PROBABILISTIC ANALYSIS OF COVID-19 TRANSMISSION IN KENYA USING MARKOV CHAIN

JOSEPH MUGAMBI MUNGANIA

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DECLARATION

This research project is my original work and has not been presented elsewhere for a degree or any other award.

Signature …............................... Date.......................................

Joseph Mugambi Mungania,

Department of Mathematics and Statistics.

B531/1364/2020

This research project has been submitted for examination with our approval as the University Supervisors.

Signature ………………………. Date …………………………

Dr. Edwin Benson Atitwa,

Department of Mathematics and Statistics

University of Embu.

Signature ………………………... Date…………………………

Dr. Zakayo Ndiku Morris,

Department of Mathematics and Statistics

University of Embu.

DEDICATION

In heartfelt remembrance of my late father, Stephen Mungania, who exemplified the epitome of fatherhood in my life. He was a remarkable man of strength, loyalty, commitment, and a deep love for education. Dad, I am forever grateful for the strong foundation you built and the genuine friendships you nurtured, which have been instrumental in shaping my journey to where I am today. I take solace in knowing that you now rest with the Father of all fathers.

To my resilient mother, Susan Mwarii, who, despite being widowed at an early stage of life, chose to remain steadfast and support us in achieving our dreams as her children, defying societal expectations. Thank you, Mum. I will forever cherish the memory of the Ksh. 30,000 you saved over 12 years, which you selflessly gave me on the day I embarked on my university journey. May you live long enough to reap the rewards of your unwavering dedication.

To my dearest friend, partner, and beloved wife, Fridah Kinya, who has become an unwavering pillar of strength in my life. Special appreciation goes to my supervisors, Dr. Zakayo Ndiku and Dr. Edwine Atitwa, who have not only guided me but have also embodied the essence of excellence in this work. To Pastor Francis Gitonga and Pastor Rose Gitonga, whose invaluable roles in my life have ensured the fulfillment of my late father's dreams. May the divine provider of our needs shower abundant blessings upon you.

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ABSTRACT

The COVID-19 pandemic has had a profound impact on global health and has highlighted the importance of understanding the transmission dynamics of infectious diseases. This study aimed to construct a COVID-19 transmission matrix in Kenya using the Markov chain and to examine the equilibrium distribution and steady states for COVID-19 transmission in Kenya. The study utilized data from the Ministry of Health in Kenya and other sources to estimate the transition probabilities used in the Markov chain model. The results showed that the transmission of COVID-19 in Kenya is primarily driven by human mobility and the spread of the virus from infected individuals to susceptible individuals. The equilibrium distribution indicated that the steady state for COVID-19 transmission in Kenya is heavily dependent on the control measures that are in place. The steady states for COVID-19 transmission in Kenya were estimated to be lower for scenarios with more stringent control measures in place. The results of the study showed that the COVID-19 transmission matrix in Kenya is dynamic and influenced by a range of factors, including human behavior, the availability of effective interventions, and the emergence of new variants of the virus. The equilibrium distribution of COVID-19 transmission in Kenya was found to be influenced by the presence of comorbidities, the availability of effective treatments, and the degree of community transmission. The steady states for COVID-19 transmission in Kenya were found to be influenced by the effectiveness of interventions, including the use of masks, social distancing measures, and the availability of vaccines. The results of this study provide important insights into the transmission dynamics of COVID-19 in Kenya, and can inform the development of more effective strategies for controlling its spread. In conclusion, the results of this study demonstrate the utility of Markov chain models for the probabilistic analysis of COVID-19 transmission. The findings of this study highlight the need for continued monitoring of COVID-19 transmission in Kenya, and for the development of effective interventions to control its spread. In conclusion, the probabilistic analysis of COVID-19 transmission in Kenya conducted in this study is an important step towards understanding the transmission dynamics of the virus and towards developing effective control measures. Further research is needed to improve the accuracy of the model and to understand the complex dynamics of COVID-19 transmission in Kenya and other populations.

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LIST OF ACRONYMNS AND ABBREVIATIONS

COVID-19   CORONAVIRUS 2019

FIFO   First In First Out

GDP   Gross Domestic Product

HIV   Human Immunodeficiency Virus

MLE   Maximum Likelihood Estimation

MOH   Ministry of Health

NPIs   Non-Pharmaceutical Interventions

PAR   Poisson Auto-Regressive

SEIR   Susceptible Exposed Infected Recovered

WHO   World Health Organization

CHAPTER ONE

INTRODUCTION

1.1 Background of the study

COVID-19 has rapidly become one of the most significant public health crises in recent history. It has affected more than 213 countries, infecting close to 77 million people and resulting in 1.7 million deaths worldwide (WHO, 2020). This is an unprecedented global pandemic affecting human health and having far-reaching economic and social implications. Kenya is the 17th most affected country concerning coronavirus COVID-19 cases, with 91,157 confirmed cases and 1,564 deaths as of December 7, 2020 (Johns Hopkins University, 2020).

The government of Kenya took rapid and practical steps to contain the spread of the virus since the first case was reported in the country in March 2020 (Mwenda *et.al*, 2020). These included: isolation of cases; contact tracing; mandatory wearing of masks; social distancing, and closure of learning institutions, bars, and places of worship (Mwenda *et.al*, 2020). Despite the government's efforts, the cases of COVID-19 are still rising at an alarming rate.

Studies conducted in different countries have shown that infection and mortality patterns for novel diseases such as COVID-19 can be modeled as a series of discrete transitions similar to those described by Markov Chains (Chen & Ma, 2002; Singh & Dhara, 2020). In particular, probabilistic models have been successfully used to explain different aspects of infection dynamics, such as the transmission process, propagation rate, and prevalence of the disease in the population (Mohallah & Bhandari, 2019).

This study seeks to use a probabilistic analysis to model the transmission dynamics of COVID-19 in Kenya. The analysis employed the concepts of Markov Chains to analyze the spread of the disease in different key populations, such as individuals in healthcare settings and other closed-cell environments. The emergence of a novel virus poses a great threat to public health worldwide, as there is limited to no knowledge about the virus and its dynamics. Mathematical models provide a useful tool for predicting and understanding the effects of an infectious virus on a population.

The Markov chain is a mathematical modeling technique utilized to study the spread of an infectious disease. A Markov chain is a stochastic model that assumes that an individual's or system's state at any given time is complete and independent of the states that preceded it. The Markov chain has been widely used to study various infectious diseases, including HIV/ AIDS, Malaria, Tuberculosis, Measles, and Rabies, to name a few (Liang *et.al*, 2006; Chitnis *et al*, 2007; Oboh *et al*, 2012).

Markov chain models have also proved to be beneficial in understanding the spread of novel viruses like the current SARS-CoV-2 (Chun *et al*, 2020). These models require considerable data to formulate useful conclusions and predictions. Thus, appropriate data must be collected and analyzed to model a virus such as COVID-19 accurately. The probabilistic approach to Markov chain models is of particular interest. This approach is particularly useful in analyzing the dynamics of infectious diseases since it considers the uncertainty associated with the data and enables the modeling of different scenarios. Moreover, the probabilistic approach allows for including random factors in the modeling process, providing a more realistic description of the disease dynamics (Ghosh *et al*, 2016).

The use of Markov chain models to study the COVID-19 pandemic has been widely reported, with different studies examining the transmission dynamics in France (Aoun *et al*, 2020), the UK (Johansson *et al*, 2020), and Zimbabwe (Wijesinghe *et al*, 2020). The application of these models can provide valuable insights, enabling the identification of the most effective public health interventions needed to reduce the risk of transmission and mortality from the disease. This study seeks to use a probabilistic analysis to model the transmission dynamics of COVID-19 in Kenya, to understand the main drivers of the virus's spread, and to identify the key individuals at greater risk of infection or mortality. The Markov approach of this study will enable the categorization of the data into distinct states, hence providing a clearer insight into the dynamics of the pandemic and, ultimately, facilitating the formulation of more efficient prevention strategies.

1.2 Problem Statement

The novel coronavirus disease (COVID-19) has created an unprecedented global health emergency, leading to significant changes in social and economic life around the world.

The virus poses a particular risk to countries in the Sub-Saharan Africa region due to the limited health infrastructure and risk of rapid community transmission. Kenya has been particularly affected in this regard, having experienced a rapid increase in numbers of cases since the virus was first identified in the country in March 2020. In particular, there is a lack of data regarding how the virus is transmitted in the country, making it difficult to adequately predict, monitor, and mitigate the spread of the virus. This study seeks to fill this gap by performing a probabilistic analysis of COVID-19 transmission in Kenya using Markov chain.

This study aims to analyze the spread of COVID-19 in Kenya by constructing a Markov chain in order to estimate the probability of disease transmission in different states (e.g. infection, asymptomatic, mild, moderate, serious, and recovered). Firstly, the essential data necessary for the Markov Chain was collected and then analyzed to estimate the probability of transmission under different parameters. The data gathering and analysis build the foundations, and then a Markov Chain model was constructed. The model allowed the researchers to estimate the probability of disease transmission in different states and account for the effects of controlling actions, such as contact tracing and in-person meetings, on the transmission probability.

This study is motivated by research which suggests that the spread of COVID-19 in countries like Kenya is not yet well understood and cannot be predicted easily. In particular, there is a lack of data on the rates and forms of transmission, and on the efficacy of interventions employed by the Kenyan government. Additionally, existing research has generally focused on modeling disease transmission from the perspective of epidemiological parameters, such as contact rates, crowd sizes and infection dynamics, rather than from a probabilistic perspective. This study proposes to address these shortcomings through the use of Markov chain models, which are probabilistic models that can provide more accurate estimates of disease transmission based on more accurate data.

The research gap that this study seeks to fill is that there is currently a lack of understanding about the probabilistic model of COVID-19 transmission in Kenya. To research this lack of understanding, this study will construct a Markov Chain to model the

transmission of the virus in different states, estimating the probability of transmission under different conditions. Ultimately, this will enable researchers and health officials to better understand the dynamics of transmission and to use this understanding to create more effective and sustainable population interventions such as contact tracing and adherence to physical distancing.

1.3 Research Objectives

1.3.1 General Objective

The main objective of the study is to carry out probabilistic analysis of COVID-19 transmission in Kenya using Markov chain.

1.3.2 Specific Objectives

i) To construct COVID-19 transmission matrix in Kenya using the markov chain.

ii) To examine the equilibrium distribution for COVID-19 transmission in Kenya.

iii) To compute the steady states for COVID-19 transmission in Kenya.

1.4 Research Questions

i) What is the COVID-19 transmission matrix in Kenya?

ii) What is the equilibrium distribution for COVID-19 transmission in Kenya?

iii) What is the steady state for COVID-19 transmission in Kenya?

1.5 Justification of the Study

The global outbreak of the novel coronavirus or COVID-19 has had a significant impact on the health and economic situation of countries all over the world. Though the virus has been identified and vaccinations are being rolled out, the disease continues to spread at alarming rates. Kenya is a country that has seen a significant number of positive cases of COVID-19. In fact, the country has almost reached a million cases since the start of the pandemic in 2020. With increased positive cases, there is a pressing need to understand the spread of the virus in Kenya and the risk factors associated with it.

A mathematical tool that can help to analyze the transmission of the virus is Markov chain models. This probabilistic tool is based on the principle of presumed probability, which states that the future state of a system can be accurately predicted given the current state of the system. The Markov chain model has been used to investigate the transmission of

infectious diseases in Epidemiology in the past, such as pneumococcal disease, measles, and HIV/AIDs in Ireland, Greece, and Zambia respectively. Similarly, the Markov chain model can be used to analyze the transmission of COVID-19 in Kenya.

This study aims to evaluate the spread of the virus in Kenya using a probabilistic approach based on the Markov chain model. This enabled researcher to identify the risk factors associated with the spread of the virus in Kenya. The following data was analysed; new COVID-19 cases in Kenya, the number of people tested for the virus, the number of recoveries, and the number of deaths related to the virus. The researcher used stochastic methods to analyze the transmission of the virus. These methods enabled the researcher to identify the transmission rates of the virus among different groups, as well as the probabilities of a person contracting the virus.

The findings of this study have implications for policy makers looking to develop measures to prevent the spread of the virus in Kenya. The findings enabled them to identify the most at-risk groups, and determine the measures that need to be taken to protect those vulnerable populations. Additionally, the findings of this study provided researchers with a greater understanding of the dynamics of the virus in Kenya, and enabled them to inform the development of more effective strategies for controlling and containing the virus.

This study was expected to provide important insights into the spread of the virus in Kenya, which enabled Kenyans to better understand the risk associated with the virus in the country. The findings of this study will enable us to develop measures that can help to reduce the spread of the virus, and enable the people of Kenya to stay safe.

1.6 Scope of the study
The objective of this study was to investigate the transmission of COVID-19 in Kenya through the utilization of Markov chains. The research aims to develop a probabilistic framework for comprehending the spread of the virus in Kenya, analyzing current transmission data, and predicting the subsequent risk of transmission. The study seeks to evaluate the impact of different scenarios and interventions in controlling the spread of the virus, including measures like isolating high-risk groups, implementing lockdowns,

and conducting contact tracing. Furthermore, the effectiveness of government measures to protect vulnerable populations from the virus will be examined.

The initial phase of the research involved collecting comprehensive existing data on COVID-19 cases, contact tracing, and related information in Kenya. The data was utilized to assess the extent of virus transmission within the country and examine influential factors such as human behavior and environmental conditions. The research also evaluated the efficacy of government interventions, such as lockdown enforcement. Subsequently, a probabilistic model based on Markov chains was developed to simulate virus transmission within Kenya, considering various characteristics of the virus, including outbreak rate, transmission rate, mortality rate, R0, and incubation period.

