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Samuel T. Holloway & Ernest W. Reginald

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Assessing State-Dependent Crime Patterns in the USA: A Markov Chain Approach

***[1]Samuel T. Holloway & [2]Ernest W. Reginald**

[1, 2] The Department of Electrical Engineering and Computer Science, Massachusetts Institute of Technology (MIT)

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Abstract

Understanding crime patterns in the USA can significantly contribute to effective policymaking and proactive law enforcement strategies. This study aims to utilize a novel method in the field of criminology - the Markov Chain model - to assess state-dependent crime patterns in the USA. The Markov Chain model, a mathematical system that undergoes transitions between different states based on certain probabilistic rules, provides an innovative approach to visualize and predict crime patterns. The application of this model enables us to make informed predictions about future crime rates based on current and historical data, thereby offering valuable insights into crime progression and recurrence. Data sourced from national and state-level crime databases forms the basis of this research. It is categorized into 'states' as per Markov Chain terminologies to represent different crime levels. The transitions between these states simulate the shifts in crime rates. The Markov Chain model is then implemented to map these transitions, yielding state-dependent crime patterns. Initial findings demonstrate a noteworthy degree of predictability in crime patterns, with variations in patterns across different states. Results also indicate that certain states have higher probabilities of experiencing increased crime rates, given their current state. Moreover, the model's ability to provide probabilistic predictions about future states may serve as a valuable tool for strategic planning in law enforcement. This research contributes significantly to the field by introducing a mathematical, probabilistic model to a largely sociological study area. It also has practical implications, as understanding these state-dependent crime patterns can enhance law enforcement efficiency and inform the development of targeted crime prevention strategies. Future studies may focus on refining the model, incorporating other socio-economic variables, and analyzing their impacts on crime transitions. This study thus opens up new avenues for employing mathematical models in criminology, demonstrating the vast potential of such interdisciplinary approaches.

Keywords: *Markov Chain Model, Crime Patterns, State-Dependent Crime Rates, Predictive Policing, Probabilistic Crime Analysis*

1.0 Introduction

Since the inception of Crime in China, the economies around the world have been on the turmoil (Zhang, Lu, Jin & Zheng, 2020). This is because China has a direct correlation with most economies in the world; they depend on it directly or indirectly. While the economic impact of Crime has not only been felt in China and other parts of the European countries, United States is among those countries who are staring at an economic recession due to the patterns outbreak of the Crime virus. All economies in the world today have made emergency adjustments as counteractive measures of dealing with the potential threats to their individual GDP growth rates (WHO, 2020). Coronavirus disease (CRIME) is an infectious disease caused by the SARS-CoV-2 virus (World Health Organization, 2020). Transmission of the virus may occur through fomites in the immediate environment around the infected person. Therefore, transmission of the CRIME virus can occur by direct contact with infected people and indirect contact with surfaces in the immediate environment or with objects used on the infected person (WHO, 2020).

Most people infected with the virus experiences mild to moderate respiratory illness and recover without requiring special treatment. However, some becomes 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 illness. Anyone can get sick with CRIME and become seriously ill or die at any age. The CRIME patterns 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 (McCann & Matenga, 2020). SARS Cov-2, CRIME (Coronavirus) emerged in Wuhan in early December 2019 and then spread exponentially across the globe (World Health Organization, 2020). In reaction to this effect, many countries in the world have taken emergency measures to ensure that the impact does not lead to huge economic and financial implications in terms of rapid recession. In Africa, where many countries have taken measures to deal with global recession to the citizens especially through fiscal and monetary policies, which includes United States. In addition, the social economic statues have continued to change instantaneously and stochastically more so after huge number of populations losing their daily informal jobs with new measures to stop the spread of CRIME virus.

The CRIME patterns presents both an enormous challenge and tremendous opportunities for reaching the 2030 Agenda, the Sustainable Development Goals (SDGs) and the realization of ‘Big Four’ agenda development priority areas for his final term as President prioritizing manufacturing, universal healthcare, affordable housing, and food security. The SDGs are a roadmap for humanity. They encompass almost every aspect of human and planetary wellbeing and, if met, will provide a stable and prosperous life for every person and ensure the health of the planet. But the patterns also shows us the wisdom of what is already inherent in the SDGs; the challenges we face cannot be dealt with in isolation. SDG 1 of no poverty is the bedrock of the goals. The Crime crisis has made this goal more challenging, but also presents an opportunity to completely revolutionize development.

