

Probabilistic analysis of COVID-19 transmission in Kenya using Markov chain



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ABSTRACT

Since the outbreak of the COVID-19 pandemic, many countries have continued to suffer economically due to trade losses. COVID-19 has evolved into different forms and hence became a problem to analyze its transmission. As a result of increased COVID-19 infections, there has been a scarcity of resources like hospital facilities, quarantine centers, and personal protective equipment (PPEs) for the medics. Therefore, accurate planning has to be made by the government of Kenya to ensure that resources are made available to combat the rising COVID-19 cases. To ensure effective future planning for the COVID-19 pandemic, proper analysis of the COVID-19 pandemic among the population is key. Therefore, this study will go a long way in providing insights on how to plan for the Kenyan population through probabilistic analysis of the COVID-19 pandemic using the Markov chain. The study used Secondary Cumulative data from the Kenya ministry of health for a period between 1st June 2021 and 1st May 2022. The data was analyzed using a steady-state Markov chain in which the transition probability matrix for the COVID-19 pandemic was computed. The number of individuals infected by the COVID-19 virus and who recovered at the end of the study period was set at zero since COVID-19 disease is not curable. The results were presented in the table and reported at a 95% confidence level. Based on the findings, the study concluded that a steady-state Markov chain is beneficial in simulating the coronavirus infection in numerous stages. Also, it is noted that the use of the steady-state Markov chain model allows for capturing short and long-term memory effects that greatly improve the estimation of the number of new cases of COVID-19 and indicate whether the disease has an upward/downward trend.

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1. Introduction

Coronavirus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus (Cihan, 2022). The virus originated in Wuhan, China in early December 2019 and then spread exponentially across the globe (Cheng and Shan, 2020; Liu et al., 2020). COVID-19 droplet transmission occurs when a person is in close contact with someone who has respiratory symptoms and is therefore at risk of having his/her mucosae exposed to potentially infective respiratory droplets (Kurniawan and Kurniawan, 2021; Peng et al., 2020; Swapnarekha et al., 2021). Transmission may also occur through

fomites in the immediate environment around the infected person. Therefore, the transmission of the COVID-19 virus can occur through direct contact with infected people and indirect contact with surfaces in the immediate environment or with objects used on the infected person. Most people infected with the virus experience mild to moderate respiratory illness and recover without requiring special treatment. However, some become seriously ill and require medical attention. Older people and those with underlying medical conditions like cardiovascular disease, diabetes, chronic respiratory disease, or cancer are more likely to develop serious illnesses. Anyone can get sick with COVID-19 and become seriously ill or die at any age. The COVID-19 pandemic is unprecedented in its global reach and impact, posing formidable challenges to policymakers and to the empirical analysis of its direct and indirect effects within the interconnected global economy (Carmody et al., 2021).

As of 30 January 2020, World Health Organization (WHO) declared the Corona Virus outbreak a Public

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Health Emergency of Global Concern and COVID-19 has since continued to spread across the world with immediate and long-term social economic effects on national economies and individual citizens (Pfefferbaum and North, 2020). Although, a series of prevention strategies such as lockdown, social distancing, and total quarantine of infected individuals were enforced to control the spread of the pandemic. During the COVID-19 pandemic, governments worldwide imposed severe restrictions on public life in order to limit the spread of the SARS-CoV-2 virus (Benke et al., 2020). A critical point in the decision-making process was the limitation of beds in intensive care units (ICU) in order to adequately treat all severe cases of COVID-19. Many countries increased the number of ICU beds substantially at the onset of the crisis; a critical issue with severe COVID-19 disease is the frequent need for prolonged ICU treatment (Benke et al., 2020). For informed decision making it is important to quantitatively assess how long the patients are expected to be in an ICU.

