

Markov Chain Models in Covid-19 Prediction: State-of-the-art and Future Perspectives

Xiafei Ding^{1,†}, Yue Ma^{2,†}, Jiachen Tang^{3,†,*}

¹ Shandong University, Shandong, China

² Washington State University, Beijing, China

³ University California of Irvine, Shandong, China

* Corresponding Author Email: jiacht3@uci.edu

[†]These authors contributed equally

Abstract. Novel tuberculosis pneumonia, caused by COVID-19, has become the most serious epidemic in the world today. In times of rampant epidemics, many countries adopt policies that restrict civil liberties, and predictive models can provide advice on the best time to predict when restrictions will begin and end, as well as provide data to support other epidemic prevention policies. In this paper, the authors will use the existing literature as well as research findings to predict the prevalence of COVID-19. This paper firstly analyzes and optimizes the models developed in the literature, mainly involving Markov Chain models. The data summarized in the literature are also analyzed and integrated, and many studies combine models other than Markov Chain for combination. Finally, the evaluation methods for each model are summarized.

Keywords: COVID-19, Markov chain, epidemic prediction.

1. Introduction

Since the first case of severe acute respiratory syndrome coronavirus 2 (SARS-COV-2) was reported in Wuhan, China, the outbreak of the disease has been declared a public health emergency of international concern. On 11 February 2020, the World Health Organization (WHO) officially named the disease COVID-19. The COVID-19 pandemic has swept the world and its strong transmissibility has infected hundreds of millions of people and killed millions. It has become one of the main public health problems in the world [1]. Although the vaccine has been created, there are still numerous issues with vaccination dissemination. There is still an urgent need for executing measures to prevent the disease from spreading. To design suitable policies within and between nations, policymakers must first understand the distribution dynamics of COVID-19 and the relative factors. As a result, projecting the epidemic's future trend, assisting key departments and individuals in developing policies to restrict the spread of COVID-19 epidemic remain critical.

Markov chain is a random process with Markov characteristics. It has essential applications in computational mathematics, finance, and diseases transmission, et al. Markov chain model is based on probability theory and uses autoregressive process method. It is used to predict stationary random phenomena quantitatively. There are many kinds of Markov chain models, taking continuous, discrete, and spatial for examples. Also, simply using Markov chain may not be enough in applications, thus extended Markov chain models are suggested, whose representative models are hidden Markov chain model (HMM) and the combination of Markov chain with other models. Markov chain Monte Carlo (MCMC) is another important method of Markov chain model.

Because of the enormous harm caused by COVID-19, it is critical to use Markov chains to design models of infectious diseases to predict the epidemic for implementing preventive measures. Since the outbreak in China, many papers have been published, as shown in Table I. However, because of discrepancies in the results of those studies, the current systematic review aimed to estimate the effect of the different methods for the propagation of COVID-19.

On the first level, the selected articles have been classified in four categories in this paper, including data source, data preprocess, model construction and optimization, and assessment method.

Finally, the paper gives the summary and prospect of the application of Markov chain in the propagation of COVID-19, and gives the problems still existing in the application, which is also the direction to continue efforts in the later period.

2. Methodology

The search engines implemented were Google scholar. All of the articles shown in this review cover the time period from 2019 until the present. Although epidemic prediction plays an significant role in the formulation of epidemic prevention measures, there are not many reviews on the application of Markov chain in epidemic prediction.

3. Main Body

Markov chain is a directed state transition expression of Template Conditional Probability Distribution (TCPD). The nodes of Markov chain are states, and the edges are transition probabilities. The Markov process jumps between states with transition probability as an automaton. Consider $\{X_n, n \geq 0\}$ is a random process that takes a finite or sortable number of values. The set of states is $S = \{0, 1, 2, \dots\}$. If $X_n = i$ shows that the process is in state i at time n , and for any $n \geq 0$, this process satisfies the following formula, it is a Markov chain.

$$\mathbb{P}(X_{n+1} = j \mid X_0 = i_0, X_1 = i_1, \dots, X_n = i) = \mathbb{P}(X_{n+1} = j \mid X_n = i) \quad (1)$$

To represent this effect in a probabilistic model, it is necessary to relax the assumption of independent identically distribution. One of the simplest ways is Markov model. Markov model represents the joint probability distribution of observation sequence[2].

