cases. Due to the fact that they take into account the pattern of spatial autocorrelation, spatial models can produce a risk calculation that is more accurate. For instance, Azevedo et al. (2020) employed a direct block sequential simulation method to model and estimate the geographical distribution of COVID-19 infection risk in Portugal. This work was carried out in Portugal. In the present investigation, it was anticipated that the direct block sequential simulation method would be able to account for the error caused by the geographic uncertainty as a function of the population size in each municipality. A spatial analysis was conducted by Cordes et al. (2020) in order to find COVID-19 clusters with high testing rates and the high proportion of positive tests across New York City and analyze the determinants associated with the clusters. The outcomes of this study revealed that high testing rates and high positive rates happened more frequently in communities that were mostly black and among those who lacked health care insurance. Mollalo et al. (2020) investigated the relationship between 35 socioeconomic, demographic, and environmental variables and the incidence of COVID-19 in the United States using global models (ordinary least squares, spatial lag model, and spatial error model) and local models (geographically weighted regression (GWR) and Multiscale GWR). This was done on a country level. According to the findings of this research, the multiscale GWR model has the highest goodness-of-fit compared to the other models. The results of the modeling revealed that the median income, the income inequality, the number of nurse practitioners, and the percentage of the black female population were major variables that contributed to the spatial diversity of COVID-19 incidence rates in the United States.

This study had several aims, one of which was to define the regional distribution of COVID - 19 risk throughout different time periods. When looking at a disease, it is crucial to take both space and time into consideration because this can help show uncommon patterns and trends in the condition. The interaction term of time and space in the model can indicate that the number of instances at various places may have different temporal trends. There have been a large number of research that have looked at the development of health outcomes in both space and time simultaneously. Ischemic heart disease (IHD) risk was studied in New South Wales, Australia, throughout the course of an eight-year period beginning in 2006 and ending in 2013 as part of a COVID-19 study that was unrelated to this investigation (Anderson & Ryan, 2017). The authors of this study compared a total of seven different spatio-temporal models. The final model was chosen by taking into consideration both the score on Moran's I statistic test and the amount of time it took to compute. It was determined that the most effective model for the IHD dataset would be a spatio-temporal one that utilized within-cluster smoothing and was proposed by Lee and Lawson. This model was useful in describing the different ways in which the temporal trend could be found across the area. When the final model was used, the findings revealed that the risk of IHD in the region decreased from 2006 to 2013. However, the findings also suggested that the risk of IHD did not decrease in every region of New South Wales. The risk of IHD remained the same throughout the study, and it was significantly higher in locations with a higher degree of isolation. In a recent study relating to COVID-19, Gayawan et al. (2020) used a two-component hurdle Poisson model to investigate the spatial and temporal distribution of COVID-19 cases and healthcare capacities in Africa a few weeks after the first COVID-19 case was identified in the continent. This study was conducted a few weeks after the first COVID-19 case was identified in Africa. According to the findings of a spatio-temporal model, the number of COVID-19 cases varied spatially across Africa. Particularly, a large number of cases were discovered in the bordering countries that are located in the western and northern sections of the continent. According to the findings of the study, nations with stronger healthcare capacities had a greater number of instances than countries with lower healthcare capacities. It seemed to imply that nations with more advanced medical facilities had a higher probability of identifying cases. This study estimated the risk of COVID-19 using Bayesian spatio-temporal modeling. This decision was made in light of the objectives of the study as well as the methodology utilized in earlier studies. Each individual zip code in the county was analyzed to determine its level of risk.

The observed number of cases does not adequately depict the risk of disease in maps on its own when one takes into account the fact that cases are mostly dispersed based on the population that is being mapped. Utilizing the SIR as a method for disease risk assessment in a region is one approach. According to Bivand et al. (2013), the SIR can be defined as the ratio between the observed number of instances (Yi) and the expected number of cases (Ei) as follows: for area I where I = 1, 2, 3,..., n, the SIR is calculated as follows:

$$SIR_i = \frac{Y_i}{E_i} \qquad (1)$$

The statistics from a larger reference population, such as a country, state, or county, are used to derive an estimate of the number of instances that should be expected. If the SIR value is equal to one, then there are no distinguishing characteristics between the two groups. A SIR value greater than one implies an increased rate of disease occurrence in comparison to that which was anticipated. When calculating SIR for illness maps, each area is treated as independent of the others, and there is no assumption made regarding the data's spatial organization. It is also possible for it to be unstable in regions that have a smaller number of people living there. As a consequence of this, there is a possibility of discovering an exceptionally low SIR in these regions. As a result, a generalized linear model is frequently utilized in the process of risk assessment. When trying to enhance local risk estimates caused by spatial autocorrelation, one potentially necessary step is to incorporate spatial features into the model. Moran's I statistic (Moran, 1950) is a useful tool for determining whether or not spatial autocorrelation is present in the data. The formula for Moran's I is as follows:

$$I = \frac{n}{\sum_{i=1}^{n}\sum_{j=1}^{n} w_{ij}} \frac{\sum_{i=1}^{n}\sum_{j=1}^{n} w_{ij}(y_i - \bar{y})(y_j - \bar{y})}{\sum_{i=1}^{n}(y_i - \bar{y})^2} \qquad (2)$$

where n is the total number of spatial units that I and j signify, y is the variable of interest with a mean of y, and wij is the spatial weight of the link that connects I and j. When it comes to a spatio-temporal model, both the aspects of space and time are taken into consideration in the model. In a spatio temporal model, just like in a spatial model, it is assumed that the number of observed cases in location I at time k is chosen from a Poisson distribution with mean Eikik. This is the case because Eikik is the difference between the mean and the standard deviation. The formula for a spatio-temporal model can be thought of as an expansion of the formula for a spatial model, which can be summarized as follows:

$$log(\theta_{ik}) = s_i + x_{ik}\beta + t_k + q_{ik} \quad (3)$$

where si stands for the spatial correlation function, refers to the set of coefficients for the variable X, tk represents the temporal correlation, and qik is the time-space interaction term.

The use of Bayesian methods in the areas of disease mapping has been well known. Bayesian approaches can process complex spatial information consisting of data points near each other that share similar characteristics, like socioeconomic and demographic (DiMaggio, 2014),

The posterior distribution, which provides a summary of the model parameters given observed data, is obtained by the Bayesian inference by multiplying the prior distribution on model parameters by the data likelihood (Lawson, 2018). The Bayesian hierarchical model has the potential to increase risk estimation because it is able to operate with a number of variables at the same time while also drawing on the expertise of surrounding regions (Bivand et al., 2013). The Markov Chain Monte Carlo (MCMC) techniques are used in the fitting process for the model. When trying to derive posterior distributions, the MCMC approaches are frequently utilized. These methods frequently require a significant investment of both time and effort on the part of the computer. In their most basic form, MCMC methods include running simulations of the model's parameters in order to obtain samples that are more likely to be actualizations of the distribution that is being targeted.

There is a possibility that the social determinants of health, such as socioeconomic and demographic status, such as race, ethnicity, education, employment, and living condition, would have a major impact on the results of COVID-19. As a result, this study incorporated some of these variables into the analysis to determine how much of an impact they have on the occurrence of COVID-19. Recent research have demonstrated that minority groups have been disproportionately affected by the COVID-19 virus. Hispanics made up 18.5% of the U.S. population (according to the U.S. Census Bureau), but they accounted for 26% of COVID-19 cases. As a result, the COVID-19 infection rate was high among Hispanics in the United States (CDC, 2020a). In spite of the fact that African Americans only made up 30 percent of Chicago's total population, they accounted for more than half of the city's COVID-19 cases (Yancy, 2020). In New York City, where the number of cases was high among people of African American and Hispanic descent, a syndrome quite similar to this one also occurred (The Official Website of the City of New

York, 2020). According to the findings of several studies (Muoz-Price et al., 2020), being African American is connected with having a positive COVID-19 test result. These studies investigated the relationship between the prevalence of COVID-19 infections and a variety of socioeconomic and demographic characteristics. People with lower socioeconomic status have a higher risk of contracting COVID-19 due to a number of factors, such as living in overcrowded housing, having limited access to outdoor space, and having working conditions that make it more difficult for them to work from home, such as those who work in supermarkets and warehouses. Those with higher socioeconomic status have a lower risk of contracting COVID-19 (Patel et al., 2020).