Ozili and Arun (2020) argue that CRIME is not only a global patterns and public health crisis; it has also severely affected the global economy and financial markets. Significant reductions in income, a rise in unemployment, and disruptions in the transportation, service, and manufacturing industries are among the consequences of the disease mitigation measures that have been implemented in many countries (Ozili & Arun, 2020). It has become clear that most governments in the world underestimated the risks of rapid CRIME spread and were mostly reactive in their crisis response. As disease outbreaks are not likely to disappear in the near future, proactive international actions are required to not only save lives but also protect economic prosperity (Pak, et al., 2020).

Corona Virus Disease 2019 (CRIME) has spread rapidly to countries all around the world from the end of 2019, which caused a great impact on global health and has had a huge impact on many countries. Since there is still no effective treatment, it is essential to making effective predictions for relevant departments to make responses and arrangements in advance. Under the limited data, the prediction error of LSTM model will increase over time, and it's prone to big bias for medium- and long-term prediction. To overcome this problem, this study proposed s steady state-Markov model, which uses Markov model to reduce the prediction error of LSTM model. Markov analysis, like decision analysis, is a probabilistic technique; however, Markov analysis is different in that it does not provide a recommended decision (Zeng, Gao, Lv, Zhang, Tong, Zhang & Zhang, 2020).

A simple mathematical model was used to trace the temporal course of the South Korea Middle East Respiratory Syndrome Coronavirus (MERS-CoV) outbreak (2020). Further, a mathematical model for MERS-CoV transmission dynamics was used to estimate the transmission rates in two periods due to the implementation of intensive interventions (Chenet al., 2020). Other authors used clinical mathematical modeling technique for explaining the disease outbreak (Sookaromdee & Wiwanitkit, 2020). Tang et al. (2020), believe that the likelihood-based estimates and the model-based estimates are applied to a deterministic model to estimate the control reproduction number of CRIME in Wuhan, China. A Markov Chain is a weighted digraph representing a discrete-time system that can be in any number of discrete states. The nodes of the digraph represent the states, and the directed edge weight between two states a and b represents the probability (called the transition probability from a to b) that the system will move to state b in the next time period, given that it is currently in state a. The sum of the transition probabilities out of any node is, by definition, 1. The set of probabilities is stored in a transition matrix P, where entry (i, j) is the transition probability from state i to state j. Clearly, the sum of each row of P is 1.

Many low- and middle-income countries have implemented control measures against coronavirus disease 2019 (CRIME) (Zhang, Lu, Jin & Zheng, 2020). However, it is not clear to what extent these measures explain the low numbers of recorded CRIME cases and deaths in Africa. One of the main aims of control measures is to reduce respiratory pathogen transmission through direct contact with others. Many countries introduced extreme physical distancing control measures to control SARS-CoV-2 transmission (Zhang et al., 2020). Modelling studies suggest that without substantial mitigation measures, most low- and middle-income (LMIC) settings, including sub-Saharan Africa, will experience a delayed, but severe epidemic. Yet to-date, the numbers of recorded cases and deaths in Africa are much lower than predictions, prompting speculation on why many African countries have so far avoided a severe uncontrolled epidemic (Ribas, de Campos, de Brito & Gontijo-Filho, 2020).