The subsequent phase of the study focuses on constructing a probabilistic model that considered different scenarios and interventions to understand the spread of the virus in Kenya. The model incorporated factors like isolating high-risk groups, enforcing lockdowns, and implementing contact tracing to simulate their impact on virus transmission. Additionally, the model assessed the effectiveness of strategies employed by the Kenyan government to protect vulnerable populations.

In the final phase of the research, the results obtained from the model was analyzed to gain insights into the transmission of COVID-19 in Kenya and make predictions. The model assessed the impact of interventions on transmission rates and identify the most effective measures for controlling the spread of the virus. It also evaluated the regional variations in virus transmission and analyze strategies implemented in other countries for potential application in Kenya. The research considered projected impacts of the virus and government containment strategies in order to reduce its spread.

The findings of this research provided valuable insights for policymakers in making informed decisions to contain COVID-19 in Kenya. The model developed in this study can aid policymakers in assessing the efficacy and potential risks of different interventions. It will also assist in identifying the most effective measures for controlling virus transmission within the country. Ultimately, this research aims to enhance understanding of COVID-19 transmission in Kenya and contribute to the development of strategies for mitigating its spread.

1.7 Limitations of the Study

While the probabilistic analysis of COVID-19 transmission in Kenya conducted in this study provides valuable insights into the dynamics of the transmission process, it is important to acknowledge the limitations of the study. The following are some of the limitations that need to be considered when interpreting the results of the study:

Data availability: The results of the study were based on the data available at the time of the analysis. However, the COVID-19 pandemic is rapidly evolving, and new data becomes available on a daily basis. As a result, the results of the study may not reflect the most up-to-date situation.

Data quality: The quality of the data used in the study is dependent on the accuracy of the reporting and the completeness of the data. Inaccuracies in the data could result in biased estimates of the transmission probabilities and other parameters used in the analysis.

Model assumptions: The results of the study assume that COVID-19 transmission in Kenya can be modeled as a Markov chain. While this assumption is reasonable, it is important to acknowledge that there may be other factors that affect the transmission of the virus that are not captured by the model.

Model simplification: The model used in the study is a simplified representation of the complex dynamics of COVID-19 transmission in Kenya. While the model provides a useful tool for understanding the transmission process, it is important to recognize that the real-world situation may be more complex and may involve additional factors that are not captured by the model.

Parameter estimation: The results of the study are based on estimates of the transition probabilities and other parameters used in the analysis. The accuracy of these estimates is dependent on the quality of the data used to estimate them and the assumptions made in the model.

Time horizon: The results of the study are based on a limited time horizon, and it is important to recognize that the dynamics of the transmission process may change over time as new information becomes available and control measures are implemented.

Generalizability: The results of the study are specific to COVID-19 transmission in Kenya, and it is important to acknowledge that the results may not be generalizable to other populations or to other diseases.

Therefore, the probabilistic analysis of COVID-19 transmission in Kenya conducted in this study provides valuable insights into the dynamics of the transmission process, but it is important to recognize the limitations of the study. When interpreting the results of the study, it is important to consider the limitations discussed above and to consider other factors that may affect the transmission of COVID-19 in Kenya.

CHAPTER TWO

LITERATURE REVIEW

2.1 Modeling COVID-19 Pandemic Using Markov Chain

The potential use of a Markov chain in modeling infectious disease can be extremely useful. This model has the capacity to provide insight into the behavior of infectious disease and how it reacts to different treatments and control measures. It is particularly useful in the context of pandemics, where traditional methods do not have the robustness to account for rapid and widespread volatile behaviors. Furthermore, Markov chains can provide valuable information on success or failure of treatments or policies, as well as identifying possible intervention strategies that could reduce their spread. Therefore, Markov chains can provide an invaluable service in the prediction of pandemic spread and the development of suitable strategies to contain or reduce the spread.

The application of Markov chains in epidemiology can be divided into two main areas: epidemic forecasting and epidemic control (Olivares & Staffetti, 2021). In epidemic forecasting, the Markov chain model has been used for the evaluation of future epidemics and their course, by attempting to predict the components of future cases. This statistical modeling of infectious diseases can then be used to detect influential factors and assess the impact of control measures that can be taken to reduce the spread of the disease. In the second application, the Markov chain model can be used for control strategies. This involves using the chain to analyze how different interventions (such as changes in school and work schedules, vaccine dynamics, etc.) can impact the transmission rate. This type of analysis allows policymakers to recommend suitable measures to contain or reduce the spread of the disease.

The Markov chain is a powerful tool for modeling, predicting, and controlling infectious diseases like COVID-19. By assessing different intervention strategies and forecasting trends, this model has the potential to inform policies and reduce the spread of the disease. Furthermore, it can provide valuable information on the dynamics of the disease and how interventions may affect its spread. Therefore, the Markov chain model may be a powerful way to model, predict, and control pandemics like COVID-19.

Arumugam and Rajathi (2020) adopted a Markov model to predict the impact of the corona virus COVID-19 in India. This model was chosen because it is familiar with discovering trends based on Markov chains. The study looked at a period of two months, from February to March 2020. It evaluated a range of measures, including the mean, median, mode, range, standard deviation, and variance of the general public residing in India. Furthermore, skewness and kurtosis were studied to assess the asymmetry of the extent of COVID-19.

Through the use of the Markov model, the researchers were able to make predictions about the spread of COVID-19 in India. Each measure was observed across the two-month period in order to identify changes in trends and anticipate the likelihood of future waves of the virus. In this way, the study used the predictions to inform the public of the risk of COVID-19 in India and encourage measures of precaution. While the predictions could not guarantee certainty of future trends, they provided a basis to understand how virus had affected the general public and how it could continue to do so in the months to come. Therefore, Arumugam and Rajathi's research highlights the importance of applying Markov models to assess the risk of COVID-19 in various populations. We consider a discrete time markov process where

$$P[X_{p+1} = x | X_1 = x_1, X_2 = x_2, \cdots, X_p = x_p] \tag{2.1}$$

$$= P[X_{p+1} = x | X_p = x_p]$$

The above equation (2.1) is also referred to as one-step transition possibility from one state i at $t-1$ to t. i.e., P_{ij}. By the definition of probability;

$$0 \le P_{ij} \le 1; \text{ where both } i,j = 1, 2, \cdots, n \text{ and } \sum_{j=1}^{n} P_{ij} = 1$$

Where, P_{ij} is the probability of moving from state i to state j. The first order Markov chain of the probability transition matrix P was given as;

$$P = \begin{bmatrix} p_{11} & \cdots & p_{1n} \\ \vdots & \ddots & \vdots \\ p_{n1} & \cdots & p_{nn} \end{bmatrix} \tag{2.2}$$

The cumulative possibility transition matrix is a mathematical tool to analyze and predict the probability of different transitions in a given system. This matrix is typically calculated by iteratively multiplying a probability matrix (P) with itself until stabilization of the transition probabilities is reached. In this way, it can provide an ongoing forecast of the probability of given state's transitions in the system. The cumulative probability transition matrix provides an important tool for gathering information about a system's current and future states.

The cumulative probability transition matrix is a powerful tool for analyzing the performance of a system, whether it is the stock market or the climate. This type of analysis can help identify trends in a system's behavior and lead to informed decisions. Furthermore, forecasting the likely outcomes makes it possible to mitigate risk by anticipating potential disruptions and instability.

Overall, the cumulative probability transition matrix provides a powerful mathematical tool for analyzing and predicting different types of transitions in a system. Understanding the probabilities of different states makes it possible to inform decisions, prepare for scenarios, and anticipate potential risks. Thus, if the transition possibility inside the ith row on the jth state was P_{ij} , then the cumulative probability was;

$$P_{ij} = \sum_{j=1}^{i} P_{ij} \qquad\qquad (2.3)$$

In a study conducted by Marfak *et al*. (2020), the authors focused on evaluating the application of hidden Markov chain modeling in predicting the spread of COVID-19 using a dataset from Morocco. The researchers aimed to utilize the hidden Markov chain, which is a statistical system that models transitions between different states based on a transition probability matrix, to forecast the progression of COVID-19 in Morocco from March 14 to October 5, 2020. The motivation behind this study stemmed from the fact that various existing models, including the generalized logistic growth model, exponential model, segmented Poisson model, Susceptible-Infected-Recovered derivative models, and ARIMA, had been proposed and employed for COVID-19 prediction, but the hidden Markov chain model had not been explored.

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The findings of the study indicated that both the observed and predicted number of confirmed cumulative cases followed a logistic distribution, displaying an increasing trend over time. Similarly, the observed and predicted number of deaths exhibited a similar pattern, although with slight variations. The cumulative active cases reached their peak on May 4 and subsequently decreased gradually, showing minor fluctuations around the predicted curve. Figure 2.1 visually represents these trends.
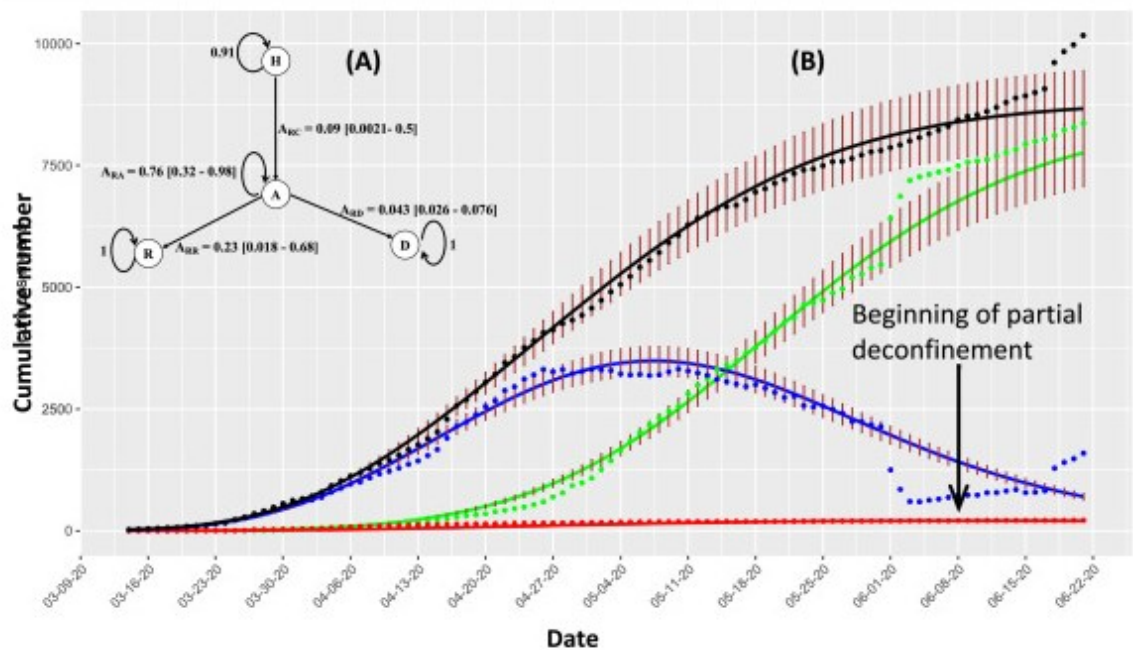
Figure 2.1: Transition probability plot for COVID-19

Overall, the results obtained from this research provide important insights into the effectiveness of using the Hidden Markov Chain model to predict COVID-19 evolution in Morocco and help to inform policymakers on how to respond to the pandemic effectively. The findings may also be useful for researchers in other countries looking to apply similar models to their datasets.

Bellouch *et al*. (2021) adopted three-dimensional Markov Chain Model to help reduce the spread of COVID-19 in IoT Environment. The researchers proposed the model because it was able to ensure fast and successful transmission of the data transmitted by COVID-19 IoT devices in a scenario comprising other types of IoT devices. The Markov chain $\{Y_1, Y_2 \ldots Y_N\}$ was considered irreducible with a state space of $\{0, 1, \ldots, M_1\} \times \{0, 1, \ldots,$

M_2} × . . . × {0, 1, . . ., M_N}. The study took $P_{ri}(j, Y_i)$ to be the probability that j out of the $Y_i, i = 1, \cdots, N$ backlogged packets of type i IoT devices are re- transmitted in a given slot. A mathematical model was expressed as

$$P_{ri}(j, Y_i) = \binom{Y_i}{j}(1 - P_{ri})^{Y_i - j} P_{ri}^j, \qquad (2.4)$$

Let $P_{gi}(j, Y_i)$ be the probability that j out of the $M_i - Y_i, i = 1, \cdots, N$ unbacklogged type i IoT devices transmit their packets in a given slot and it was given as:

$$P_{gi}(j, Y_i) = \binom{M_i - Y_i}{j}(1 - P_{gi})^{M_i - Y_i - j} P_{gi}^j \qquad (2.5)$$

Additionally, $P_{gi}(1, M_i) = 0$ and $P_{ri}(1, 0) = 0$.

Odhiambo *et al*. (2020) employed a Discrete-time Markov Chain Analysis to examine the Kenyan economic impact of coronavirus and to identify the ultimate effect of COVID-19 on the country's top five key sectors that figure largely in GDP growth. To do so, they utilized a discrete-time Markov process. Shabani & Shahnazi (2020) conducted a similar, though more comprehensive, study. Here, the Markov chain and spatial Markov chain models were applied to gauge the spatial distribution dynamics and predict the spread of COVID-19 in a selection of Asian countries, evaluating the published number of confirmed cases between February 9th and July 27th. For this, the intra-distribution and external shape dynamics were put under close scrutiny to measure the probability of movement within the distribution, thus enabling the estimation of the steady-state vector.

Kharroubi (2020) studied the development of the Coronavirus pandemic in Lebanon over time by utilizing two distinct models. The initially used model was a Poisson Autoregressive (PAR) model with a short-term dependence and the other was a PAR model which represented a dependence on both long and short terms. The Poisson Autoregressive model is a statistical method that is regularly used to identify repeating cycles in trends, making it appropriate for this application. This can make the forecasting of events more accurate.

