Journal of Technology Management and Business (ISSN: 2289-7224)
Vol 5, No 1, Special Edition, 2018
Managing Epidemic and Natural Disaster using Mathematical Modelling

MODELLING THE SPREAD OF PNEUMONIA IN THE PHILIPPINES USING SUSCEPTIBLE-INFECTED-RECOVERED (SIR) MODEL WITH DEMOGRAPHIC CHANGES

Bill William M. Soliman[1], Aldous Cesar F. Bueno[2]

[1, 2] Philippine Science High School-Central Luzon
Campus Lily Hill, Clark Freeport Zone, Pampanga,
Philippines
[2] University of the Philippines Baguio, Baguio City, Philippines

*Corresponding E-mail : bwsoliman@clc.pshs.edu.ph

Abstract

Epidemic modeling is an important tool used by mathematicians in analyzing the rate of spread of an epidemic by taking in account of the parameters and vectors that facilitate the transmission rate of the disease. The measurement of the average transmission rate through mathematical analysis helps in finding the proper approach of disease control methods in mitigating the spread of diseases. The study aims to analyze and predict the rate of transmission of the global epidemic pneumonia in the Philippines population through epidemic modeling. The study methodology used the standard epidemic model known as the SIR model to quantify real-world data on pneumonia cases into a set of differential equations while taking in consideration of changes in the population experienced due to demographic change. The study yielded results that suggested positive correlation in real-world data and the modeled data points mostly for SIR models that assumed linear change in the infection rate and recovery rate. In addition, the implementation of population models showed increases in the infection rate and the recovery rate due to increasing trend observed in the given population. The study evaluated linear rate SIR assuming exponential population growth as the most applicable epidemic model from the selection in modeling real-world epidemic data. In addition, the study compared the effectiveness of using quarantine method and vaccination method in mitigating the spread of pneumonia.

Keywords: *Pneumonia, Mathematical model, Susceptible-Infected-Recovered (SIR) Model*

Received: January 16, 2018 Accepted: January 25, 2018 Published: February 15, 2018

1.0 Introduction

Pneumonia is a respiratory disease, denoted by an inflammation of the alveoli in the lungs due to pathogens. It has several vectors for transmissions through different types of bacteria and virus, making it highly prominent due to how easily these pathogens can be transmitted from the air to the lungs of a susceptible individual (WebMD, 2005).

It is a common yet severe illness that is one of the leading causes of disease-related deaths, resulting to deaths up to 4 million annually (Ruuskanen et al, 2011). Due to the contributing vectors for its transmission by different pathogens, pneumonia is a rampant communicable infectious disease that is in the need rapid treatment and immunization in order to control and further reduce the spread of the disease. The severity of chronic pneumonia that often leads to hospitalization of the patient is an added justification of the need to closely monitor the disease. Several health departments all over the world, headed by the World Health Organization (WHO), had taken considerable action in the eradication of prominent epidemic diseases

Epidemic modelling is an important tool involving numerical simulation of the infected population per unit time gathered from health records. Epidemic models are often utilized by health organizations in order to analyze and predict the rate of transmission of the disease in a population based on the trend observed in the data sets. These models generally follow a set of assumptions based on the population and the transmission mechanism of the disease, while using the data points provided to create the pattern for differential change of the number of infected over time. Other factors such as population density and rate of immunization can be additionally added in the model as a way of creating a more accurate epidemic model.

As of 2014, the World Health Organization recorded 18% of deaths of children under 5 years old due to pneumonia at a 1.1 million deaths every year. Poor and rural communities, especially in sub-Saharan Africa and South Asia, experience the most casualties due to pneumonia. Due to the lower living standards of these countries, there is high financial burden and insufficient budget to fund a mass health immunization programs for all populations in the country afflicted by pneumonia. The Philippines is classified as one of the top countries that account for 75% of all pneumonia cases for children at 2.34 million recorded deaths on 2009 (World Health Organization, 2016). It is important for health organizations to better understand the dynamics of the disease in order to suggest precautions that should be applied by all communities against the spread of pneumonia.

Epidemic modelling is an important mathematical tool utilized by the department of epidemiology for assessing the current infectivity status of an epidemic, based on real-life data on the outbreaks of the disease in a population. The analysis of epidemic models helps in understanding the mechanisms involved in the spread of the disease throughout the population. The knowledge that can be gathered from the epidemic models can be used in order to help health organizations deliberate the most efficient approach and mode of disease control in mitigating the disease transmission rate.