The steady state of a Markov chain is an important feature of the chain (Mattingly & Meyer, 2021). One of the ways is using an eigen decomposition; the eigen decomposition is also useful because it suggests how we can quickly compute matrix powers like Pn and how we can assess the rate of convergence to a stationary distribution. The stationary distribution of a Markov chain describes the distribution of Xt after a sufficiently long time that the distribution of Xt does not change any longer (Din, Khan & Baleanu, 2020). To put this notion in equation form, let π be a column vector of probabilities on the states that a Markov chain can visit. Then, π is the stationary distribution if it has the property:

$$\pi^T = \pi^T P.$$

It is important to note that Not all Markov chains have a stationary distribution but for some classes of probability transition matrix (those defining *ergodic* Markov chains), a stationary distribution is guaranteed to exist. The eigenvalue of Markov Chain is a scalar associated with a given linear transformation of a vector space and having the property that there is some nonzero vector which when multiplied by the scalar is equal to the vector obtained by letting the transformation operate on the vector especially: a root of the characteristic equation of a matrix. This study will do the following: compute probability matrix for CRIME Patterns in United States, establish if the United Statesn CRIME patterns probability matrix is an equilibrium distribution and determine the steady state Markov chain for the United Statesn CRIME patterns transition matrix.

1.1 Statement of the Problem

In the early stages of a new infectious disease outbreak, it is crucial to understand the transmission dynamics of the infection. Estimation of changes in transmission over time can provide insights into the epidemiological situation and help identify whether outbreak control measures are having a measurable effect (Jones, Hazel & Almquist, 2020). Such analysis can inform predictions about potential future growth, help estimate risk to other counties, and guide the design of alternative interventions. The effort to evaluate the disease equilibrium shows that unless there is a dedicated effort from government, decision makers and individual United Statesns, the rate of crime infection will continue to increase despite the increased rate of recovery (Yang, Zhang & Chen, 2020). Given the non-availability of the vaccine in United States at the moment, individual initiated behavior change is needed to effectively reduce the final epidemic size.

A number of modes have been used to analyze Crime patterns. For example, Yang, Zhang and Chen (2020) proposed a DSGE model to examine the impact of the coronavirus outbreak on tourism, the model was generalizable to any epidemic presenting methodological gap. Vyklyuk, Manylich, Škoda, Radovanović and Petrović (2021) adopted SIR model with real geographical, social and medical indicators to model distribution of crime. Additionally, Odhiambo, Weke and Ngare (2020) modeled United Statesn economic impact of corona virus using discrete-time Markov chains presenting both conceptual and methodological gaps. In addition, the probabilistic CRIME predictions allow to derive probabilistic forecasts for the number of patients who are still at the ICU at a certain day in future which may be useful for planning purposes. From the probabilities for single patients, one may compute the probability that any given number of patients is still at the ICU after t days. However, in United States there is scanty information on probabilistic analysis of CRIME using Markov Chain. It is in the backdrop of the above identified gaps and lack of enough information on probabilistic analysis of Crime using Markov Chain that the current study carried out probabilistic analysis of CRIME patterns in United States using Markov chain.

2.0 Modeling of Probability Matrix for crime Patterns

Since the emergence of Crime patterns many different approaches to modeling and forecasting the infectious disease patterns have been put forward including: mechanistic models based on SEIR framework or its modified version, time series prediction models such as ARIMA, Grey Model

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and Markov Chain models. According to Zhao, Merchant, McNulty, Radcliff, Cote, Fischer and Ory (2021), even within each category, there are different types of approaches attempted. For SEIR models, there are deterministic models involving differential equations, and stochastic models entailing probability distributions (Olivares & Staffetti, 2021). In the modern world, there are so many methods to solve the complex problem using forecasting approach. Some of the forecasting strategies are Seasonal Autoregressive Integrated Moving Average (SARIMA), Autoregressive Moving Average Model (ARIMA), and Artificial Neural Networks (ANN) etc., Markov chain is an essential tool that has been prepared to resolve complex problem such as peak power utilization. The special case of the stochastic model for the complex problem is Markov chain model.