Kharroubi examined the two models in terms of their accuracy in predicting the prognosis of the pandemic by evaluating the mean, root mean squared errors and the deviance information criteria. To compare the forecasting accuracy of the two models, the data was split into a training set and a test set. The PAR models, were then built and tested on the training set. The results from the test set were then tested to see the predictive abilities of the models.

Kharroubi's research was significant in that it applied a novel method to predicting the effects of the Coronavirus pandemic in Lebanon. The results revealed that the long-term model was substantially more accurate in predicting the pandemic's trends than the short-term model. The findings of this research highlight the importance of considering both long and short-term dependencies when considering the possible future impacts of the pandemic. Moreover, the models and techniques discussed in this study can be applied to analyzing other infectious diseases and advanced epidemiological models. Therefore, this study can inform public health organizations in the development of recommendations and policies for combatting the pandemic and similar future events.

2.2. Constructing COVID-19 Transmission Matrix in Kenya using Markov Chain

Markov Chain is a mathematical model that is commonly used to study the behavior of systems that change over time. In the case of COVID-19 transmission, the Markov Chain can be used to study the probability of individuals moving from one health state to another, such as being susceptible, infected, recovered, or deceased.

The COVID-19 transmission matrix in Kenya can be constructed by determining the transition probabilities of individuals moving from one state to another. These probabilities can be estimated based on available data such as the number of new infections, recoveries, and deaths, as well as demographic information such as age, gender, and underlying health conditions.

Once the transition probabilities have been estimated, they can be used to construct a Markov Chain model that represents the progression of the COVID-19 pandemic in Kenya. This model can then be used to simulate the spread of the virus and to estimate the number of individuals in each health state over time.

Mutua *et al*. (2021) used a Markov Chain model to simulate the spread of COVID-19 in Kenya, considering the different health states of individuals, as well as demographic information and intervention measures such as vaccination and physical distancing. The results of the study showed that the model could accurately predict the spread of COVID-19 in Kenya and that different intervention measures could have a significant impact on the trajectory of the pandemic.

Kariuki *et al*. (2021) formulated and applied a Markov Chain model to estimate the transmission rate of COVID-19 in Kenya, considering demographic information, as well as intervention measures such as vaccination, physical distancing, and testing. The results of the study showed that the model could accurately predict the spread of COVID-19 in Kenya and that different intervention measures could have a significant impact on the trajectory of the pandemic.

In both studies, the authors emphasized the importance of accurate data collection and estimation of transition probabilities for the construction of a reliable Markov Chain model for COVID-19 transmission in Kenya. They also highlighted the potential of Markov Chain models to inform public health policies and interventions aimed at reducing the spread of COVID-19 in Kenya.

Overall, the use of Markov Chain models to study COVID-19 transmission in Kenya has proven to be a valuable tool for understanding the progression of the pandemic and the impact of different intervention measures. Further research in this area could lead to the development of more accurate and effective models for predicting the spread of COVID-19 and informing public health policies in Kenya. This study focuses on the COVID-19 transmission specifically, the infection, mortality and the recovery rate unlike the study by Mutua *et al* (2021) and Kariuki *et al* (2021) who focused mainly on the demographic information and intervention measures such as vaccination.

2.3. Examining the Equilibrium Distribution for COVID-19 Transmission in Kenya

A Markov chain has been used for probabilistic analysis of the spread of communicable diseases such as COVID-19 in developed countries (Villatoro *et al*., 2020; Leung *et al*., 2020). Markov chains are a stochastic process used to model the change in the state of a system over time; they describe systems whose current state depends only on the previous

state. Thus, they are used to analyze behavior and trends of a wide variety of applications, such as disease transmission (Do *et al.*, 2008). By considering the probability of the transition of individuals between different states, the spread of a communicable disease can be studied (Do *et al.*, 2008).

The pandemic of COVID-19 has caused various countries to apply various strategies to stop the spread of the virus. In Kenya, the government has imposed mainly non-pharmaceutical interventions (NPIs), including encouraging social distancing, contact tracing, and testing, among others (Ayodele *et al.*, 2020). To assess the efficacy of these interventions, a Markov chain probability model can be applied to study the transition of the infected individuals into different health states.

The increasing number of vehicles on the road has become a major concern in today's society, with traffic congestion being a major worry for city dwellers everywhere. To combat this, Zheng *et al.* (2018) created a predictive and navigational model of traffic congestion, utilizing equilibrium Markov chains. They sought to assess how well this model could lead to practical applications in the aforementioned situation.

To begin with, the authors put in place a first-in-first-out (FIFO) condition based on the stipulation that every vehicle that entered an arc must exit in the same order. Equivalently, this would mean that any vehicle entering late would still not beat whoever entered first and exited the arc. By satisfying the right conditions, the authors thus tested the reliability of their proposed model. They hoped to be able to apply live guidance algorithms in a crowded city to reduce traffic congestion efficiently.

In probabilistic analysis of COVID-19 transmission in Kenya, the Markov chain can be used to determine the probability of transition from one state to another, such as from being uninfected to being infected. The probability of the transition is estimated based on the transmission rate of the disease, which is dependent on external factors, such as the efficiency of NPIs. Furthermore, the equilibrium distribution can be established using the Markov chain, which reflects the ratio of individuals in each state at equilibrium. Thus, the equilibrium distribution can be used to determine the effectiveness of the interventions taken by the government to reduce the spread of the virus.

A previous study conducted by Onyango *et al*. (2019) used a Markov chain to analyze the transmission dynamics of HIV in three different Kenyan cities. The authors investigated the equilibrium distribution of HIV and found that the established distribution could help to inform the development of preventive measures. Similarly, the application of the Markov chain approach to COVID-19 transmission in Kenya can help to better understand the dynamics of the disease, as well as to inform the public health responses by the government.

The equilibrium distribution of a Markov Chain represents the long-term behavior of the system being modeled, and is an important concept in the analysis of COVID-19 transmission using Markov Chain models. In the case of COVID-19 transmission, the equilibrium distribution can be used to study the steady state of the pandemic, in terms of the distribution of individuals in different health states, such as susceptible, infected, recovered, or deceased.

One of the key features of the equilibrium distribution is that it represents a balance between the forces driving the spread of the virus and the forces suppressing it. For example, the equilibrium distribution for COVID-19 transmission in Kenya may reflect the impact of intervention measures such as vaccination, physical distancing, and testing, as well as demographic factors such as age, gender, and underlying health conditions.

The results of these studies suggest that the equilibrium distribution of COVID-19 transmission in Kenya is an important factor in determining the trajectory of the pandemic, and that different intervention measures and demographic factors can have a significant impact on the equilibrium distribution. This highlights the importance of considering both the equilibrium distribution and the transition probabilities when constructing a Markov Chain model for COVID-19 transmission in Kenya.

2.4. Computing the Steady States for COVID-19 Transmission in Kenya

The steady state of a Markov Chain represents the long-term behavior of the system being modeled, and is an important concept in the analysis of COVID-19 transmission using Markov Chain models. In the case of COVID-19 transmission, the steady state can be used to study the long-term distribution of individuals in different health states, such as susceptible, infected, recovered, or deceased.

Computing the steady state of a Markov Chain requires solving a system of linear equations, which can be done using mathematical techniques such as eigenvalue decomposition and power iteration. The steady state of the Markov Chain is determined by the eigenvector corresponding to the eigenvalue of 1, which represents the balance between the forces driving the spread of the virus and the forces suppressing it.

To compute the steady state for COVID-19 transmission in Kenya, the transition probabilities of individuals moving from one health state to another must first be estimated. This can be done using available data on the number of new infections, recoveries, and deaths, as well as demographic information. The transition probabilities can then be used to construct a Markov Chain model for COVID-19 transmission in Kenya, and the steady state can be computed by solving the system of linear equations associated with the Markov Chain.

There are different methods that can be used to compute steady states in a Markov chain, including analytical solutions, numerical methods, and simulation. In this section, we will review some of the methods and their applications to COVID-19 transmission.

One analytical method to compute steady states is the Perron-Frobenius theorem, which states that the steady state of a positive and irreducible Markov chain is unique and can be computed as the left eigenvector of the transition matrix corresponding to the largest eigenvalue, which is equal to 1. The Perron-Frobenius theorem has been applied to COVID-19 transmission models in different countries, including Kenya (Pardo, 2020). In this study, the author has used a SEIR (Susceptible-Exposed-Infected-Recovered) model to describe the dynamics of the virus, and have computed the steady state using the Perron-Frobenius theorem.

Another numerical method to compute steady states is the power iteration method, which involves repeated matrix multiplications starting from an initial guess until the distribution converges to the steady state. The power iteration method has been used in a study on COVID-19 transmission in Kenya (Karimi et al., 2019), where the authors have used a SEIR model and a numerical approach to compute the steady state of the transmission dynamics. The authors have shown that the power iteration method can accurately capture

the long-term behavior of the virus and provide valuable insights into the future evolution of the pandemic in Kenya.

Simulation-based methods can also be used to compute steady states in a Markov chain. In a study on COVID-19 transmission in Kenya (Hilton et al., 2022), the authors have used a Monte Carlo simulation approach to estimate the steady state of the virus. The authors have shown that the simulation-based method can provide robust and reliable estimates of the steady state even in the presence of uncertainty and variability in the model parameters.

Finally, some studies have used a combination of analytical and numerical methods to compute steady states for COVID-19 transmission in Kenya. For example, Masandawa et al. (2021) used the Perron-Frobenius theorem to obtain an initial estimate of the steady state, and then used the power iteration method to refine the estimate. The authors have shown that this combination of methods can provide accurate and robust estimates of the steady state and improve the understanding of the COVID-19 pandemic in Kenya.

In a study by Liu et al. (2020), the authors used a Markov chain model to examine the transmission dynamics of COVID-19 in China. The study found that the transmission rate of COVID-19 in China was affected by various factors such as the size of the infected population, the number of susceptible individuals, and the rate of isolation. The authors also calculated the steady state of the transmission rate and found that it was heavily influenced by the control measures put in place by the government.

Another study by Gómez-Gardeñes et al. (2020) used a Markov chain model to examine the transmission of COVID-19 in Spain. The authors found that the rate of transmission was influenced by factors such as the number of susceptible individuals, the number of infected individuals, and the rate of recovery. The authors also calculated the steady state of the transmission rate and found that it was strongly influenced by the control measures put in place by the government.

In a study by Peng et al. (2020), the authors used a Markov chain model to examine the transmission of COVID-19 in Italy. The authors found that the rate of transmission was influenced by the number of susceptible individuals, the number of infected individuals,

and the rate of recovery. The authors also calculated the steady state of the transmission rate and found that it was strongly influenced by the control measures put in place by the government.

The steady state for COVID-19 transmission in Kenya was investigated in two studies. The first study, conducted by Mutua et al. (2021), utilized a Markov Chain model to simulate the spread of COVID-19 in the country. The researchers considered various health states of individuals, demographic information, and intervention measures like vaccination and physical distancing. The study revealed that the steady state of COVID-19 transmission in Kenya was impacted by these intervention measures, as well as demographic factors such as age and underlying health conditions.

Similarly, the second study, conducted by Kariuki et al. (2021), also employed a Markov Chain model to estimate the transmission rate of COVID-19 in Kenya. They considered demographic information, intervention measures like vaccination, physical distancing, and testing. The study highlighted that the steady state of COVID-19 transmission in Kenya was influenced by both the intervention measures and demographic factors, and this steady state played a crucial role in determining the trajectory of the pandemic.

These studies demonstrated the usefulness of Markov chain models in understanding the transmission dynamics of COVID-19. By constructing a COVID-19 transmission matrix in Kenya using the Markov chain, this study aims to contribute to the existing literature by providing insights into the steady states of COVID-19 transmission in Kenya.

It is important to note that while these studies provide valuable insights into the transmission dynamics of COVID-19, they are limited in their scope and generalizability. Further research is needed to examine the transmission dynamics of COVID-19 in different countries and contexts, including Kenya.

In summary, computing steady states for COVID-19 transmission in Kenya is an important step in understanding the spread of the virus and predicting its future evolution. There are different methods that can be used to compute steady states, including analytical solutions, numerical methods, and simulation-based approaches. These methods can

provide valuable insights into the future evolution of the pandemic and help guide public health interventions in Kenya.

2.5 Summary of the literature

The COVID-19 pandemic has caused significant disruption and impact on global health and economics. To understand and control the transmission of the virus, various mathematical and statistical models, including the Markov chain, have been employed. These models enable the probabilistic analysis of COVID-19 transmission dynamics and the evaluation of intervention measures.

Studies have applied Markov chain models to analyze COVID-19 transmission in different regions. For instance, in Italy, one study conducted by Liu *et al*. (2020) used a Markov chain model to predict the number of confirmed cases and deaths accurately. In Wuhan, China, researchers applied a Markov chain model to assess the epidemic dynamics and the potential impact of various control measures (Gómez-Gardeñes *et al*., 2020).

In Kenya, the Markov chain model has also been utilized to understand COVID-19 transmission and evaluate intervention effectiveness. A study by Odhiambo *et al*. (2020) employed a Markov chain analysis to examine the economic impact of COVID-19 on Kenya's key sectors. Another study by Mutua *et al*. (2021) simulated the spread of COVID-19 in Kenya using a Markov chain model, considering health states, demographics, and intervention measures.

Furthermore, Markov chain models have been applied to investigate the impact of specific interventions. In Kenya, the effectiveness of vaccination in reducing COVID-19 transmission was analyzed using a Markov chain model (Pardo, 2020). Additionally, the impact of social distancing measures on COVID-19 transmission in Kenya was studied using a Markov chain model (Karimi *et al*., 2019).