Throughout the duration of the pandemic, Cook County remained one of the counties in the United States with the highest number of COVID-19 cases. In previous years, the number of COVID-19 cases in Cook County began to rise in March of that year and reached their highest point on May 1 of that same year. The number of newly reported cases remained relatively stable until May 11 before beginning an upward trend once more. After this, the number of cases of COVID-19 continued to gradually decrease until the middle of June 2020. Despite this, the number of newly reported cases continued to rise until it reached a new high point at the beginning of September of the same year (USA Facts, 2020). Over time, there has been a shift in the demographic features of people who have had confirmed cases. According to the data from IDPH COVID-19, the majority of the instances that occurred in Cook County in late May were reported among persons in their 40s and 50s. Early in September, the demographics changed as a result of an increase in the number of cases among adults in their 20s and 30s. This is an indication that the number of cases increased among younger people over the summer of 2020. The number of newly reported cases varied greatly from one part of the county to another and from one time period to another. The spread of COVID-19 in Cook County has been halted thanks to the combined efforts of state and local authorities. In March of 2020, the governor of Illinois issued a number of executive measures in an effort to contain the situation as effectively as possible. At the municipal level, Chicago west suburb regions such as Oak Park, River Forest, and Forest Park have mandated a shelter-in-place order for their community by the date of March 20, 2020. (Schering, 2020). The mayor of Chicago and the governor of Illinois worked to focus on the mitigation measures in predominantly Hispanic areas, such as Little Village and Archer Heights, in order to respond to the surge in new cases among Hispanic residents in Chicago. They did this by launching a multilingual digital and video campaign and holding virtual town hall meetings for seniors and immigrant youth in Hispanic communities. Little Village and Archer Heights are just two of the predominantly Hispanic neighborhoods in Chicago (Spielman & Sfondeles, 2020).

Chapter 3

METHODOLOGY

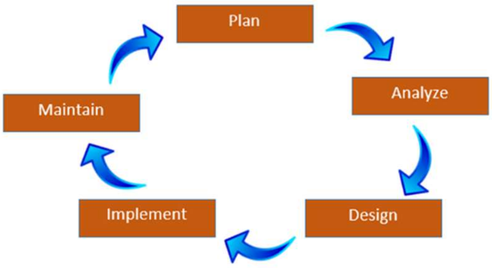
3.1 Research Design

During the process of developing the system, researchers utilized both descriptive and developmental research approaches. In the descriptive technique, the behaviors of certain individuals are observed and reported in great detail, but the individuals themselves are not influenced in any manner. This also clarifies or validates certain objectives or assumptions pertaining to a particular category of individuals (Gutcheck 2018). The developmental method is a systematic study of the design, development, and evaluation of instructional programs, products, or processes that meet the criteria of consistency and effectiveness, which is very important in the field of instructional technology. In other words, the developmental method looks at how instructional programs, products, or processes are designed, developed, and evaluated (Ritchie, 1994). The essential information is cultivated through developmental research, and designs that have the potential to be realized as prototypes are produced. 2014, authored by Martin.

3.2 Data and Process Modelling

Analyzing and defining an organization's data requirements within the context of its information systems is what data and process modelling is all about. Documenting the intricate system architecture of software is the primary focus of data modelling. This is done in order to make the design and diagrams, which make use of symbols and language to show flow, simply understandable (Techtarget, 2019).

The software development life cycle (SDLC) method is a technique that guarantees that the end-user requirements are satisfied in order to support strategic business goals and solutions. When designing, developing, replacing, or maintaining an information system, its application is required. Through its methodical, step-by-step procedures, SLDC makes the construction of a system easier, which ultimately helps the company fulfil all of its customers' expectations (Stackify, 2017). The Software Development Life Cycle, or SDLC, can be broken down into the following steps, as indicated above:



Credit to Stackify (2017)

Fig. 2. Systems Development Life Cycle Model

3.2.1 Plan:

During this step of the SDLC process, the data were gathered, and the needs were determined in order to make an in-depth study of the data by collecting the COVID-19 data that was provided by the legitimate organizations. The most essential inputs, such as the required data from COVID-19, particularly their geographical location, are examined. Other inputs, such as the data, are also considered. The information was collected from reliable sources so that it could be used as a component in an analysis of the best way to depict the information on infected people on the map using the appropriate level of detail.