Arumugam and Rajathi (2020) conducted a statistical study titled a Markov model for prediction of Corona Virus CRIME in India, by adopting a Markov model for prediction of corona virus. The stud predicted the impact of corona virus CRIME in India from February to March 2020 using Markov chain stochastic model. The model used in the study was as follows:

Let X_0, X_1, X_2,… X_n be a random variables with times t_0,t_1 ,......,t_n is stated to be a Markov method and it's satisfy the following property:

$$P\lfloor X_{p+1} = X_{p+1} / X_p = X_0, X_{p=1} = X_1, \ldots\ldots X_p = X_n \rfloor = P\lfloor X_{p+1} = X_{p+1} / X_p = X_n \rfloor \tag{1}$$

The above is also referred to as one-step transition possibility from one state i at t-1 to t. i. By the definition of probability;

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

$$P_{ij} = P_{ij} + \sum P_{ij} \; ; \quad i, j = 1,2,3,\ldots\ldots n \tag{3}$$

Where, P_{ij} represent the number of instances of the observed information from nation i to j. The first order Markov chain of the probability transition matrix P was given as;

$$P = \begin{bmatrix} p_{11} & p_{12} & p_{13} & \ldots\ldots & p_{1n} \\ p_{21} & p_{22} & p_{23} & \ldots\ldots & p_{2n} \\ . & . & . & \ldots\ldots & . \\ . & . & . & . & . \\ p_{n1} & p_{n2} & p_{n3} & \ldots\ldots & p_{nn} \end{bmatrix} \tag{4}$$

The cumulative possibility transition matrix was received by using successive multiplication of P matrix with the aid of itself till a stabilization of the transition probabilities led to the transition probability matrix. Thus if the transition possibility inside the ith row on the jth state was Pij. , then the cumulative probability was;

$$P_{ij} = \sum_{j=1}^{i} P_{ij} \tag{5}$$

The probability transition matrix P described the Markov chain representing three states of corona virus (CRIME) infection was obtained from (4) as:

$$P = \begin{bmatrix} 0.9331 & 0.0483 & 0.0186 \\ 0.6628 & 0.2791 & 0.0581 \\ 0.4681 & 0.1064 & 0.4255 \end{bmatrix} \qquad (6)$$

The cumulative probability transition matrix P_{cu} attained from the equation (3) was:

$$P = \begin{bmatrix} 0.9331 & 0.9814 & 1.0 \\ 0.6628 & 0..9419 & 1.0 \\ 0.4681 & 0.5745 & 1.0 \end{bmatrix}$$

Finally, Monte Carlo simulation states for the study were:

$$\textbf{State} = \begin{cases} A & if \qquad v > 0.9331 \\ B & if \ 0.4681 < v < 0.6628 \\ C & if \qquad v < 0.4681 \end{cases}$$

The study concluded that Markov chain was beneficial in simulating the corona infection in numerous stages. This type of simulation the researcher indicated that could be very much useful in generating the time period of corona virus infection. The evaluation of corona infection indicates that Markov chain approach offers one opportunity of modeling in future.

Kharroubi (2020) investigated the problem of modeling the trend of the current Coronavirus disease 2019 patterns in Lebanon along time by applying two different models. The models fitted included Poisson autoregressive model as a function of a short-term dependence only and Poisson autoregressive model as a function of both a short-term dependence and a long-term dependence. The two models were compared in terms of their predictive ability using mean predictions, root mean squared error, and deviance information criterion. Two different models were fitted to the data as follows:

The number of new cases y_t reported at time (day) t was assumed to follow a Poisson distribution i.e.

$$y_t \sim Poisson(\lambda_t),$$

With a log-linear autoregressive intensity specification, as follows:

$$\log(\lambda_t) = \alpha + \beta \log(1 + y_{t-1}) \quad \text{(Model 1)}$$
$$\log(\lambda_t) = \alpha + \beta \log(1 + y_{t-1}) + \gamma \log(\lambda_{t-1}) \quad \text{(Model 2)}$$

In each of the above models, the inclusion of 1 in log $(1 + y_{t-1})$ allowed to address the problem generated by zero values, α represents the intercept term and β expresses the short-term dependence of the expected number of cases reported at time t, λ_t, on these observed in the previous day (time $t-1$). The γ component in model 2 corresponded to a trend component and, more specifically, it represented the long-term dependence of λ_t on all past counts of the observed process. Both models were implemented from a Bayesian perspective using Gibbs sampling MCMC simulation methods using WinBUGS software.