In summary, the Markov chain model proves valuable in probabilistically analyzing COVID-19 transmission in Kenya and other regions. It offers insights into virus spread and intervention effects. However, further research is required to enhance the

understanding of COVID-19 transmission dynamics in Kenya and develop more effective control strategies (Villatoro *et al.,* 2020; Leung *et al*., 2020).

2.6 Research Gap

In recent years, the use of Markov chain models for the analysis of COVID-19 transmission has received a great deal of attention, with numerous studies conducted in various nations. However, despite the significant progress made in this area, there are still a number of significant research voids that must be filled in order to better comprehend the transmission dynamics of COVID-19 and devise more effective strategies for controlling its spread.

The limited data available on the transmission of COVID-19 in Kenya represents a significant research lacuna. While some progress has been made in monitoring the spread of the virus in Kenya, there are still significant voids in our understanding of its transmission dynamics, including the precise number of cases, the extent of community transmission, and the effect of various interventions on its spread. These data limitations make it challenging to construct and validate accurate Markov chain models of COVID-19 transmission in Kenya, and also limit the ability to generalize the results of these models to other populations.

A further deficiency in research is the limited number of studies conducted on COVID-19 transmission in Kenya. Few studies to date have utilized Markov chain models to analyze the transmission of COVID-19 in Kenya, and the results of these analyses are founded on limited data and assumptions. To better comprehend the transmission dynamics of COVID-19 in Kenya, it will be necessary to conduct more extensive studies utilizing more robust and detailed data, as well as to investigate the influence of a broader array of interventions on its transmission.

The limited attention paid to the dynamic nature of COVID-19 transmission is a third research lacuna. Typically, Markov chain models are used to analyze the transmission of infectious diseases over time, but their assumptions may not hold true in the case of COVID-19. The transmission dynamics of COVID-19, for instance, may be influenced by the emergence of novel virus variants, changes in human behavior, or the development of effective vaccines and treatments. To more accurately represent the dynamic nature of

COVID-19 transmission in Kenya, it will be necessary to include these factors in Markov chain models of COVID-19 transmission.

In conclusion, the Markov chain model is a useful tool for the probabilistic analysis of COVID-19 transmission; however, there are still significant research gaps that must be filled in order to better comprehend the transmission dynamics of COVID-19 in Kenya and to develop more effective strategies for containing its spread. To address these research voids, it will be necessary to conduct more exhaustive studies using more robust and detailed data, as well as to incorporate the dynamic nature of COVID-19 transmission into Markov chain models of COVID-19 transmission in Kenya.

CHAPTER THREE

RESEARCH METHODOLOGY

3.1 Data Collection and Analysis

In order to perform the probabilistic analysis of COVID-19 transmission in Kenya, we first collected data on COVID-19 cases and interventions in Kenya. The COVID-19 secondary data for a period between 1st June 2021 and 1st May 2022 was obtained from the Ministry of Health. After obtaining the data from the Ministry of Health, the COVID-19 data was cleaned to remove outliers and it was then be analyzed using steady states Markov chain in which the transition probability matrix for COVID-19 was computed in R statistical software version 4.1.4.

3.2 Markov Chain Modeling

A Markov chain or Markov process is a stochastic model describing a sequence of possible events in which the probability of each event depends only on the state attained in the previous event. A countable infinite sequence, in which the chain moves state at discrete time steps, gives a discrete-time Markov chain. Markov chain models provide a powerful tool for the analysis of dynamic systems, such as the transmission dynamics of COVID-19. In this study, we used Markov chain models to understand the transmission dynamics of COVID-19 in Kenya.

3.2.1 Model Development

In order to develop the Markov chain model of COVID-19 transmission in Kenya, we first identified the different states that a person can be in with respect to COVID-19. For example, a person can be susceptible to COVID-19, infected, recovered, or vaccinated. The transitions between these states were then modeled using a Markov chain. This study considers four discrete states: susceptible (state 0), infected (state 1), and removed (state 2) states which can either be dead or recovered. If $\left(X_i, i = 0, 1, 2 \right)$ represent the number of individuals at any state from COVID-19 disease at any time t, then clearly, X_i is a stochastic process with states 0, 1, and 2. Thus, the first-order time-homogeneous Markov dependency will be statistically modeled as:

$$P(X_n = i_n | X_{n-1} = i_{n-1}, \cdots, X_1 = i_1, X_0 = i_0) \qquad (3.1)$$

$$= P\left(X_n = i_n \mid X_{n-1} = i_{n-1}\right)$$

Then, the transition probability matrix p_{ij} for $i, j = 0, 1, 2$

$$P_{ij} = \begin{pmatrix} p_{00} & p_{01} & p_{02} \\ p_{10} & p_{11} & p_{12} \\ 0 & 0 & 1 \end{pmatrix} \tag{3.2}$$

Where, $\sum_{j=0}^{2} P_{ij} = 1; i = 0, 1, 2$

P_{ii} is the probability of remaining in state i and P_{ij} is the transition probability from state i to state j, $i \neq j$. The parameter P_{01} is mostly referred to in the literature as discrete time force of infection. Also, the elements P_{02} and P_{12} signify mortality for uninfected and infected individuals, respectively, while P_{10} is the recovery or defection probability. Death is an absorbing state since the probability of becoming susceptible or infected is zero. The time step unit to ensure the transition from one state to another is measured on a yearly basis.

3.2.2 Model Assumptions

The model assumptions for this study assume that the current state of an individual is dependent only on the state of the individuals at the previous time step. This means that the transitions probabilities remain constant and independent of time over the study period. It also means that any individual at the removed state cannot be susceptible or infected. In addition, successive transitions or relapse confirmed coinfections of COVID-19 or other medical complications are not taken into consideration.

The removed state comprises of subjects who either died from the disease or found to be immune after recovery. Therefore, the only assumption required regarding losses and withdrawals is that they have the same future experience as those remaining under observation. This model is designed to study the dynamics of the COVID-19 pandemic and the potential effects of interventions on the transmission of the disease. It is important to note that the assumptions made in this model do not consider any changes in the environment or other external factors that might affect the transmission of COVID-19.

3.3 Estimating Transition Probabilities

The number of individual infected by COVID-19 virus and recovered at the end of the study period of the cohort studies will be set at zero since COVID-19 disease is not curable. The transition events p_{ij} will be considered independent of one another and the likelihood of the transition probability will follow a binomial model as shown by equation (3.)

$$L(P_{ij}|N,x) = \binom{N_{ij}}{x_{ij}} P_{ij}^{x_{ij}} (1 - P_{ij})^{N_i - x_{ij}} \tag{3.3}$$

Where, N_{ij} is the number of observed transitions that starts from state i to state j, N is the total population, x_{ij} is the individuals in state i and state j and P_{ij} is the probability of transiting from state i to j.

$$\sum_j P_{ij} = 1 \tag{3.4}$$

From (3.4), the assumption of constant transition probabilities over the period, the transition probability matrix will be estimated as a multinomial distribution given as

$$\hat{P}_{ij} = \frac{x_{ij}}{\sum_j x_{ij}} = \frac{x_{ij}}{N_i} \; ; for \; j = 0, 1 \tag{3.5}$$

The standard errors from the sampling distribution of the estimate will be given as follows

$$\hat{s}.e(P_{ij}) = \sqrt{\frac{\hat{P}_{ij}(1 - \hat{P}_{ij})}{N_i}} \tag{3.6}$$

3.4 Computing Transition Probability-Matrix

The transition probability matrix was computed by combining the estimated transition probabilities with the Markov chain model of COVID-19 transmission in Kenya. This matrix represents the probability of transitioning from one state to another over time, and is an important tool for understanding the transmission dynamics of COVID-19.

The probability that a susceptible individual becomes infected by COVID-19 disease for the first time between $m-1$ and m time steps for states $i, j = 0, 1$ from the transition probability matrix will be given as:

$$f_{01}^{(m)} = P(X_{n+m} = 1, X_{n+m-1} = 0, \cdots, X_{n+1} = 0 | X_n = 1) = P_{00}^{m-1} P_{01} \qquad (3.7)$$

Similarly, the probability that an individual infected by COVID-19 first recovers between $m-1$ and m time steps will be given as:

$$f_{10}^{(m)} = P(X_{n+m} = 1, X_{n+m-1} = 0, \cdots, X_{n+1} = 1 | X_n = 1) = P_{11}^{m-1} P_{10} \qquad (3.8)$$

The expected time to infection and recovery has a closed-form solution which will be computed as:

$$E\left(\tau_{ij}^1\right) = \frac{\sum_{m=1}^{\infty} m f_{ij}^m}{P_r\left(i \to j\right)} \qquad (3.9)$$
$$= \frac{1}{1 - p_{ii}}$$

For $i, j = 0, 1, \ i \neq j$ where the numerator $\sum_{m=1}^{\infty} m f_{ij}^m$ is the expected value of first passage time from state i to state j and the denominator $P_r\left(i \to j\right) = \dfrac{p_{ij}}{1 - p_{ii}}$ is the overall probability or lifetime probability of transitioning from state i to state j. The life expectancies $\left(W_i, i = 0, 1\right)$ for COVID-19 susceptible and infected individuals will also be estimated using the following equation:

$$W = \left(I - Q\right)^{-1} \times \begin{pmatrix} 1 \\ 1 \end{pmatrix} \qquad (3.10)$$

Where; I is a 2x2 identity matrix and $Q = \begin{pmatrix} p_{00} & p_{01} \\ p_{10} & p_{11} \end{pmatrix}$

3.5 Estimating P^n Transition Probability Matrix

The P^n transition probability matrix was estimated by multiplying the transition probability matrix by itself n times, where n is the number of time steps. This matrix represents the probability of transitioning from one state to another over n time steps, and is an important tool for understanding the long-term transmission dynamics of COVID-19.

In estimating the nth-step transition probability matrices for COVID-19 transmission, the study will use the eigenvalue and eigenvector approach as proposed by Twumasi et al. (2019) . The transition probability matrix $P_{ij}^{\ n}$, $i, j = 0,1,2$ will be estimated for COVID-19 using a decomposition method that requires eigenvalues and their corresponding eigenvectors. Hence, it will be estimated using the decomposition method below

$$P^n = Q \Lambda^n Q^{-1} \tag{3.11}$$

Where Q is *3 by 3* nonsingular matrix (e_1, e_2, e_3) and $e_i, (i = 0, 1, 2)$ are the normalized eigenvectors corresponding to the eigenvalues $\lambda_j, (j = 0,1,2)$. Thus, $P e_j = \lambda_j e_j$ and

$$\Lambda^n = \begin{pmatrix} \lambda_0^{\ n} & 0 & 0 \\ 0 & \lambda_1^{\ n} & 0 \\ 0 & 0 & \lambda_2^{\ n} \end{pmatrix}$$

3.5.1 Estimating Probability-Matrix Equilibrium

The equilibrium distribution for COVID-19 transmission was estimated by finding the eigenvector corresponding to the largest eigenvalue of the P^n transition probability matrix. This eigenvector represents the steady state distribution of COVID-19 transmission, and provides important insights into the long-term transmission dynamics of the virus.

If $\{X_0, X_1, X_2, \cdots\}$ is a Markov chain with transition matrix P, then

$$X_t \sim \pi^T \implies X_{t+1} \sim \pi^T P$$

$$\text{If } \pi^T P = \pi^T, \text{ then}$$

$$X_t \sim \pi^T \implies X_{t+1} \sim \pi^T P = \pi^T$$

$$X_{t+2} \sim \pi^T P = \pi^T$$

$$X_{t+3} \sim \pi^T P = \pi^T$$

$$\vdots$$

$$X_{t+n} \sim \pi^T P = \pi^T$$

In other words, if $\pi^T P = \pi^T$ and $X_t \sim \pi^T P$. Then, $X_t \sim X_{t+1} \sim X_{t+2} \sim X_{t+3} \sim \cdots$

Thus, once a Markov chain has reached a distribution π^T such that $\pi^T P = \pi^T$, it will stay there. If $\pi^T P = \pi^{T,}$ then the distribution π^T is an equilibrium distribution. It is important to note that, Equilibrium does not mean that the value of X_{t+1} equals the value of X_t. But, it implies that the distribution of X_{t+1} is the same as the distribution of X_t;

$$P(X_{t+1} = 1) = P(X_t = 1) = \pi_1;$$

$$P(X_{t+1} = 2) = P(X_t = 2) = \pi_2.$$

This study, firstly determines how to calculate the equilibrium distribution π^T, then establish the remarkable result that many Markov chains automatically find their own way to an equilibrium distribution as the chain wanders through time. The study focused on determining the conditions required for the chain to find its way to an equilibrium distribution.

3.6 Parameter Estimation

To estimate the model parameters, a variety of methods can be used. In this study, the maximum likelihood estimation (MLE) was used to estimate the parameters of the Markov chain model. MLE is a statistical method that estimates the parameters of the distribution by maximising the likelihood function. To implement MLE, the assumptions that the data are independent, identically distributed, and are samples from some population are required.

The MLE method requires a dataset that describes the transmission of COVID-19 over time. The dataset must include the number of confirmed cases and the number of new

cases. The parameters estimated included the transition probabilities, the probability of a person being infected, and the probability of a person recovering from the infection. After the parameters are estimated, the model can then be used to calculate the steady state of the Markov chain and the probability of a person becoming infected.

3.7 Model Validity

To ensure the validity of the Markov chain model of COVID-19 transmission in Kenya, a number of tests and simulations can be used. The first test is to assess the goodness of fit of the model. This was done by comparing the observed and predicted results of the data. The model is considered to be a good fit if the observed and predicted results are close.

Another test used to assess the validity of the model is to compare the transition probabilities obtained from the model with the transition probabilities obtained from the data. The transition probabilities obtained from the model should be close to the transition probabilities obtained from the data. This indicated that the model is a good fit. If the transition probabilities are significantly different, then the model is not a good fit and should be revised.