3.2.2 Analyze:

The information that was gleaned from the data was subjected to thorough examination and processing. The data were organized so that the system would receive useful input from them. In order to achieve the desired outcomes, careful consideration was given to each of the goals. The benefits and drawbacks of the existing system were also noted, and the new system that was presented was envisioned and drawn. During this phase, the new system proposal was evaluated in order to provide the specifications necessary for the system's development.

3.2.3 Design:

The blueprint was created right here. Using a flowchart, we were able to illustrate the flow of the system, and the sequence was also established. All of the documentation was arranged in an orderly fashion to make certain that the path taken by the system was consistent with the objectives of the research. During this time, coding was also completed. In order to demonstrate how the system functions, the layout of the system was also drawn and displayed. Both the enlarged system layout and design were developed in order to fulfill the system's technological and functional needs, with both the logical and physical components of the system being taken into consideration.

3.2.4 Implement:

The construction of the system is what this phase is all about. The software was configured and the necessary codes were written so that it could communicate with one another via the network. The completed system was put through a battery of practical examinations. In addition to testing the functionality, users were given training to ensure that they were able to utilize the system appropriately. During the phase devoted to implementation, it is intended to incorporate the results into the official website in order to provide a reference to the current standing of Covid-19 in the area. This can be of assistance to the parents, students, employees, and management in monitoring to raise their understanding of the status of the areas being monitored. People can gain the awareness they need to immediately implement additional countermeasures to combat the threat posed by a pandemic as a result of this. Because the system is just concerned with District 2, it offers convenient access because the amount of time it takes users to search for information is reduced.

3.2.5 Maintain:

During this phase, we make certain that there will be no interruptions to the normal operation of the system. Training was provided for both the regular users of the system and the administrators of the system. The methods for maintaining and providing assistance for the system have been laid out in step-by-step format. During this stage, a maintenance plan was put into effect.

4.0 Software Evaluation:

In order to conduct an acceptability analysis of the software, the researcher utilized the standard ISO/IEC 2510:2011, focusing on the characteristics that were relevant to the analysis, as shown in Figure 3:

Fig. 3. Eight (8) Characteristics of Software Product Quality Model and System Quality in Use Model

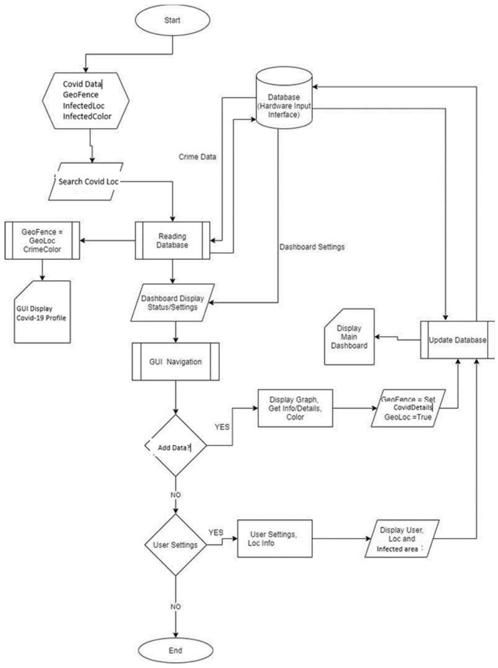


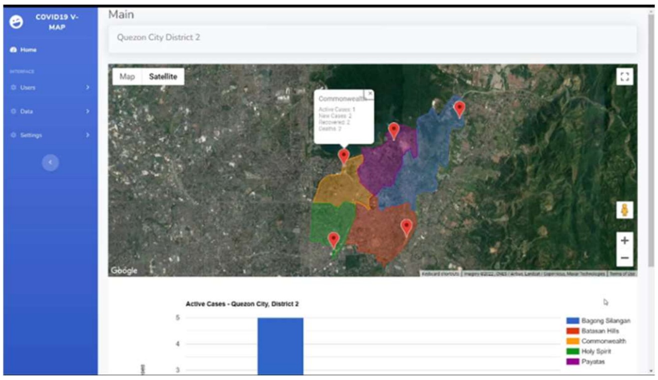
Fig. 4. Flowchart of the System

The flowchart outlines the steps that need to be taken in order to arrive at the solution. This began with the setup of the locations using Global Information System (GIS), followed by the assignment of colors to each barangay and finally the assignment of colors to indicate the people who were sick. The information from the COVID 19 will be entered into the system, and then the system will be able to record its findings in the database for use by the various barangays. The data will be used to build the dashboard, which will then be able to provide specifics regarding the current status of the affected areas. It would be possible to produce bar graphs in order to provide a more graphical representation of the afflicted areas.