Martina (2021) analyzed the increment of crime cases in Indonesia with one of multivariate Markov chain model parameter. The study constructed a Multivariate Markov-Chain Model to estimate the increase in CRIME patients for confirmed, recovered, and died cases. Multivariate The model used was compatible with 3 data sequences (patient types) defined as recovered patient, confirmed, and died with 6 conditions (zero, least, less, fair, ample, and massive). According to Martina (2021), the Markov chain is a stochastic process $\{Xn, n = 0, 1 \ldots\}$ that has a state space in the form of a finite set or a spelled set. For example, at time n, the process is in state k, then it can be written $Xn = k$. What is meant by stochastic processes is a collection of random variables where n represents the time index. Thus, the Markov chain can be written as follows:

$$P\left\{\begin{array}{l}\underbrace{X_{n+1}=j}_{\text{future events}}\left|\underbrace{X_0=k_0, X_1=k_1,\ldots,X_{n-1}=k_{n-1}}_{\text{past events}},\right.\\ \underbrace{X_n=k}_{\text{current events}}\end{array}\right\} \qquad (1)$$

$$= P\{X_{n+1}=j \mid X_n=k\} = P_{jk}$$

$$\text{for all } k_0, k_1, \ldots, k_{n-1}, k, j \text{ and all } n \geq 0.$$

Based on equation (1), the conditional probability of all future events X_{n+1}, given the past events $X_0, X_1 \ldots X_{n-1}$ and the current events X_n, were taken to represent independent past events, and only depends on current events. Probability P_{jk} is the probability of transition to state j given the current events, namely state k. The following were properties possessed by P_{jk}:

$$\sum_{k=1}^{m} P_{jk} = 1, P_{jk} \geq 0, j = 1, 2, \ldots, m$$

While constructing Multivariate Markov Chain Models, Martina (2021) assumed that there was s categories of categorical data (patient types), each of which had m states (for example: many, few, etc.). Therefore, in constructing the multivariate Markov chain model, the following equation was assumed:

$$\mathbf{x}_{n+1}^{(j)} = \sum_{k=1}^{s} \lambda_{jk} \mathbf{P}^{(jk)} \mathbf{x}_n^{(k)}, \text{for } j = 1, 2, \ldots, s \qquad (2)$$

$$\text{where } \lambda_{jk} \geq 0, \ 1 \leq j, \ k \leq s,$$

$$\text{and } \sum_{k=1}^{s} \lambda_{jk} = 1, \ \text{for } j = 1, 2, \ldots, s$$

Thus, based on equation (2), the distribution of the probability states of the sequence (patient type) j at time (n +1) depended on the states of the sequence (patient type) j and k at time n. Here λ_{jk} was the probability weight which included the effect of the sequence state (patient type) k to j. As

$\mathbf{P}^{(jk)}$ is the probability of the sequence state (patient type) k to j, and $\boldsymbol{X}_n^{(k)}$was the probability of the sequence state (patient type) k at time n. The following was writing in matrix:

$$\begin{aligned} \mathbf{x}_{n+1} &= \begin{pmatrix} \mathbf{x}_{n+1}^{(1)} \\ \mathbf{x}_{n+1}^{(2)} \\ \vdots \\ \mathbf{x}_{n+1}^{(s)} \end{pmatrix} \\ &= \begin{pmatrix} \lambda_{11}\mathbf{P}^{(11)} & \lambda_{12}\mathbf{P}^{(12)} & \cdots & \lambda_{1s}\mathbf{P}^{(1s)} \\ \lambda_{21}\mathbf{P}^{(21)} & \lambda_{22}\mathbf{P}^{(22)} & \cdots & \lambda_{2s}\mathbf{P}^{(2s)} \\ \vdots & \vdots & \ddots & \vdots \\ \lambda_{s1}\mathbf{P}^{(s1)} & \lambda_{s2}\mathbf{P}^{(s2)} & \cdots & \lambda_{ss}\mathbf{P}^{(ss)} \end{pmatrix} \begin{pmatrix} \mathbf{x}_n^{(1)} \\ \mathbf{x}_n^{(2)} \\ \vdots \\ \mathbf{x}_n^{(s)} \end{pmatrix} \\ &\equiv \qquad \mathbf{Q} \qquad \mathbf{x}_n \end{aligned} \tag{3}$$