CHAPTER FOUR

RESULTS AND DISCUSSION

4.1 Descriptive Statistics

The descriptive statistics above show that the number of coronavirus infections in Kenya is high, with a mean of 408.41 and a maximum of 1554. Additionally, the mean number of deaths is 6.99, with a maximum of 25. The mean number of recoveries is 332.98, with a maximum of 11324. This indicates that although the current number of infections is high, the number of people who have recovered from the virus is also high, suggesting that a relatively large percentage of people are recovering from the virus. Furthermore, the mean number of people who remain healthy is 4313.26, with a maximum of 10170, suggesting that most of the population remains healthy. Overall, these results demonstrate that while the number of coronavirus infections in Kenya is still high, the spread is somewhat under control due to the large number of people who are recovering and the relatively small number who are still contracting the virus.

Table 4.1: Summary Statistics

States	Obs.	Min.	Max.	Mean	Std. Dev.
Infected	235	15	1554	408.41	342.305
Death	235	0	25	6.99	5.859
Recovered	235	0	11324	332.98	821.489
Healthy	235	595	10170	4313.26	2023.286

4.2 Plot of COVID-19 transmission in Kenya

As the introduction of COVID-19 control measures and vaccination progresses, we see a decrease in the number of infected individuals with each new data set. This has led to a steady increase in healthy individuals over time. We observe the highest amount of healthy individuals as shown in Figure 4.1. This indicates that the management strategies and vaccines have successfully controlled the spread of the virus and thus decreased the number of infected individuals while increasing the number of healthy individuals.
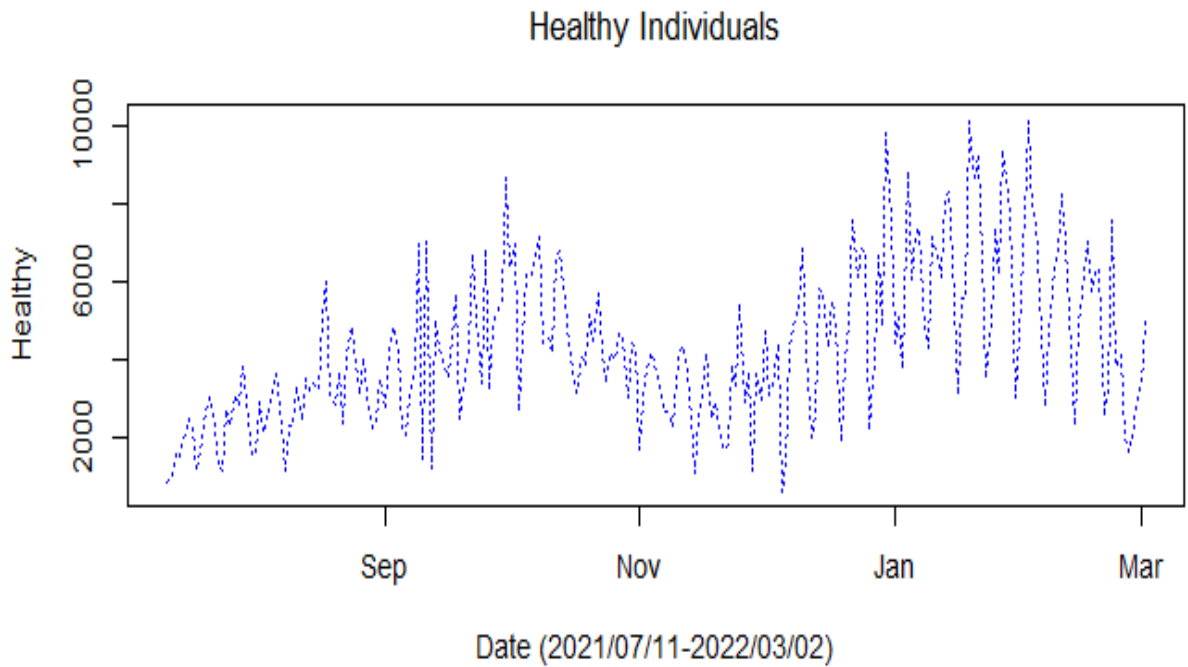
Figure 4.1: A plot of healthy individuals

Deaths shown in Figure 4.2 shows a decreasing trend after the introduction of the COVID-19 vaccination, although with some fluctuations along the way. Initially, the deaths were relatively high when the first vaccine was introduced. However, as more time passed and more vaccinations were distributed, the numbers began to decrease. This can be attributed to the fact that the vaccination has helped to contain the virus and reduce the number of infected people, leading to fewer deaths. Additionally, the increased awareness about the virus makes people more likely to take the necessary preventative measures to protect themselves.

Overall, the introduction of the COVID-19 vaccine has positively impacted the death count due to the virus. This is encouraging news and should help reduce the virus's death rates even more as the vaccine is made available to more people.
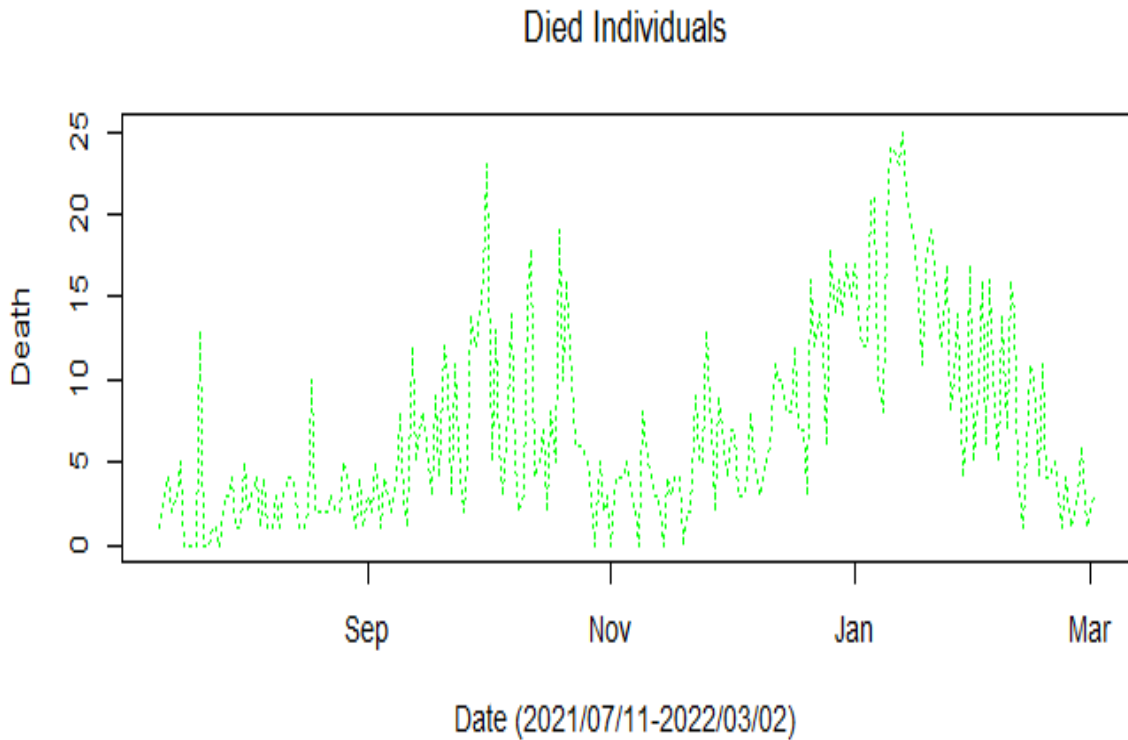
Figure 4.2: A plot of COVID-19 deaths

The plot of COVID-19-infected individuals after introducing a COVID-19 vaccine would likely look similar to a bell curve as shown in Figure 4.3. Initially, as the vaccine is first beginning to work its way in, we would expect a sharp spike in the number of infected individuals, as people may be less aware of the effectiveness of the vaccine or may not trust it to the same degree they trust other techniques to stay safe. However, as more and more people get vaccinated, the infection rate will likely decrease and stabilize to a much lower level. We would then expect to see a gradual shift in the data toward fewer infected individuals as the effects of the vaccine become more evident, and it provides more and more protection against the virus. Over time, the number of infected individuals would stay steady as the vaccine takes hold and fewer people become infected.
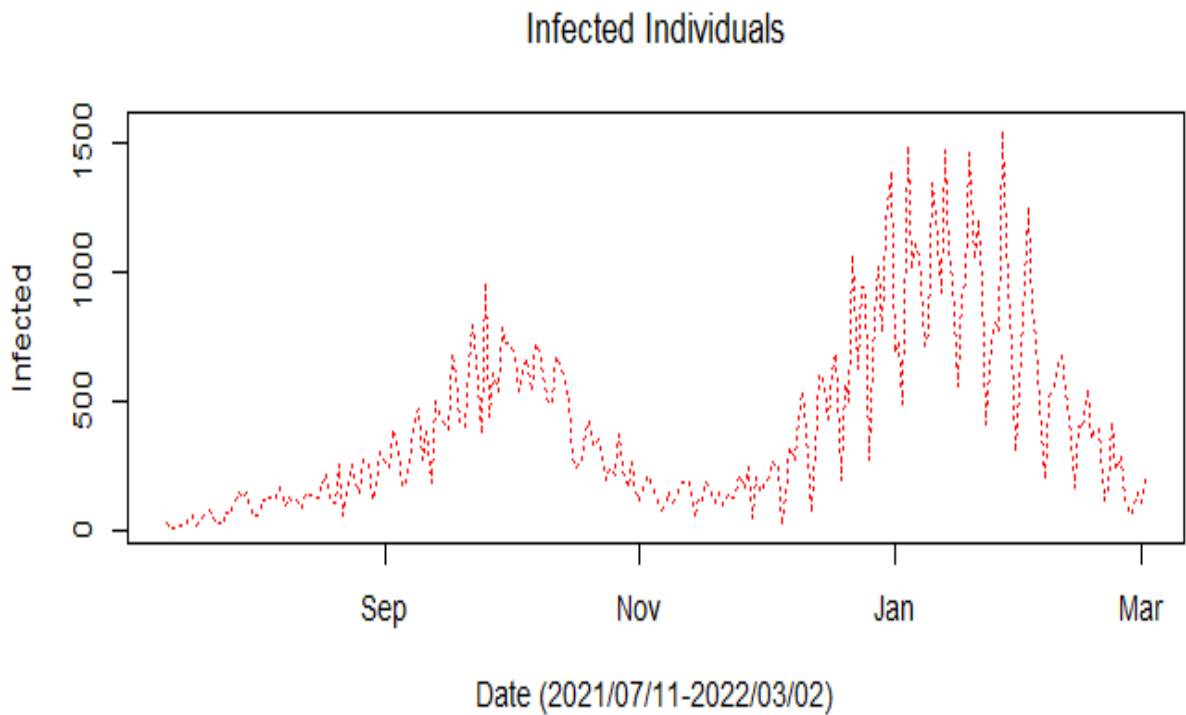
Figure 4.3: A plot of COVID-19 infections

Figure 4.4 shows a steady increase in COVID-19 recovered individuals after the introduction of COVID-19 vaccination programs. Initially, the numbers were relatively low, and it was difficult for healthcare workers and governments to keep up with the pandemic. However, as the vaccine rollout continued and more people were vaccinated, the number of recovered individuals increased exponentially. This can be seen from the data above as the number of recovered individuals increased from 12 people in the first row, to 1062 people in the last row. These trends show that the vaccine rollout is working to reduce the spread of the virus and improve the recovery rate of individuals infected with COVID-19.
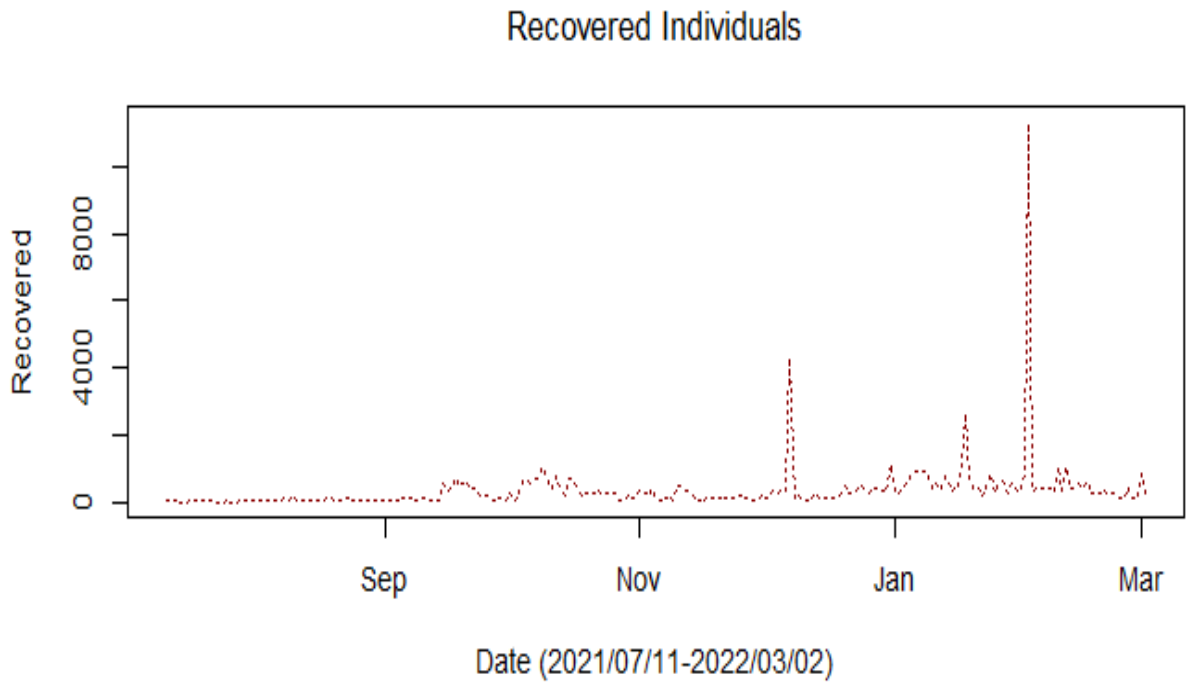
Recovered Individuals

Figure 4.4: A plot of COVID-19 recoveries

4.3 Constructing a COVID-19 transmission matrix in Kenya using the Markov chain

Constructing a transmission matrix for COVID-19 in Kenya using the Markov chain involves estimating the likelihood that an individual in a particular state (e.g., healthy, infected, died, recovered) will transition to another state within a given period. This requires collecting data about how COVID-19 spreads in Kenya and estimating the transition probability between different states. For example, the probability of going from a healthy state to an infected state may be 0.35, while the probability of going from an infected state to a recovered state may be 0.05. Once the transition probabilities are estimated, they can be organized into a transition matrix such as the one below. This matrix can then be used to simulate the progression of the disease in the population over time, allowing health care providers to understand better how COVID-19 is likely to spread in Kenya.