3.1. Data Source

The experimental data sources for the paper on using the Markov chain model to study covid19 related problems can be divided into three categories, as shown in Table II. First is the authoritative organizations around the world, such as WHO, ECDC; Secondly, the source of data can be collected from the national and regional government medical departments like DSHS and DPH. Moreover, Related research done by different universities (Northwestern University, John Hopkins University) are also be included in the data source. The obtained data is mostly based on confirmed cases and fatalities in a certain nation or area within a specified time period. The directions and objectives of these selected research papers are mainly concentrating on predicting the evolution of COVID-19, which includes evaluating the peak position and the number of confirmed COVID-19 developers, estimating the infection and mortality rates, forecasting the end time of the outbreak) and finding the factors that may affect the spread of COVID-19, such as social contacts, governmental policy, mobility restriction. Besides, Other data are also used in some studies as the objectives and areas of these study are not the same. For example, to establish the most probable sequence of observable symptoms, and compare the whole process of these symptoms in COVID-19 to the progression of other respiratory diseases, the influenza, MERS, SARS patient's dataset were also used.

3.2. Data Process

3.2.1 Data Cleaning

Data cleaning is the process of identifying and fixing (or deleting) corrupt or erroneous data from a record set, table, or database. The process of data cleansing begins with identifying missing, inaccurate or irrelevant data, then supplementing, replacing original data or removing coarse data, resulting in filtered, desired data. Specifically, completing missing values, smoothing or eliminating outliers, and resolving data discrepancies consists the fundamental part of data cleaning. If users believe the data is tainted, they will be less trusting of the mining results obtained from it, signaling that the output results are erroneous. In Suryaningrat's research, After obtaining the data set required

for the experiment, they first delete the unnecessary variables and select only a few types of data for the attributes required by the research, which are “id”, “create at” and text[3]. Then they found two outliers in the dataset by observing the data graph. Outliers may have an effect on the performance of the models produced. The two outliers deviate significantly from the mean of the whole set of data. This issue is then resolved by either deleting outlier data and substituting the median of all data for them, or by computing the state space using the median. Besides, In Mas research, they use statistical methods(normal distribution) to find the outliers: If the data has a normal distribution, it deviates beyond 3 sigma from the mean. Points within the range of $P(|x-u|>3\sigma)\leq 0.03$ are usually defined as outliers. Fortunately there is no outliers in their datasets after data cleaning[4]

3.2.2 Data Normalization

Inconsistencies in the data's dimensions and wide discrepancies in its values are common in data processing and the results of data analysis may be impacted by these errors. Under that circumstances As a result, the data must be scaled to fit into a certain region in order to permit complete the data analysis, which is called data normalization. Data normalization is used in Omran's research, they use MinMaxScaler, which is a library in Python, to scale dataset between 0 and 1. The reason for this is because LSTM and GRU models prefer to deal with data inside the range of their activation function[5]. Also, in order to better fit the selected data with Adam optimizer, Ma and other researchers normalized the data using the following formula[4].

$$X_i = \frac{(X_i - \min)}{(Max - Min)} \quad (2)$$

Table 1. Summary:Direction & Objective Of Research

Author	Direction & Objective
Donsimoni, Jean Roch, et al. [6]	Expect the peak numbers of Coronavirus sick people in Germany. Analyze the impact of government rules Predict the expected end date of the CoV-2 epidemic.
Marfak, Abdelghafour, et al. [7]	Predict the COVID-19 evolution in Morocco
Dehghan Shabani, et al. [8]	The dynamics of COVID-19's geographical distribution and its prediction in 40 Asian nations.
Larsen, Joseph R., et al. [9]	Determine the most probable order of visible symptoms in COVID-19 individuals Compare the evolution of these symptoms in COVID-19 to the progression of symptoms in other respiratory illnesses to identify if the illnesses manifest differently.
Ma, Ruifang, et al. [4]	Predict the COVID-19 evolution
Du, Z. C., et al. [10]	Estimate the age-specific case fatality rate of COVID-19.
Hassan, Md Nazmul, et al. [11]	Estimate the probability of Covid-19 outbreak Predict the COVID-19 evolution
Oka, Tatsushi, et al. [12]	Evaluate the influence of mobility restrictions on the transmission of diseases across areas
Wong, George N., et al. [13]	Estimates the peak position and severity (Predict the COVID-19 evolution) Forecast the regional-dependent results of releasing stay-at-home orders