The first case of COVID-19 was confirmed in Kenya on 13th March 2020 and ever since, the pandemic has continued to ravage the Country (Odhiambo et al., 2020a; Maurice et al., 2021). The COVID-19 pandemic is a global shock like no other, involving simultaneous disruptions to both supply and demand in an interconnected world economy (Zhang et al., 2020). According to Güder (2020), on the supply side, infections reduce labor supply and productivity, while lockdowns, business closures, and social distancing also cause supply disruptions. On the demand side, layoffs and the loss of income reduced household consumption and firms' investment. The extreme uncertainty about the path, duration, magnitude, and impact of the pandemic could pose a vicious cycle of dampening business and consumer confidence and tightening financial conditions, which could lead to job losses and investment. Mathematical models have been developed and used to trace the temporal course of the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) outbreak 2020 (Olivares and Staffetti, 2021). Other authors used clinical modeling techniques for explaining the disease outbreak (Al-Qahtani, 2020).

Markov analysis, like decision analysis, is a probabilistic technique; however, Markov analysis is different in that it does not provide a recommended decision (Zeng et al., 2020). Instead, Markov analysis provides probabilistic information about a decision situation that can aid the decision maker in making a decision. It is important to note that Markov analysis is not an optimization technique; it is a descriptive technique that results in probabilistic information (Zeng et al., 2020). Markov analysis is specifically applicable to systems that exhibit probabilistic movement from one state (or condition) to another, over time. COVID-19 has evolved into different forms and hence became a problem to analyze its transmission. Odhiambo et al. (2020b) modeled the Kenyan economic impact of coronavirus using

steady-state discrete-time Markov chains presenting both conceptual and methodological gaps but they did not focus on the chances of transmission of COVID-19 in Kenya. Thus this study will focus on modeling probabilistic analysis of COVID-19 to understand the chances and transmission of COVID-19 transmission in Kenya using the Markov chain.

2. Materials and methods

2.1. Data collection and analysis

The COVID-19 secondary data was obtained from Kenya's Ministry of Health. The collected data was based on facts and figures collected by the Ministry of Health officials. After collecting the cumulative data, it was cleaned and analyzed using steady states Markov chain in which the Probability matrix was computed. The R statistical software was used to analyze and visualize the data.

2.2. 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.

2.2.1. Model development

This study considers three discrete states: susceptible (state 0), infected (state 1), and removed (state 2) states. If $(X_i, i = 0, 1, 2)$ represent the number of individuals in 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:

$$P(X_n = i_n | X_{n-1} = i_{n-1}, \dots, X_1 = i_1, X_0 = i_0) = P(X_n = i_n | X_{n-1} = i_{n-1}). \quad (1)$$

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

$$P_{ij} = \begin{bmatrix} P_{00} & P_{01} & P_{02} \\ P_{10} & P_{11} & P_{12} \\ 0 & 0 & 1 \end{bmatrix} \quad (2)$$

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.

2.2.2. Model assumptions

The current state of an individual is dependent only on the state of the individual at the previous time step; No individual at the removed state can be susceptible or infected; Transitioning probabilities are independent of time and remain constant over time or the study period; Successive transitions or relapse confirmed infections of COVID-19 or other medical complications do not take into consideration or does not meet the eligibility criteria of the study. The removed state comprises subjects who either died from the disease or were found to be immune after recovery; the only assumption required regarding losses and withdrawals is that they have the same future experience as those remaining under observation.

2.3. Estimating transition probabilities

The number of individuals infected by the 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:

$$L(P_{ij}|N, x) = \binom{N_i}{x_{ij}} P_{ij}^{x_{ij}} (1 - P_{ij})^{N_i - x_{ij}} \quad (3)$$

where, N_{ij} is the number of observed transition that starts from state i to j then,

$$\sum_j P_{ij} = 1. \quad (4)$$

From Eq. 4, the assumption of constant transition probabilities over the period, the transition probability matrix will be estimated as a multinomial distribution given as

$$\hat{P}_{ij} = \frac{x_{ij}}{\sum_j x_{ij}} = \frac{x_{ij}}{N_i} \quad (5)$$

For $i, j = 0, 1$, with standard errors from the sampling distribution of the estimate will be given as

$$\hat{s.e}(P_{ij}) = \sqrt{\frac{\hat{P}_{ij}(1 - \hat{P}_{ij})}{N_i}} \quad (6)$$