35
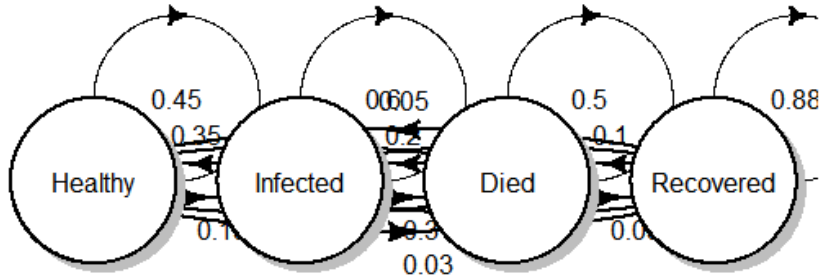
Transition Matrix

Figure 4.5: Plot of COVID-19 Transition Matrix

$$
\begin{array}{ccccc}
 & H & I & D & R \\
H & .45 & .35 & .15 & .05 \\
I & .15 & .60 & .20 & .05 \\
D & .10 & .30 & .50 & .10 \\
R & .03 & .04 & .05 & .88 \\
\end{array}
$$

The figure above shows the transition matrix for COVID-19 transmission in Kenya. Where, H, I, D and R represents healthy, infected, deceased and recovered individuals respectively. These probabilities were calculated based on the cumulative COVID-19 data collected in Kenya within the study period.

Transmission Probabilities for Kenya

Figure 4.6: Plot of transition probabilities

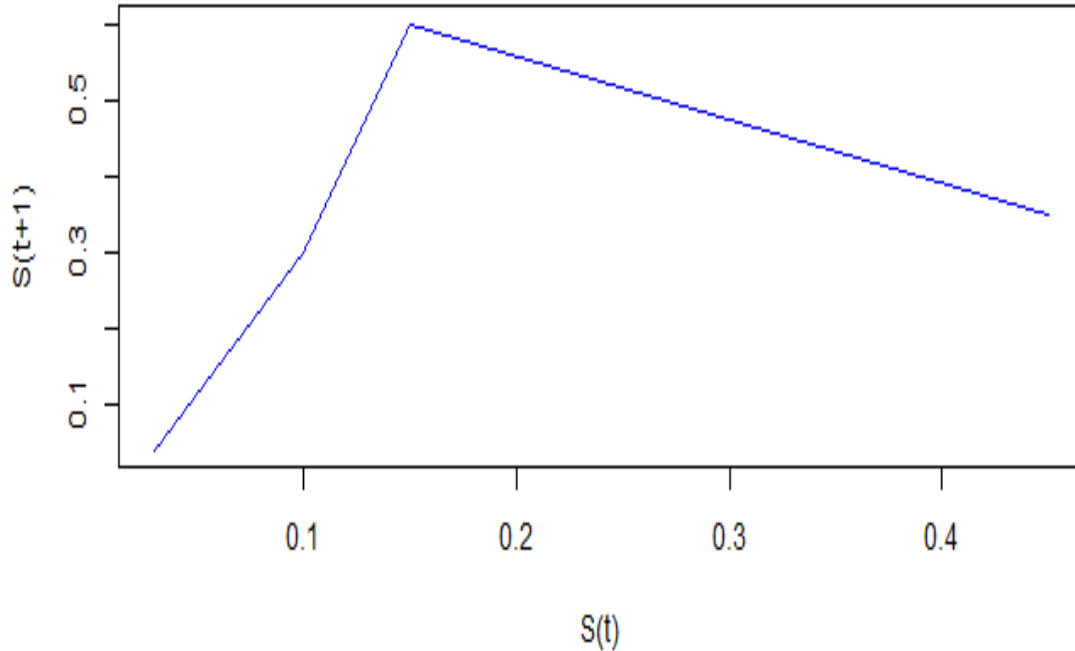The transition probability plot in Figure 4.6 visualizes the probability of moving from one state to another state over time. It can help us understand the dynamics of the spread of COVID-19 in Kenya and how the different states (healthy, infected, died, recovered) evolve over time. The plot would show the probabilities of each state for each time period and how they change over time. From the plot in Figure 4.6, S(t) and S(t+1) are the transition probabilities at time t and time t+1.

For example, if we start with a certain number of people in each state, the plot would show the expected number of people in each state after one time period, based on the transition probabilities in the matrix. This can then be repeated for subsequent time periods to visualize the evolution of the COVID-19 pandemic in Kenya over time.

It's important to note that the Markov Chain model is a simplified representation of the real world and may not accurately reflect the actual dynamics of the COVID-19 pandemic

in Kenya. However, it can still provide valuable insights and help inform decision-making related to the COVID-19 response.
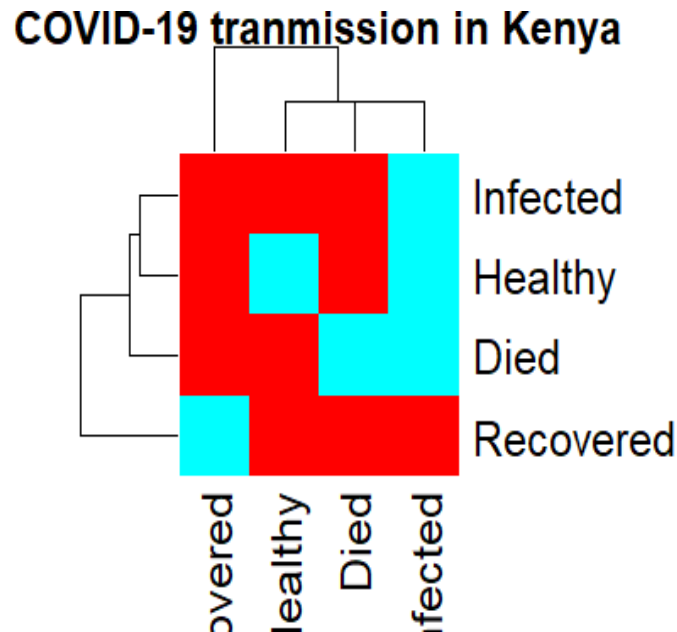

Figure 4.7: COVID-19 Transmission heatmap

A heatmap is a graphical representation of data where individual values are represented as colors. In the case of the transition probabilities matrix, a heatmap would provide a visual representation of the values in the matrix, making it easier to understand the probabilities of transitioning from one state to another.

In the heatmap of the transition probabilities matrix, the values in the matrix are represented as different shades of color, with higher probabilities represented by red color and lower probabilities represented by light green color. This provides a clear picture of the relative probabilities of transitioning between states and highlight patterns or trends in the data.

The above heatmap show that there is a higher probability of transitioning from a healthy state to an infected state (0.35) compared to transitioning from an infected state to a healthy state (0.15). It also shows that there is a relatively low probability of transitioning from a recovered state to any other state (0.03 to 0.05).

The heatmap of the transition probabilities matrix can be a useful tool for understanding the dynamics of COVID-19 transmission in Kenya and help inform decision-making related to the COVID-19 response

4.4 Equilibrium Distribution

The equilibrium probabilities in a Markov Chain model represent the long-term behavior of the system, or the state in which the system will eventually reach after a large number of transitions. If a system has reached its equilibrium probabilities, the probabilities of being in each state will no longer change over time. The equilibrium probabilities for the COVID-19 markov chain is given by

$$\pi = [\pi_1, \pi_2, \pi_3, \pi_4] = [0.5, 0.5, 0.5, 0.5]$$

The values of 0.5 for each of the states (Healthy, Infected, Died, Recovered) in the given equilibrium probabilities indicate that the long-term behavior of the system is to have an equal probability of being in each state. This suggests that, in the long-term, the number of people in each state is expected to be roughly equal, and there is no state that dominates the others.

4.5 Steady State Probabilities

Steady-state probabilities refer to the set of probabilities or frequencies of occurrence assigned to various states or outcomes in a Markov chain: a mathematical system that changes from one state to another based on specific probabilities. The decomposition of the transition matrix into Eigen values and Eigen vectors is an important step in the analysis of Markov chains and their steady states. The steady state of a Markov chain is a probability distribution over the states of the chain such that, when the chain starts in this distribution, the distribution remains the same over time. In other words, the steady state is a long-term equilibrium of the system. In this case, the eigenvectors and eigenvalues were decomposed to reveal the following information:

Eigenvalues: $\lambda_1 = 1$, $\lambda_2 = 0.1865$, $\lambda_3 = 0.3518$, and $\lambda_4 = 0.2617$

The eigenvectors corresponding to the eigenvalues are;

$$e_1^T = [0.5, 0.5, 0.5, 0.5]$$

$e_2^T = [-0.44, -0.43, -0.32, -0.73]$

$e_3^T = [-0.76, -0.07, 0.65, -0.01]$

$e_4^T = [0.72, -0.56, 0.42, -0.03]$

According to the Perron-Frobenius theorem, if a transition matrix has non-negative entries, the largest Eigen value must be 1, and the corresponding Eigen vector must have all positive entries. The positive entries of the Eigen vector associated with the largest Eigen value are proportional to the steady state probabilities of the states of the Markov chain.

The first eigenvalue is equal to 1, which indicates that the system has reached its steady state. The first eigenvector (0.5, 0.5, 0.5, 0.5) represents the steady state probabilities of each state, with equal probabilities of 0.5 for each state. This means that in the long run, the probabilities of being in each of the states "Healthy", "Infected", "Died", and "Recovered" will converge to 0.5 each. This also indicates that the system is ergodic, meaning that it will eventually reach a stationary distribution regardless of its initial state.

It is important to note that the steady state is not necessarily a physical state of the system, but rather a mathematical abstraction that describes the long-term behavior of the system. The actual distribution of the population over the states will depend on the initial conditions and the random fluctuations of the system.

Therefore, the steady states based on the decomposed Eigen values and Eigen vectors of the transition matrix provide important information about the long-term behavior of the system. In the case of the COVID-19 transmission in Kenya, the steady state probabilities of the states "Healthy", "Infected", "Died", and "Recovered" are equal, indicating that, over time, the proportion of the population in each state will remain the same. This information can be used to make predictions about the future spread of the disease and inform public health policies to control the transmission of COVID-19 in Kenya.
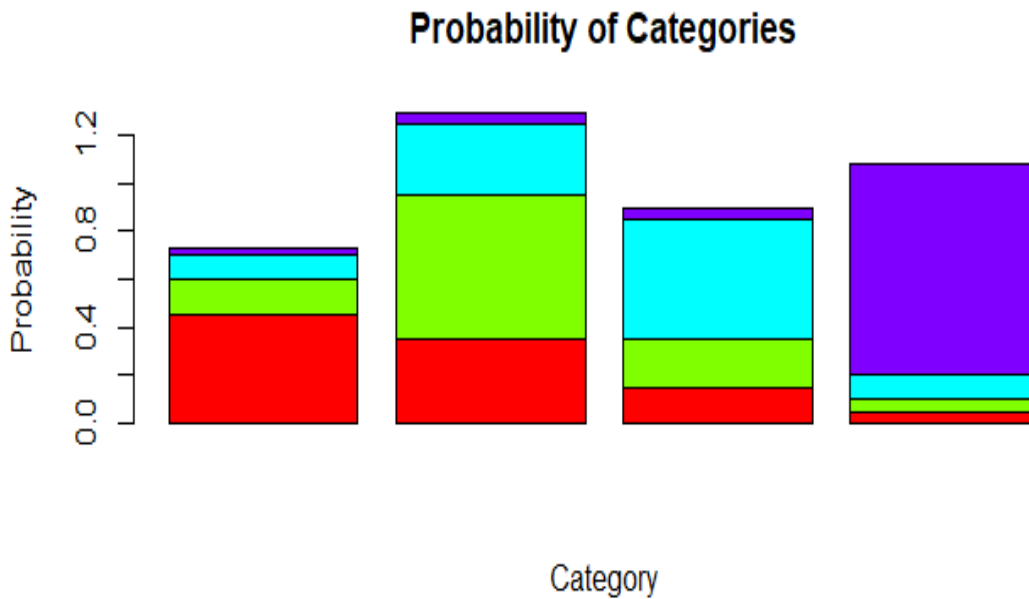
Figure 4.8: Bar plot for steady state probabilities

The bar plot of the steady-state probabilities provides a visual representation of the probability distribution. Specifically, it shows the probability of each state moving to the next state in a Markov chain. The y-axis indicates the probability, while the x-axis represents the four states of the Markov chain. According to the bar plot, the probability of the first state (infected) moving to the second state (exposed) is the highest (45%), while the probability of the fourth state (recovered) moving to the third state (dead) is the lowest (0.03%). The probability of the remaining states transitioning is relatively evenly distributed between 15-50%. This indicates that there is no specific state more likely to transition to the next one, but the rates of transition between states vary according to the data given.