2.0 Methodology

2.1 Data Gathering and Plotting

A letter of request, regarding data on the number of people infected by pneumonia was sent to the Department of Health (DOH) Office. The data samples span annual cases of pneumonia infections in country from 1990 to 2010. All the number of infected cases over total population versus time are incorporated over a scatter plot. Different parameters, like the instance of population change, for each of the data sets in each model. Since demographic population change in one of the focus of the study, a separate letter of request was sent to the Philippines Statistics Authority (PSA) Office on the Philippine population per year,

2.2 Plugging in all SIR Models

The SIR Model serves as the epidemic model used in the study, focusing on the populations for (1) susceptible, (2) infected, and (3) recovered compartments. These compartments are represented by the following set of equations:

Equation 1 (Susceptible Compartment):

$$\frac{dS}{dt} = -\alpha SI$$

Equation 2 (Infected Compartment):

$$\frac{dI}{dt} = \alpha SI - \beta I$$

Equation 3 (Recovered Compartment):

$$\frac{dS}{dt} = \beta I$$

The first parameter that was implemented in the SIR models is the assumption of constant and linear rate of change in the infection rate α and the recovery rate β of all compartments in the population, which means that from time $t = 0$ until the end, the coefficients for α and β may vary based on the assumption given in the model. The second parameter that was implemented is the addition of demographic changes due to instances of births and deaths in the population. Two different population models were used for the SIR models, namely:

Equation 4 (Linear Population Change):

$$N(t) = m + N0$$

Equation 5 (Exponential Population Change):

$$N(t) = Ae^{kt} + B$$

All in all, there are a total of six SIR models used for this research study based on rate of changes in the compartment populations and total population per unit time.

2.3 Finding the Infection Rate Constants for the Epidemic Models

Wolfram Mathematica is an essential statistical program that is effective in the creation and analysis of mathematical models by analysing various trends in the derivative changes in several data points observed. The program was used to find the infection rate α and recovery rate constant β on the infected and recovered ratio equation provided, respectively, through the FindFit() function from Mathematica for these variables, based on the peaks and changes of all variables over a period of time. This procedure was also done for all SIR model of varying assumptions. The slope constants *m* and *k* in Equations 4 and 5, respectively, are calculated as a Taylor function in the Wolfram Mathematica based on real-life data acquired from the PSA Office. The values for the total Philippine population per time *t* changes through the addition of these slope constants in their respective population change models.

The basic reproductive number R_0, given by the infection rate α over the recovery rate β, represents the number of secondary infections that result per infected individual. Finding the basic reproductive number will help describe the rate at which the pneumonia is transmitted. If R_0 is greater than 1, the disease can be classified as an epidemic since the coefficient for α is greater than coefficient for β. The findings for these procedures will help give disease control methods that can be done to control the rate of pneumonia spread.

2.4 Statistical Analysis

Pearson Correlation Test is the statistical analysis used to measure the degree of correlation of a data set relative to another data set in comparison. The value for the Pearson Correlation test varies from -1 to 1 which denotes positive correlation and negative correlation, respectively. The closer the value to 1, the more varied are the values relative to the plotted data points. These statistical analysis tests were used for each model in order to find how their varying parameters affect their respective correlations with the data gathered from DOH.

2.5 Simulation of Disease Control

The implementation of different methods that hinder disease transmission rate and promote immunization were used as a way of fitting in the rate of infection and recovery to the data sets provided. This was done by decreasing the values of infection or increasing the values for

recovery rate, thus significantly changing the value of the basic reproductive number for each model. The first disease control method evaluated is the quarantine method which involves reducing the rate of contact between the infected and susceptible population, thereby decreasing the rate of infection (Safi & Gumel, 2011). In the SIR model, quarantine method involves decreasing the coefficients of α by 0.5%, 1%, and 1.5%. Vaccination also reduces the rate of infection by promoting immunization on a number of the susceptible population, thus effectively converting the susceptible population into the recovered population where there is no chance of being infected (Safi & Gumel, 2011). Vaccination was simulated by increasing the coefficients of recovery rate by 0.5%, 1%, and 1.5%. The graphs for the corresponding methods were compared and analysed in order to assess which method is more effective.

3.0 Results and Discussion

3.1 Data parameters for SIR models

The plotted values for the SIR Models span the number of annual pneumonia cases recorded by DOH in the Philippines from the year 1990 to 2010. The initial number of infected population is at 235,947 cases of pneumonia over the initial Philippine population at 60,703,206, back in the year 1990. The infectivity peak for pneumonia cases in the Philippine is at t = 12 at 776,562 annual cases of pneumonia experienced in the Philippines.