2.4. Computing probability-matrix

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:

$$f_{01}^{(m)} = P(X_{n+m} = 1, X_{n+m-1} = 0, \dots, X_{n+1} = 0 | X_n = 1) = P_{00}^{m-1} P_{01} \quad (7)$$

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

$$f_{10}^{(m)} = P(X_{n+m} = 1, X_{n+m-1} = 0, \dots, X_{n+1} = 1 | X_n = 1) = P_{11}^{m-1} P_{10} \quad (8)$$

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

$$E(\tau_{ij}^1) = \sum_{m=1}^{\infty} \frac{m f_{ij}^{(m)}}{P_r(i \rightarrow j)} = \frac{1}{1 - P_{ii}} \quad (9)$$

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

$$W = (I - Q)^{-1} \begin{pmatrix} 1 \\ 1 \end{pmatrix} \quad (10)$$

where, I is a 2x2 identity matrix and $Q = \begin{pmatrix} P_{00} & P_{01} \\ P_{10} & P_{11} \end{pmatrix}$

3. Results and discussion

3.1. Transition probability matrix

This analysis is modeled by the Markov chain process where five health states were considered Infected (I), Hospitalized (Ho), Home Based (HB), Recovered (R), and Dead (D). Table 1 shows the computed transition probability matrix for the COVID-19 transmission in Kenya from state i to state j . The Markov property is observed since the sum of the rows of each state adds to one.

Table 1: Transition probability from state i to state j in one cycle

From state i to state j		Infected (I)	Hospitalized (Ho)	Home-based (HB)	Recovered (R)	Dead (D)
COVID-19	Infected (I)	0.07	0.05	0.07	0.80	0.01
	Hospitalized (Ho)	0.05	0.00	0.00	0.94	0.01
	Home-based (HB)	0.07	0.00	0.00	0.92	0.01
	Recovered (R)	0.80	0.19	0.00	0.00	0.01
	Dead (D)	0.01	0.00	0.99	0.00	0.00

Figs. 1 and 2 show the Markov chain transition diagram for COVID-19 with their corresponding transition probability matrix. The COVID-19 patient who is in state i (Infected state) are Hospitalized,

then the patient can either remain in the same state or transit to state j that is, the patient either dies or recovers from the virus.