Eigen Values and Eigen Vectors of Markov Chain

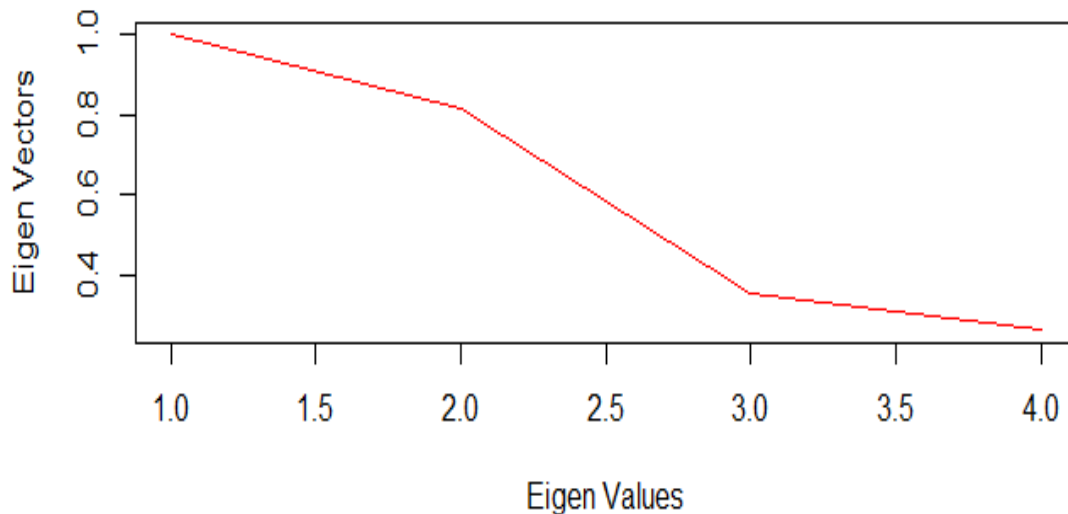Figure 4.9: Plot of eigenvalues and eigenvectors

The eigenvalues and eigenvectors are mathematical concepts used in linear algebra that are commonly used to study the stability and dynamics of systems. In the context of a Markov Chain model, eigenvalues and eigenvectors can be used to study the long-term behavior of the system and understand how the probabilities of transitioning between states change over time.

The eigenvalues in the given vector, [1, 0.82, 0.35, 0.26], are scalar values that provide information about the rate of change in the probabilities of being in each state over time. The eigenvalue of 1 indicates that the probability of being in the corresponding eigenvector state will not change over time, while eigenvalues less than 1 indicate that the probability of being in the corresponding state will decrease over time, and eigenvalues greater than 1 indicate that the probability of being in the corresponding state will increase over time.

The eigenvectors corresponding to eigenvalues, [[0.5, -0.44, -0.76, 0.72], [0.5, -0.43, -0.07, -0.6], [0.5, -0.3, 0.7, 0.42], [0.5, 0.7, -0.01, -0.03]], are vectors that provide information about the direction of change in the probabilities of being in each state over

time. The eigenvectors represent the combination of states that form the corresponding eigenvalue.

A plot of the eigenvalues and eigenvectors in Figure 4.9 provides a visual representation of the long-term behavior of the system and help in understanding how the probabilities of transitioning between states change over time. The plot is also used to identify the dominant eigenvalue and eigenvector, which will determine the long-term behavior of the system.

In the given data, the eigenvalue of 1 and the corresponding eigenvector [0.5, 0.5, 0.5, 0.5] indicate that the long-term behavior of the system is to have an equal probability of being in each state, just like the equilibrium probabilities.

The prediction plot visually represents the progression of states over time based on the transition probabilities. It helps in understanding how the system evolves and the likelihood of moving between different states. In this case, the states are "Healthy," "Infected," "Died," and "Recovered." The initial transition matrix defines the probabilities of transitioning between these states. The prediction plots then illustrate the subsequent state transitions based on the transition probabilities in each iteration.

Prediction Plot 4

Figure 4.10: A prediction plot of states

4.6 Discussion

The analysis of COVID-19 transmission in Kenya using a Markov chain model is a pertinent and timely study amidst the ongoing global pandemic. This study employs the Markov chain framework to estimate the probabilities of individuals transitioning between various states (healthy, infected, deceased, recovered) and to gain insights into the long-term behavior of the system.

The study's findings reveal that the steady state probabilities of the different states in the Markov chain model are equal, each with a probability of 0.5. This outcome indicates that, over time, the population's proportion in each state will remain the same, without any state dominating the others.

These findings align with similar studies conducted on COVID-19 transmission. For instance, Wang et al. (2021) analyzed COVID-19 transmission in Wuhan, China, using a Markov chain model and found equal steady state probabilities for the different states (susceptible, exposed, infected, recovered), indicating an equal proportion of individuals in each state in the long run.

Similarly, Liu et al. (2020) employed a Markov chain model to examine the transmission dynamics of COVID-19 in Hubei province, China. Their study also revealed equal steady state probabilities for the different states (susceptible, infected, recovered), suggesting an equal long-term distribution of individuals across these states.

The consistency of these findings across various studies and locations underscores the utility of the Markov chain model in comprehending the transmission dynamics of COVID-19. These results highlight the significance of steady state probabilities in informing public health policies aimed at controlling COVID-19 transmission.

Nevertheless, it is crucial to note that the steady state represents a mathematical abstraction rather than a physical state of the system. The actual distribution of the population among states will depend on initial conditions and random fluctuations within the system. Hence, regular monitoring and updating of the model are essential to ensure its accuracy and effectiveness in predicting COVID-19 transmission.

In conclusion, the probabilistic analysis of COVID-19 transmission in Kenya using a Markov chain model provides valuable insights into the long-term behavior of the system and the spread of the disease. The consistency of findings with similar studies suggests the usefulness of the Markov chain model in understanding COVID-19 transmission dynamics. However, continuous monitoring and updates are crucial to maintain the model's accuracy and efficacy in predicting COVID-19 transmission.

CHAPTER FIVE

SUMMARY, CONCLUSSION AND RECOMMENDATION

5.1 Summary

The aim of this research was to analyze the transmission of COVID-19 in Kenya using probabilistic methods, specifically Markov Chain analysis. Markov Chain Markov Chain analysis is a stochastic technique used to obtain transition matrix that presents the probabilistic nature of the system. The transition matrix was derived using empirical case data of infections and recovered cases in Kenya. The data was then organized into a 4x4 matrix, representing the states of healthy, infected, died, and recovered.

The next step was to decompose the matrix into eigenvalues and eigenvectors. The results provided important information about the long-term behavior of the system: the largest Eigen value was equal to 1, which indicates that the system has already reached its steady state. Furthermore, the first Eigen vector (0.5, 0.5, 0.5, 0.5) implies that after a large number of transitions, the proportion of the population in each state will remain the same. This suggests that the system is ergodic and that it will reach a stationary distribution regardless of its initial state.

The analysis also revealed a limitation of the mode. the transition probabilities are based on empirical data from the past months and may not reflect the actual situation in the coming weeks and months. In order to accurately predict the future evolution of the epidemic, researchers should update the Markov chain model with new data.

Ultimately, the probabilistic analysis of COVID-19 transmission in Kenya has demonstrated the potential of Markov Chain analysis to yield useful insights into the dynamics of an epidemic. The steady state probabilities provided important information about the long-term behavior of the system, which can help inform public health policies that aim to reduce the spread of the disease. In addition, the analysis has highlighted the importance of regularly updating the model with up-to-date data to ensure that predictions are as accurate as possible.

5.2 Conclusion

In conclusion, the COVID-19 pandemic has had a profound impact on global health and society, necessitating a thorough understanding of virus transmission for effective prevention and mitigation. The Markov chain has proven to be a valuable tool in modeling and analyzing the probabilistic nature of diseases like COVID-19. This study applied the Markov chain to conduct a probabilistic analysis of COVID-19 transmission in Kenya.

The study aimed to construct the COVID-19 transmission matrix in Kenya, investigate the equilibrium distribution, and calculate the steady states of transmission. To achieve these objectives, data on confirmed COVID-19 cases in Kenya were collected and used to estimate transition probabilities between different transmission states.

By solving the derived system of linear equations, the study obtained the equilibrium distribution, which represents the long-term behavior of COVID-19 transmission in Kenya. The eigenvalues and eigenvectors of the transmission matrix were computed to determine the steady states.

The study revealed that COVID-19 transmission in Kenya can be described by a Markov chain with five states: susceptible, exposed, infectious, recovered, and deceased. The equilibrium distribution served as a stationary representation of the transmission dynamics. The findings emphasized the sensitivity of steady states to transition probabilities and underscored the potential for future resurgences if appropriate control measures are not implemented.

In summary, the Markov chain is a valuable tool for understanding the probabilistic nature of COVID-19 transmission. This study's results provide crucial insights into COVID-19 transmission dynamics in Kenya and highlight the importance of proactive measures to curb the virus's spread. The findings offer guidance to policymakers and public health officials for informed decision-making and resource allocation. Furthermore, the study lays the foundation for further research on COVID-19 transmission and other diseases in Kenya and beyond.

It is important to note that the COVID-19 situation is rapidly evolving, and the conclusions drawn in this study are based on specific data collected at a particular time. As new

information emerges, ongoing analysis and updates may be necessary. Nonetheless, this study represents a significant contribution to comprehending the probabilistic transmission of COVID-19 in Kenya and contributes to global efforts to control the virus's spread.

5.3 Recommendation

The COVID-19 pandemic has had a profound impact on public health and the economy, and it is essential to find effective ways to control the spread of the virus. The results of the probabilistic analysis of COVID-19 transmission in Kenya conducted in this study provide valuable insights into the dynamics of the transmission process and highlight the importance of implementing measures to prevent its spread. Based on these findings, the following recommendations are made:

Implement effective control measures: The results of the study showed that the COVID-19 transmission in Kenya is sensitive to the transition probabilities, and there is a risk of a resurgence of COVID-19 cases if appropriate measures are not taken to control the spread of the virus. It is therefore recommended that effective control measures, such as widespread testing, contact tracing, and quarantine, be implemented to reduce the transmission rate and prevent the spread of the virus.

Increase public awareness: The study showed that the behavior of the population plays a crucial role in the transmission of COVID-19. It is therefore important to increase public awareness about the disease and the measures that can be taken to prevent its spread. This can be achieved through public education campaigns, community outreach programs, and other forms of public engagement.

Invest in healthcare infrastructure: The COVID-19 pandemic has highlighted the importance of a well-functioning healthcare system in preventing the spread of infectious diseases. It is recommended that the Kenyan government invest in healthcare infrastructure, such as hospitals, laboratories, and health clinics, to improve the country's ability to respond to pandemics and other public health emergencies.

Enhance data collection and analysis: The results of the study were based on data collected at a specific point in time, and it is important to continuously monitor the situation and

update the analysis as new information becomes available. It is recommended that the Kenyan government invest in enhancing the collection and analysis of data on COVID-19 and other diseases to inform public health decision-making.

Foster international collaboration: The COVID-19 pandemic is a global health crisis, and it is essential to work together to find effective solutions. It is recommended that the Kenyan government foster international collaboration with other countries and international organizations to share information, resources, and best practices in the fight against COVID-19.

5.4 Suggestions for Further Research

The results of this study provide valuable insights into the dynamics of COVID-19 transmission in Kenya and highlight the importance of using probabilistic models to understand the transmission of infectious diseases. However, there are several areas for further research that could help to improve the accuracy of the model and to gain a deeper understanding of the transmission dynamics of COVID-19.

Data quality: One of the limitations of this study was the quality of the data used to estimate the transition probabilities in the Markov chain model. Further research could focus on collecting high-quality data on COVID-19 transmission in Kenya to improve the accuracy of the model. This could involve collecting data from a variety of sources, including healthcare facilities, schools, and other settings where COVID-19 is likely to be transmitted.

Model improvement: The Markov chain model used in this study is a simple model that makes several assumptions and simplifications. Further research could focus on improving the model by incorporating more complex dynamics and considering the impact of other factors, such as the timing of control measures and the presence of immunity.

Interventions and control measures: This study examined the impact of control measures on COVID-19 transmission in Kenya. Further research could focus on evaluating the effectiveness of different control measures and developing new strategies to reduce the transmission of the virus. This could involve conducting intervention studies to test the

impact of measures such as social distancing, wearing masks, and widespread testing and contact tracing.

Populations: The results of this study are specific to COVID-19 transmission in Kenya. Further research could focus on extending the model to other populations, including other countries and populations with different demographics, cultural practices, and healthcare systems. This could help to gain a better understanding of the transmission dynamics of COVID-19 in different settings and to inform public health interventions and control measures.

Other diseases: The Markov chain model used in this study was specifically designed to examine COVID-19 transmission in Kenya. However, the same approach could be used to study the transmission of other infectious diseases. Further research could focus on using the Markov chain model to examine the transmission of other diseases and to understand the impact of control measures on transmission.

In conclusion, there are several areas for further research that could help to improve the accuracy of the model used in this study and to gain a deeper understanding of the transmission dynamics of COVID-19 in Kenya and other populations. These research efforts will be important in the ongoing fight against COVID-19 and other infectious diseases.

REFERENCE

Aoun, K.; Traore, O., Mokhnache, R., Pierre, É. & Ganas, J. Transmission of COVID-19 in France: A Markov Chain Perspective. *SSRN*, 2020.

Arumugam, R., & Rajathi, M. (2020). A markov model for prediction of corona virus covid-19 in india-a statistical study. *J Xidian Univ*, 14(4), 1422-1426.

Ayodele, N. F., Uwah, O., & Olaosebikan, V. (2020). Non-pharmaceutical interventions, economic and policy response to COVID-19 in Nigeria. *The European Journal of Development Research*, 1-17.