Chapter 4

RESULTS AND DISCUSSIONS

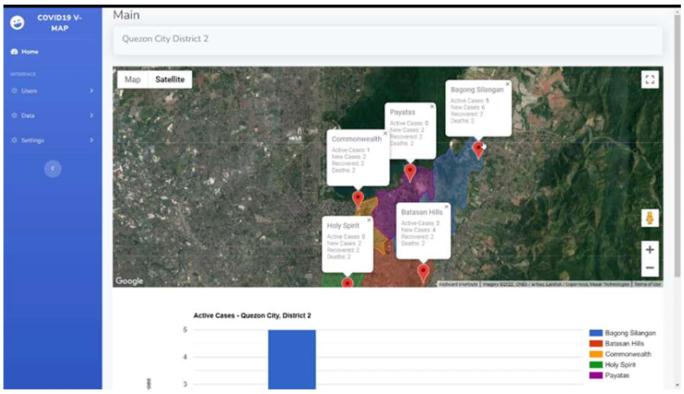
The information regarding the Covid-19 casualties that occurred in the 2nd District of Rizal will be captured by the digital map. This will be accomplished by collecting data on those who have been infected, as well as death records from the Department of Health and the World Health Organization, as well as information from the Rizal local health office that is concentrating on District 2, and encoding it into the system that has been developed. The data that was retrieved from the system will be presented in the form of a map, with the region that is afflicted by the virus indicated by a shaded portion of the map. It will receive the data updates in a timeframe that is described as "near real-time."



Commonwealth
Active Cases: 1
New Cases: 2
Recovered: 2
Deaths: 2

Fig. 5. Mapping of Covid-19 using Spatial Analysis

Web-based applications may now make it possible for automatic graphical representations to be applied using Google Maps (Pokorn, P., 2017). This was made possible with the assistance of technology. The map of Rizal District 2, which serves as the primary focus of the investigation, is presented below. After being input, the data that was gathered from the Department of Health (DOH) will be shown with the correct colors serving as an indicator. Each individual location within the aforementioned district is denoted by a distinct hue. The status of the infected COVID-19 will be shown as soon as the mouse is pointed in the direction of each marker. This contains the number of instances that are currently active, new cases, patients who have recovered, and several fatalities.



Quezon City District 2

Bagong Silangan
Active Cases: 5
New Cases: 6
Recovered: 2
Deaths: 2

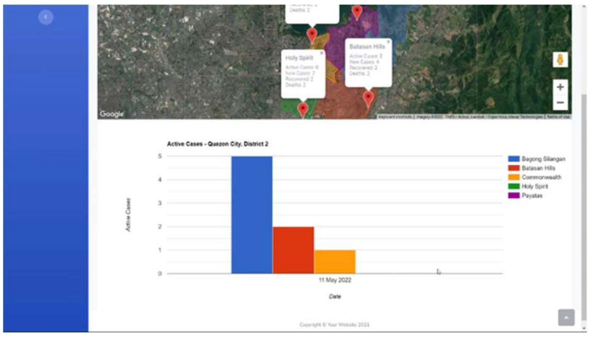
Payatas
Active Cases: 0
New Cases: 2
Recovered: 2
Deaths: 2

Commonwealth
Active Cases: 1
New Cases: 2
Recovered: 2
Deaths: 2

Batasan Hills
Active Cases: 2
New Cases: 4
Recovered: 2
Deaths: 2

Holy Spirit
Active Cases: 0
New Cases: 2
Recovered: 2
Deaths: 2

Fig. 6. Mapping of Covid-19 Specifying Details per Area.



Deaths: 2

Holy Spirit
Active Cases: 0
New Cases: 2
Recovered: 2
Deaths: 2

Batasan Hills
Active Cases: 2
New Cases: 4
Recovered: 2
Deaths: 2

Fig. 7. Mapping of Covid-19 Specifying Details and Graphical Result per Area.