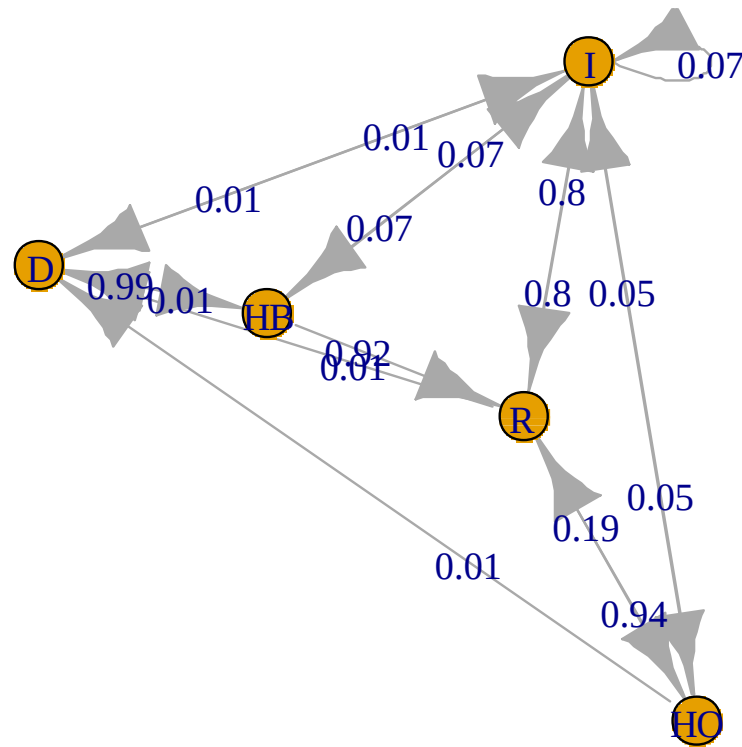


Fig. 1: Diagram of transitions in the Markov chain for COVID-19

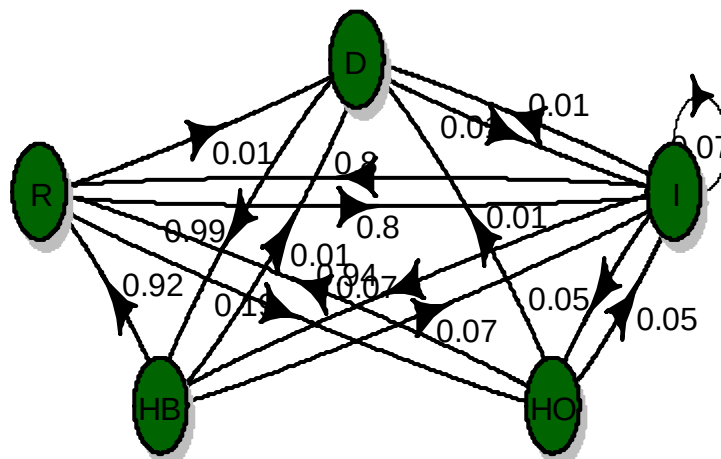


Fig. 2: Diagram of transitions in the Markov chain for COVID-19

3.2. Discussion

This study presents a steady-state Markov chain model to predict the Kenyan COVID-19 pandemic transition matrix. The findings revealed that one of the most important uses of the steady-state Markov chain in analyzing the COVID-19 pandemic situation in Kenya is that it compares performances for different states of affairs and courses of action within the health sector, by using system steady-state performance measurements. In the inefficient case, when infection rates are 10% instead of CDC suggested 5%, there is a higher percentage of patients hospitalized or have a higher rate of entering the Hospital (29% instead of 18%). This shows how, letting the infection rate increase above the suggested upper bound of 5%, results in saturating the Health Care system with too many

patients. A similar situation occurs with times between two successive visits to a state i .

The eigenvector associated with the eigenvalues of 1 is the stationary vector. This stationary vector is called the Markov chain ergodic distribution vector (steady-state vector). The ergodic vector shows the prediction of COVID-19 spread as the current status continues, including the current policies. Convergence speed towards steady-state distribution and mobility index was calculated using a transition probability matrix. As indicated in a study by [El-Hadidy \(2021\)](#) on developing a detection model for a COVID-19-infected person based on a probabilistic dynamical system. The study findings revealed that Markov Chains have a unique steady state distribution regardless of the initial state that is approached by successive iterations from any starting distributions. Other researchers ([Din et al., 2020](#); [Kharroubi, 2020](#); [Raherinirina et al., 2021](#))

have also applied the Markov chain probability analysis to model the COVID-19 transmission, and their findings agree with our findings.

4. Conclusion

On the basis of the findings above, this study concludes that the state transition probability matrix of a Markov chain gives the probabilities of transitioning from one state to another in a single time unit and it is important that the concept is extended to longer time intervals. In addition, the steady-state situation has been discussed to get the probability and the mean time of detection for the infected person. The study also concludes that a steady-state Markov chain is beneficial in simulating the coronavirus infection in numerous stages. This type of simulation could be very much useful in generating the time period of coronavirus transmission. The evaluation of COVID-19 transmission indicates that the Markov chain approach offers one opportunity for modeling in the future. Moreover, the use of the steady-state Markov model allows for capturing short and long-term memory effects that greatly improve the estimation of the number of new cases of COVID-19 and indicate whether the disease has an upward/downward trend. This can help decision-makers to plan for health policy interventions and take the appropriate actions to contain the spread of the virus.

Compliance with ethical standards

Conflict of interest

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

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