The figure below shows the summary for the coefficient values of α, β, and R_0 for all parameters in the SIR models used in the study.

Table 1: Fit coefficient values for all SIR models

	SIR without demography		SIR with linear population change		SIR with exponential population change	
	Constant Rate	Linear Rate	Constant Rate	Linear Rate	Constant Rate	Linear Rate
α	1.30903	1.11413	1.44753	1.07187	1.45549	0.91423
β	1.13764	1.2529	1.28617	1.19678	1.29087	1.03213
R_0	1.15065	0.889242	1.12546	0.8957	1.12753	0.88577

The general trend observed for the models, assuming constant rate of infection and recovery, is a higher coefficient value for α compared to β; this suggests that there is active transmission of pneumonia in the population ($R_0 > 1$). In the case of linear rate, there is derivative changes in the coefficients for α and β throughout time. As mentioned before, the infectivity peak for the SIR models is located at t = 12. This means that there is steady increase for both α and β from $t = 0 \rightarrow 12$. At $t > 12$, the coefficient values of both α and β go from positive and negative as the value of β exceeds the value α. After the infectivity peak, the lower decrease in recovery rate makes it higher than the infection rate, hence, leading to the decline in the infected fraction in the population (Chowell et al., 2004).

Thus, SIR models assuming linear rate of change for α and β have lower transmission rate of pneumonia by $t > 12$ in the ($R_0 < 1$). The advantage of linear rate of change over constant rate of change is there are more specific points or ranges of time t in which α and β experience derivative change (Tassier, 2005).

3.2 Statistical Analysis

The table below shows the degree of correlation between the data gathered from DOH compared to the theoretical values modelled by incorporating the values of α and β:

Table 2: Pearson Correlation test statistics for all SIR models

	SIR without demography		**SIR with linear population change**		**SIR with exponential population change**	
	Constant Rate	**Linear Rate**	**Constant Rate**	**Linear Rate**	**Constant Rate**	**Linear Rate**
Pearson Correlation Test	**0.903582**	**0.955688**	**0.861105**	**0.9349**	**0.8887**	**0.936445**

From the values shown in Table 2, it can be observed that there is higher correlation between the model and the data for SIR models that assume linear rate of change in infection and recovery rate. Although the SIR model without demographic change yielded the highest correlation, it can be attested that there is an increase in the basic reproductive ratio for SIR models that experience demographic change since there are more individuals that are added into the S(t) compartment per unit time (Naresh et al., 2009; Chowell et al., 2004). From the models shown in Table 2, the SIR model assuming demographic change and linear rate of change in α and β are most applicable of use in a realistic setting.

3.3 Disease Control Simulation

As expected of the simulation of disease control methods, there is an observed decrease in the infectivity peak per incremental fraction of the population applied by these methods as shown in the figures below.

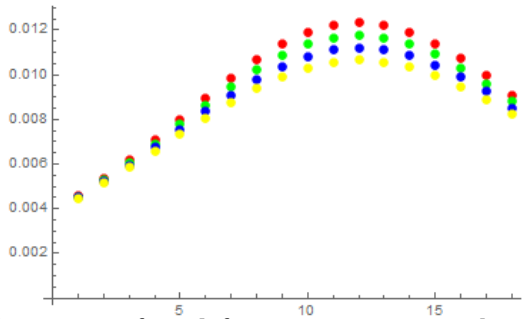

Figure 1: Infected fraction vs time graph of SIR model implementing Quarantine method (1.00α, 0.995α, 0.990α, 0.985α)

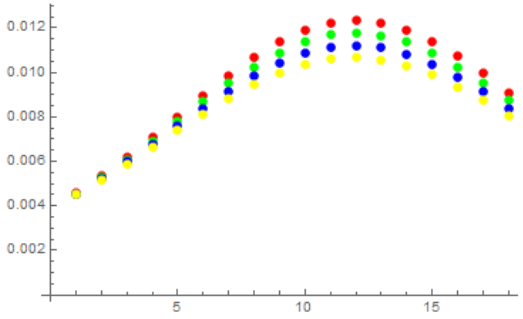

Figure 2: Infected fraction vs time graph of SIR model implementing Vaccination method (1.00β, 1.005β, 1.010β, 1.015β)

The infected fraction of the population at the infectivity peak (t = 12) for each 0.5% increment in the recovery rate and infection rate, respectively, for quarantine and vaccination methods is shown by the table below:

Table 3: Infectivity Peak per 5% population fraction increment of Quarantine and Vaccination methods

	Quarantine Method				**Vaccination Method**			
	1.000α	**0.995α**	**0.990α**	**0.985α**	**1.000β**	**1.005β**	**1.010β**	**1.015β**
Infected Fraction	0.123564	0.0117715	0.01122028	0.0106509	0.0123564	0.0117742	0.0112134	0.0106736

Through calculation of the average decrease in the infected fraction per 0.5% increment in α or β, there is found to have higher decrease in infected fraction for quarantine method ($\Delta iquar = 5.685 \times 10^{-4}$) compared to vaccination method ($\Delta ivacc = 5.6093 \times 10^{-4}$). This shows that at the infectivity peak, decreasing the infection rate has bigger impact in reducing the basic reproductive number of pneumonia compared to increasing the recovery rate. Since pneumonia is found to have a high rate of infection compared to recovery rate, it is of higher priority to reduce the infected population by isolation of the infected population from the susceptible population. Although the costs for implementing constant vaccinations and construction of quarantine compartments has high demerit on the national health organization budget, a combination of both methods could be done in order to ensure that pneumonia transmission is hindered through cost-effective disease control strategies (Department of Health, 2015).

4.0 Conclusion and Recommendation

This study demonstrated the modeling of pneumonia spread in the Philippines through the use of SIR model while incorporating the parameters of demographic change in the population as a real measure over time. In addition, the SIR models yielded values estimatedly close to 0.9 accuracy as given by the Pearson Coefficient Test. The most applicable SIR models that were used in the study exhibited assumptions of linear changes in the infection rate and recovery rate constants, as well as the incorporation of population changes along with the SIR models. These models yielded the highest correlation values for the modeled data and real-world data, showing the applicability of these models in measuring and predicting the spread of pneumonia in the Philippine population. These SIR models can be used in order to predict the future changes of pneumonia based on the derivative changes in the values of infection rate and recovery rate over time (Brauer & Castillo-Chávez, 2001).

The simulated health interventions demonstrated their effectivity in reducing the transmission rate of epidemic diseases by limiting the rate in which a fraction of the susceptible population moves on to the susceptible population by either ensuring that their contact with infected population is hindered or by moving them to the recovered compartment. The simulation of disease control justifies necessary priority in reducing the contact rate between the infected and the susceptible populations due to the high transmission rate of pneumonia especially in urbanized areas (Ruuskanen *et al.*, 2011). The simulation of these methods in the SIR model is a step in determining the best approach in hindering and ultimately, eliminating the spread of pneumonia through health initiatives.

For further study, the use of epidemic data recorded in shorter time intervals such as by weekly intervals is suggested. Epidemic modeling is more ideally done for long time spans composed of weekly records for the number of infected in the population. This means that more data points in the infection curve may mean a higher correlation between the data values and for more variance that can be observed from the values.

In addition, future studies regarding demographic change in SIR model may opt to include the parameters of birth rate and death in the SIR models as this allow the evaluation of changes in the total population for each compartment model (Naresh *et al.*, 2009).

References

Brauer, F. & Castillo-Chávez, C. (2001). Mathematical Models in Population Biology and Epidemiology. NY: Springer.

Chowell, G., Hengartner, N., Castillo-Chavez, C., Fenimore, P., Hymann, J. (2004). The basic reproductive number of Ebola and the effects of public health measures: the cases of Congo and Uganda. Journal of Theoretical Biology. 229. 119-126.

Department of Health. (2015). Field Health Service Information System 2015 Annual Report.

Naresh, R., Sharma, D., Tripathi, A. (2009). Modelling the effect of tuberculosis on the spread of HIV infection in a population with density-dependent birth and death rate. Mathematical and Computer Modelling. 50. 1154-1166.

Ruuskanen, O; Lahti, E; Jennings, LC; Murdoch, DR (2011). Viral pneumonia. Lancet. 377 (9773): 1264– 75

Safi, M. A., & Gumel, A. B. (2011). Mathematical analysis of a disease transmission modelwith quarantine, isolation and an imperfect vaccine.Computers & Mathematics with Applications, 61(10), 3044-3070.

Tassier, T. (2005). SIR Model of Epidemics.

WebMD (2005). Pneumonia-topic overview. Retrieved November 12, 2016, from http://www.webmd.com/lung/tc/pneumonia-topic-overview

World Health Organization. (2016). Pneumonia. Retrieved November 14, 2016, from World Health Organization, http://www.who.int/mediacentre/factsheets/fs331/en/