The shaded regions that correspond to where the markers are pointed are shown in figure 7. The portion that is shaded indicates the locations of the five barangays as well as the specifics of the status of Covid 19 that occurred in the respective places. In addition, a bar graph that illustrates the data of the affected locations is displayed on the primary screen. This will present a distinct image of the event that took place in each barangay. A graph might be used to create a virtual image that would illustrate how many people are affected in the aforementioned places.

Software Evaluation

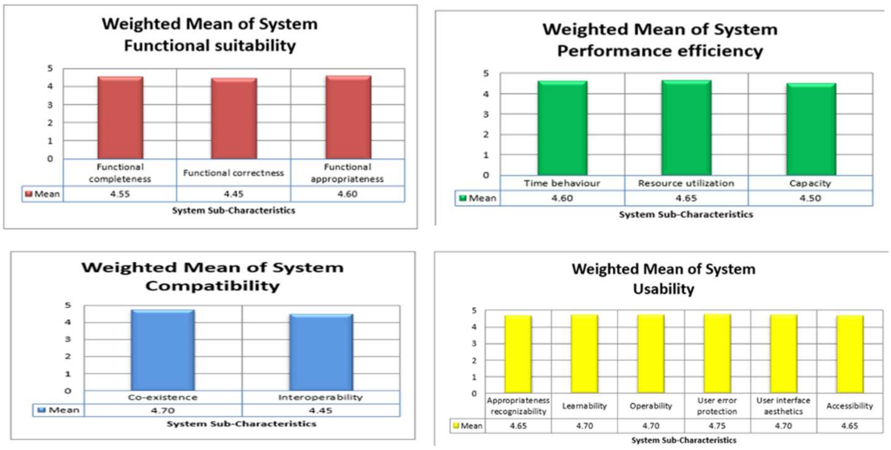
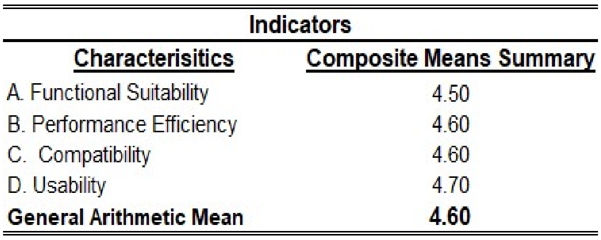


Fig. 8. Mapping of Covid-19 Specifying Details and Graphical Result per Area.

The outcome of the evaluation of the program, which was conducted by applying the characteristics and sub-characteristics of ISO 25010, is presented in Figure 8. This demonstrates that the users were satisfied with the system that was built by using the general weighted mean of 4.60, which is equivalent to "Strongly Agree (Outstanding)".

Table 1: General Arithmetic Mean of Characteristics



Indicators	
Characterisitics	**Composite Means Summary**
A. Functional Suitability	4.50
B. Performance Efficiency	4.60
C. Compatibility	4.60
D. Usability	4.70
General Arithmetic Mean	**4.60**

This demonstrates not only that the program is capable of performing the necessary work, but also that it is successful in acquiring the intended results. Additionally, this demonstrated that the system can be included into any existing system. The system also demonstrated that it is capable of responding to the actions taken by the users and that it is efficient in its use of the available resources. The system is intuitive, and there are no known bugs in it. The user interface is intuitive and attractive all at the same time.

CONCLUSIONS

The purpose of designing and developing the virtual map that has the capability of gathering data on the COVID-19 casualties in the 2nd District of Rizal is to display data to the people in each barangay of the 2nd District in order to raise their level of awareness. This can also aid the people by providing them with further knowledge about the area, which can protect them from being sick by preventing them from going to infected places.

The design and development of the map using Spatial Analysis were done in order to identify and plot the location of the confirmed cases of Covid-19, as well as the number of people who died from the infection and those who were exposed to it in the aforementioned district. This is a visual representation of the current situation regarding infections in the region. Because of this, people are aware of the problem and will likely steer clear of the locations where the infection is spreading.

The system's acceptability and functionality were evaluated based on how well it met the requirements of the pertinent sub-characteristics of the ISO/IEC 25010:2011 standard. The overall weighted mean for the acceptability assessment is 4.60, which translates to "Strongly Agree." This indicates that users have indicated that they are satisfied with the system based on the results of the evaluation that was conducted using the characteristics and sub-characteristics of the standard.

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