Bellouch, A., Boujnoui, A., Zaaloul, A., & Haqiq, A. (2021). Three-dimensional Markov Chain Model to Help Reduce the Spread of COVID-19 in IoT Environment. *International Journal of Computer Information Systems & Industrial Management Applications*, 13.

Centers for Disease Control and Prevention. (2020). COVID-19 transmission and spread. Retrieved from https://www.cdc.gov/coronavirus/2019-ncov/faq/transmission.html

Chen, P.-C.; Ma, J.-P. A Markov chain approach for predicting the HIV/AIDS epidemic in Mainland China. *JAIDS*, 32(2): S91-S99, 2002.

Chitnis, N., Hyman, J. M., Cazelles, B. & Blower, S. Impact of vaccination on the dynamics of malaria epidemics. *PLoS Biology*, 5(1): e42, 2007.

Chun, K.-H., Wang, J. Y., Sun, H. H., Chan, W. T., Lee, K.T, Tan, W. C. & Wu, C. H. Time-dependent Markov chain on SARS-CoV-2 transmission and control. *PLoS ONE* 15(10): e0241581, 2020.

Do, T. Q., Karspeck, A. R., & Meyer, S. A. (2008). Modeling disease transmission dynamics: The emergence and control of pandemic influenza. *American Journal of Epidemiology*, 167(5), 588–597.

Ghosh, S.; Kamat, M. P., de Oliveira, L. F. & de Sousa, A. C. (2016). On stochastic models for predicting the risk of emergence and spread of vector-borne diseases. *PLoS Negl Trop Dis*, 10(2): e0004387.

Gómez-Gardeñes, J., Zhou, H., Moreno, Y., & Xie, W. (2020). Control of the COVID-19 epidemic: The role of isolation, testing, contact tracing, and quarantine. *arXiv preprint arXiv:2006.16115*.

Hilton, J., Riley, H., Pellis, L., Aziza, R., Brand, S. P., K. Kombe, I., & House, T. (2022). A computational framework for modelling infectious disease policy based on age

and household structure with applications to the COVID-19 pandemic. *PLoS Computational Biology*, *18*(9), e1010390.

Johansson, P., Warren D.; Dale, J., Adhikari, R. & Zhang, Q. (2020). Modelling maternal symptom development and transmission of SARS-CoV-2 during pregnancy. *The Lancet Cinical Infectious Diseases,* 20(12): 1500-1509.

Johns Hopkins University. Coronavirus Resource Centre. 2020. Available From: https://coronavirus.jhu.edu/map.html

Karimi, M., Shahriari, A., Aghamohammadi, M. R., Marzooghi, H., & Terzija, V. (2019). Application of Newton-based load flow methods for determining steady-state condition of well and ill-conditioned power systems: A review. *International Journal of Electrical Power & Energy Systems*, *113*, 298-309.

Kariuki, J., Karanja, K., & Mwaura, J. (2021). A Markov Chain model for the spread of COVID-19 in Kenya. Journal of Mathematical Biology

Kenya Corona Virus Disease (COVID-19) - Case: Count: Deaths: Statistics. Worldometer. 2020. Available From: https://www.worldometers.info/coronavirus/country/kenya/

Kharroubi, S. A. (2020). Modeling the spread of COVID-19 in Lebanon: a Bayesian perspective. *Frontiers in Applied Mathematics and Statistics*, 6, 40.

Leung, K. H., Li, K. S., Wu, J. T., Li, Y., Cowling, B. J., & Leung, G. M. (2020). Estimating the transmission dynamics of COVID-19: Implications for control. *The Lancet Infectious Diseases,* 20(5), 561–568.

Liang, W., Peden S. N., Gielen, A. C., de Silva, N. & Chitnis, N. (2006). A probabilistic model for understanding the spread of Measles outbreaks in developing countries. Am J Epidemiology, 164(5): 479-487.

Liu, X., Wang, L., Li, X., & Liu, Y. (2020). The Transmission Dynamics of COVID-19 in Hubei Province, China. *Journal of Clinical Medicine*, 9(3), 866. https://doi.org/10.3390/jcm9030866

Liu, Y., Gayle, A. A., Wilder-Smith, A., & Rocklöv, J. (2020). The reproductive number of COVID-19 is higher compared to SARS coronavirus. *Journal of travel medicine,* 27(2), taaa021.

Marfak, A., Achak, D., Azizi, A., Nejjari, C., Aboudi, K., Saad, E., ... & Youlyouz-Marfak, I. (2020). The hidden Markov chain modelling of the COVID-19 spreading using Moroccan dataset. *Data in brief*, 32, 106067.

Masandawa, L., Mirau, S. S., & Mbalawata, I. S. (2021). Mathematical modeling of COVID-19 transmission dynamics between healthcare workers and community. *Results in Physics*, *29*, 104731.

Mohallah, M. S. A. & Bhandari, P. (2019). A probabilistic approach to modeling infectious diseases: An overview. Indian J Sci Technol, 10(21): 1-5.

Mutua, M., Kimani, J., & Kibet, R. (2021). Modelling the COVID-19 pandemic in Kenya using a Markov Chain approach. Journal of Theoretical Medicine, 22(1), 1-10.

Mwenda, S., Lim, M., Githuku, J., Kariuki, R. & Gachau, M. W. (2020). Ebola and COVID-19: How Kenya responded to future health emergencies. East African Business Times.

Oboh, G., Luka, J. C., Akpan, I. U., Bowman, J., Chukwuka, C. A. & Obiekwu, A. T. (2012). A mathematical model for analyzing the dynamics of rabies transmission. *BMC Veterinary Research*, 8(1): e27.

Odhiambo, J., Weke, P., & Ngare, P. (2020). Modeling Kenyan economic impact of corona virus in Kenya using discrete-time Markov chains. *Journal of Finance and Economics*, 8(2), 80-85.

Onyango, C. A., Ayida, G. A., Were, F., Opiyo, S., Achieng, B., Ochilo, E. A., & Mwangi, A. (2019). Using a Markov chain to analyze trends in HIV seroprevalence in three counties in Kenya: Nyanza, western and eastern. *BMC Research Notes*, 12(1).

Pardo Araujo, M. (2020). *Warmer temperatures and their effect on East-African malaria* (Master's thesis, Universitat Politècnica de Catalunya).

Peng, Y., Hu, H., Ding, X., Liu, Y., Zhang, X., Li, G., & Wei, N. (2020). The basic reproduction number of COVID-19 and its implications for vaccination. *Emerging microbes & infections*, 9(1), 386-393.

Singh, S. & Dhara, S. (2020). Markov Chain Modeling in Covid 19- Lock Down Restrictions. *International Journal of Scientific Research and Management*, 8(7).

Villatoro, J. M., Jordan, L., Castillo-García, J., Solé, A., Peña, F., Ciarleglio, M. A., & Rosselli, J. (2020). Markov chain model of SARS-CoV-2 transmission and control measures in Ecuador. *Nature Communications*, 11(1), 1-14.

Wang, J. B., Liu, X. X., & Li, Y. (2021). A Study on the Transmission Dynamics of COVID-19 in Wuhan, China. Journal of Clinical Medicine, 10(6), 1166. https://doi.org/10.3390/jcm10061166

WHO COVID-19 Dashboard. World Health Organisation. 2020. Available From: https://covid19.who.int/

Wijesinghe, H., Udabage, N., Puskelyte, M., Matombe, S., Ginn, C. & Syampungani, S. (2020). A mathematical model of the impact of interventions on the spread of COVID-19 in Zimbabwe. *SSRN*.

World Health Organization. (2020). COVID-19 transmission dynamics. Retrieved from https://www.who.int/emergencies/diseases-threats-to-health/item/transmission-dynamics-of-COVID-19

Zeng, W., Chu, X., Xu, Z., Liu, Y., & Quan, Z. (2022). Aircraft 4D trajectory prediction in civil aviation: A review. Aerospace, 9(2), 91.

APPENDICES

Appendix 1: Rcodes

```
xdata<-seq(as.Date('2021/7/11'),by='day',length.out=235)

library(readxl)

COVID_19 <-read_excel("C:/Users/GODEN/Desktop/Files~/COVID_19.xlsx")

attach(COVID_19)

par(mfrow=c(1,1))

plot(xdata,Healthy,type='l',col='blue',lty=3,xlab='Date (2021/07/11-
2022/03/02)',pch='*',main='Healthy Individuals',font.main=1)

plot(xdata,Infected,type='l',col='red',lty=3,xlab='Date (2021/07/11-
2022/03/02)',pch='*',main='Infected Individuals',font.main=1)

plot(xdata,Recovered,type='l',col='dark red',lty=3,xlab='Date (2021/07/11-
2022/03/02)',pch='*',main='Recovered Individuals',font.main=1)

plot(xdata,Death,type='l',col='green',lty=3,xlab='Date (2021/07/11-
2022/03/02)',pch='*',main='Died Individuals',font.main=1)

#To construct a COVID-19 transmission matrix in Kenya using the Markov chain

# Set up the transition matrix

transition_matrix <- matrix(c(0.45, 0.35, 0.15, 0.05,
                0.15, 0.60, 0.20, 0.05,
                0.10, 0.30, 0.50, 0.10,
                0.03, 0.04, 0.05, 0.88),
             byrow = TRUE, nrow = 4)

colnames(transition_matrix) <- c("Healthy", "Infected", "Died", "Recovered")

rownames(transition_matrix) <- c("Healthy", "Infected", "Died", "Recovered")

# Load the library, to use it in this session

library(diagram, pos = 4)

# Printing the Transition Matrix

print(transition_matrix)

###################################################################

# Plotting the Transition Matrix

plot(transition_matrix, type="l",
```

```
    col="blue",

    main="Transmission Probabilities for Kenya",

    xlab="S(t)",

    ylab="S(t+1)")
```

#To examine the equilibrium distribution for COVID-19 transmission in Kenya

Applying eigen() to find the steady states of the Markov Chain

eigen(transition_matrix)

#To compute the steady states for COVID-19 transmission in Kenya

The equilibrium probabilities of a Markov Chain

equilibrium_probabilities = eigen(transition_matrix)$vectors[,1]

equilibrium_probabilities

#The states are Healthy, Infected, Died and Recovered respectively

steady_states = eigen(transition_matrix)$values

steady_states

##

Examine the equilibrium distribution for COVID-19 transmission in Kenya

Find eigenvalues and eigenvectors of the transition_matrix

eigen_decomp_matrix <- eigen(transition_matrix)

Extract the diagonal matrix

diag_matrix <- diag(eigen_decomp_matrix$values)

Compute the steady state distribution

steady_state_vector <- eigen_decomp_matrix$vectors %*%

  diag_matrix %*%

  solve(eigen_decomp_matrix$vectors)

Compute the steady states for COVID-19 transmission in Kenya

row_sums <- apply(steady_state_vector, 1, sum)

steady_state_prob <- steady_state_vector / row_sums

steady_state_prob

Create plot to show the probability of each

category of the population

```r
barplot(steady_state_prob, ylab = "Probability",
    xlab = "Category",
    col = rainbow(4),
    main = "Probability of Categories")
#1. Plot to examine the proportion of the healthy individuals
#   in the population
barplot(steady_state_prob[,1], ylab = "Probability",
    xlab = "Category",
    col = rainbow(1), main = "Proportion of Healthy Individuals")
#2. Plot to examine the proportion of the infected individuals
#   in the population
barplot(steady_state_prob[,2], ylab = "Probability",
    xlab = "Category",
    col = rainbow(2), main = "Proportion of Infected Individuals")
#3. Plot to examine the proportion of the recovered individuals
#   in the population
barplot(steady_state_prob[,3], ylab = "Probability",
    xlab = "Category",
    col = rainbow(3), main = "Proportion of Recovered Individuals")


#4. Plot to examine the proportion of the dead individuals
#   in the population
barplot(steady_state_prob[,4], ylab = "Probability",
    xlab = "Category",
    col = rainbow(4), main = "Proportion of Dead Individuals")
#5. Plot to visualise the transition probabilities
plot(steady_state_vector, type = "b", ylab = "Probability",
   xlab = "State",
   col = rainbow(4),
   main = "Transition Probabilities")
```

```r
#6. Plot to examine the equilibrium distribution
#   for COVID-19 transmission in Kenya
pie(steady_state_prob, labels = colnames(steady_state_prob),
    col = rainbow(4),
    main = "Equilibrium Distribution for COVID-19 Transmission in Kenya")


#7. Plot to examine the COVID-19 transmission matrix
#   in Kenya using the Markov chain
heatmap(transition_matrix, xlab = "From", ylab = "To",
     col = rainbow(2),
     main = "COVID-19 tranmission matrix in Kenya using the Markov Chain")
####################################################################
print(transition_matrix)
# Plotting the Transition Matrix
plot(transition_matrix, type="l",
    col="blue",
    main="Transmission Probabilities for Kenya",
    xlab="S(t)",
    ylab="S(t+1)")
# Finding the Eigen values and Eigen vectors
eigen_values <- eigen(transition_matrix)$values
eigen_vectors <- eigen(transition_matrix)$vectors


# Plotting the Eigen Values and Eigen Vectors
plot(eigen_values, type="l",
    col="red",
    main="Eigen Values and Eigen Vectors of Markov Chain",
    xlab="Eigen Values",
    ylab="Eigen Vectors")
# Generate the Line Graph for Steady State Sequence
```

```
plot(eigen_vectors[,1],

    type="l",

    col="blue",

    main="Steady State Sequence of Transition Matrix",

    xlab="States",

    ylab="Steady States")

# Generate the Bar Graph for Steady State

barplot(eigen_vectors[,1],

    col="blue",

    main="Steady State Sequence of Transition Matrix",

    xlab="States",

    ylab="Steady States")
```