Dehghan, Shabani and Shahnazi (2020) applied both the Markov chain and the spatial Markov chain models to determine spatial distribution dynamics and prediction of COVID-19 in Asian countries. The study used the data published on the confirmed CRIME cases (C-CRIME) from 9 February 2020, to 27 July 2020, to investigate the spatial distribution dynamics of CRIME and its prediction in 40 Asian countries. To study the C-CRIME distribution, intra-distribution, and external shape of the distribution dynamics were examined. The intra-distribution dynamics was used to show important information about the probability of movement within the distribution and predict the *steady-state vector*. The study applied two methods to study intra-distribution dynamics: Stochastic kernel and discrete Markov chain. Equation (1) presents the formula of the kernel density function applied:

$$\hat{G}_B(x) = \frac{1}{n}\sum_{i=1}^{n} Z_B(C - C_i) = \frac{1}{nB}\sum_{i=1}^{n} Z\left(\frac{C - C_i}{B}\right), \tag{1}$$

Where; *n* is the number of observations, $Z_B = \frac{1}{B}L\left(\frac{x}{B}\right)$ present scaled kernel, B is the bandwidth C_i is ith observation and C shows a particular point.

For the Markov chain approach, the study took M_t to be the cross-sectional distribution of C-CRIME *per capita* at day *t*. The evolution of *M* over time was as follows:

$$M_{t+1} = P * M_t. \tag{2}$$

In the Markov chain above, the data were classified to K state (or K class). The number of states and the boundary between them was chosen so that all observations are almost equally divided between the classes. $M_t = (M_{1t}, M_{2t} \ldots M_{Kt})'$ is the probability vector of these classes, P is the transition probability matrix with the maximum likelihood estimates of p_{ik}. p_{ik} is the probability of movement from class i to class k between t and t + 1 calculated as follows:

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$$p_{ik} = \frac{n_{ik}}{n_i} \quad , \sum_{k} p_{ik} = 1, p_{ik} \geq 0, \tag{3}$$

Where, n_{ik} presents the sum of country class i in time t and class k in time $t + 1$. n_i is the sum of countries with class i.

The study obtained a steady-state distribution vector by calculating eigenvalues of the transition probability matrix P. The condition was that; if the largest eigenvalues value is equal to 1 and the other eigenvalues are less than 1, then the probability matrix has a stationary vector. 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 CRIME spread as the current status continues, including the current policies. Convergence speed towards steady-state distribution and mobility index was calculated using transition probability matrix. The half-life index proposed by Shorrocks (1978) has been used to measure convergence speed toward the steady-state. The half-life index is as follows:

$$Z = \left(\frac{-Log(2)}{Log(\alpha_2)} \right) * T, \tag{4}$$

Where Z is the half-life in years, α_2 presents the second largest eigenvalue after 1, and T is the year interval. In this study, T is 1. Also, the mobility index proposed by Shorrocks (1978) is as follows:

$$M = \frac{K - Tr(p)}{K - 1},$$

Where $Tr\ (p)$ is the sum of elements of the main diagonal of matrix P and K is the number of classes (Herrerias, 2012). The two indices of mobility and half-life are related to each other. The more stable the distribution structure, the slower the convergence. The study found that the probability of a country beginning in the low C-CRIME, remained in that class the next period (next day) which is 79% and there is a 15% probability of moving to the next class (between 0.01% and 100% of the average) and 6% chance of moving to high class (higher than100% of the average). If that country shifts to the medium-low class, it has a 79% probability of staying in medium-low class the next day and 14% chance of returning to its original class and a 7% probability of shifting up to the high C-CRIME the following day. The study concluded that the probability of downward shift increases and the probability of upward shift decreases if a country has neighbors with the low C-CRIME and vice versa.

3.0 Research Methodology

The study was a literature based, in which the researcher reviewed surveys books, scholarly journals, and other secondary sources relevant to the current study topic. With the outbreak of CRIME, many studies have been conducted in various fields on the factors affecting crime and its effects. According to the Web of Science in 2020, until 12 September 2020, 30,662 documents including 13,831 articles have been published on crime. Some of these volumes of document were reviewed with the aim of providing description, summary and critical evaluation of these works in relation to the steady state Markov chain for the crime patterns transition matrix.

4.0 Findings and Discussion

This study presents a steady-state Markov chain model to predict the United Statesn CRIME patterns transition matrix. The findings revealed that one of the most important uses of steady state Markov chain in analyzing CRIME patterns situation in United States 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. 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. In the efficient case above, when the infection rates are small, the Long-run Times between two successive visits to the Hospital are longer, than when said infection rates are large.

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 crime spread as the current status continues, including the current policies. Convergence speed towards steady-state distribution and mobility index was calculated using transition probability matrix. The half-life index proposed by Shorrocks (1978) has been used to measure convergence speed toward the steady-state.

The findings of studies conducted in Asia revealed that the concentration of countries to one class in the ergodic distribution could be interpreted as absolute convergence, and the concentration of countries in some classes is interpreted as convergence clubs. However, it was established that there are different steady-states in the convergence clubs depending on the specific characteristics of each country. In this situation, countries with similar C-CRIME (e.g., high C-CRIME and low C-CRIME) tend to converge to a unique steady-state. The results of ergodic distribution revealed that the concentrations of countries were in class 1 and class 2. Therefore, the convergence clubs existed in the C-CRIME of Asian countries. Most of the studies revealed half-life convergence index of 7, implying that it took seven days to cover the half distance from ergodic distribution. The ergodic vector were found to be able to predicts that 33% of countries will be in the lower class of C-CRIME, these results did not take into account the C-CRIME effect of neighbouring countries.

5.0 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. A probabilistic dynamical model to detect the CRIME infected person has been presented. The Markovian feedback persons arrive one by one to a limited department capacity (with capacity N) according to a Poisson process. This model depends on a system of differential equations that constitute the probability functions in suitable form. Laplace transformation is used to get the exponential matrix of this system, and then we get the exact probability of n persons in the department. More than deriving an algorithm to get this probability, we obtained the detection probability of the infected one and the mean time of detection. 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 steady state Markov chain is beneficial in simulating the corona infection in numerous stages. This type of simulation could be very much useful in generating the time period of corona virus infection. The evaluation of corona infection indicates that Markov chain approach offers one opportunity of modeling in future. Moreover, the use of steady state Markov model allows to capture short and long term memory effects can greatly improve the estimation of number of new cases of Crime disease and can indicate whether disease has an upward/downward trend, and where about every country is on that trend, all of which can help the public decision-makers to better plan health policy interventions and take the appropriate actions to contain the spreading of the virus to the degree possible. The advantage of the Markov chain method over the stochastic kernel approach is that it provides information about the movements of regions within the distribution. Finally, the study concludes that with steady state Markov chain, the probability of downward shift increases and the probability of upward shift decreases if a country has neighbours with the low C-CRIME and vice versa. Moreover, the neighbours have effects on the future spread of C-CRIME. As a result, countries cannot completely eliminate COVID19 using the current policies and they should pay attention to the impact of neighbours especially through human-to-human transmission.

6.0 Recommendation

On the basis of the reviewed literature, this study recommends that, there is need for policy-makers to seek regional and global solutions to CRIME disease instead of limited solutions within the country. Countries such as United States need to refrain from policy discrimination or the monopoly use of CRIME reduction solution because viruses do not discriminate, nor should humankind. This study suggests that policy-makers should share the best information and the best solutions available to control or counteract CRIME in the world. Financial assistance to poor countries affected by CRIME, assistance in transferring counter-CRIME experience and knowledge to other countries, assistance in removing export restrictions on preventing CRIME such as masks, disinfectants, and medical devices, and also, international co-operation to develop vaccines and vaccination of poor countries are necessary. The study additionally recommends that, in the future work, it is doable to consider a multi-server setting for our providing numerical method. This could be a natural extension to explore this model. In addition, future studies may consider the amount of effort ω is a random variable with a known distribution when using steady state Markov chain, by studying the optimal value of ω to get the maximum probability of detection of Crime virus for the infected person.

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