Table 2. Summary:Contents of data in resarch

Author	Data Source	Data type	Time	Country	Sample Number
Donsimoni, et al. [6]	1) The World Health Organisation's Situation reports on the progress of COVID-19 2) The dataset put together by the nCoV-2019 Data Working Group	Confirmed COVID-19 Cases	2020	Germany	Daily cases
Marfak, et al. [7]	Laboratory of Health Sciences and Technology, Higher Institute of Health Sciences, Hassan First University of Setta	The data matrix consists of cumulative number of the COVID-19 confirmed, recovered, active and death cases	Mar 13,2020-- Jul 10, 2020	Morocco	15328(243 deaths)
Dehghan Shabani, et al. [8]	ECDC (European Centre for Disease Prevention and Control)	Confirmed COVID-19 Cases	Feb 9, 2020— Jul 27, 2020	40 Asian Countries	6,680
Larsen, et al. [9]	1)The World Health Organisation's Situation reports on the progress of COVID-19 2) The China Medical Treatment Expert Group for COVID-19 3) University of Michigan 4) Northwestern University Feinberg School of Medicine	1,2) Confirmed COVID-19 Cases) 3) The influenza dataset 4) MERS patients, and SARS patients	1) Feb 16-- 24, 2020 2) Dec 11,2019 -- Jan 29, 2020 3) 1994-- 1998	1,2) China 3) North America, Europe, Southern Hemisphere	1)55,924 2)1099 3)2470 4) MERS (245) SARS (357)
Ma, et al. [4]	The dataset put together by the nCoV-2019 Data Working Group at Johns Hopkins University	Confirmed COVID-19 Cases	Mar 1, 2020--Dec 31, 2020	USA, Britain, Brazil, and Russia	Daily cases
Du, et al. [10]	The National Health Commission and China CDC (Chinese Center for Disease Control and Prevention)	Confirmed & Death COVID-19 Cases	Jan 20,2020— Mar 24, 2020	China	Daily cases
Hassan, et al. [11]	The Texas Department of State Health Services (DSHS)	Confirmed COVID-19 Cases	Mar 6, 2020-- Jan 31, 2021	America	Daily cases
Oka, et al. [12]	1)The National Health Commission of China and its affiliates 2)Baidu Migration	1) Confirmed COVID-19 Cases 2) Individuals' mobility	Jan 11,2020--- Mar 15, 2020	China	Daily cases
Wong, et al. [13]	Illinois Department of Public Health (IDPH)	Hospital and ICU room occupancy by patients, the number of daily deaths of COVID-19	2020	America	Daily cases

3.3. Model Construction and Optimization

The models of Markov chain in prediction of the epidemic section were divided into sub-categories including naïve Markov chain model, extended Markov chain model, and Markov chain Monte Carlo (MCMC). The related papers are organized in the structure shown in Fig. 1.

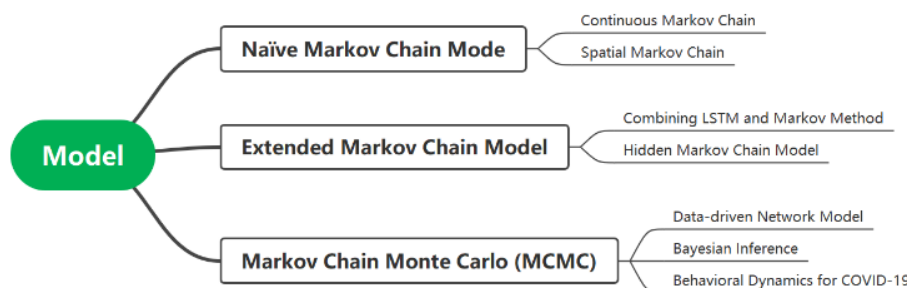


Fig 1. The structure of the arrangement of the papers related with models

3.3.1 Naïve Markov chain Models

One example of naïve Markov chain applications is using continuous Markov-chain model to forecast the spread of COVID-19 infection [14]. To begin with, some parameters reflecting the space-time change of the epidemic effectively were selected to construct an infection probability matrix. Then the mutational effect of the virus and the attenuation of antibodies were added to Markov chain model. Afterwards, real data was used to examine the effect of the expanded model including the aforesaid aspects. Finally, the full equipped model is able to estimate the COVID-19 pandemic. Another study that used for epidemic prediction developed a spatial Markov chain for examining the space effects on dynamics of epidemic distribution[15]. First, this study determined the COVID-19 spread dispersion dynamics and the steady-state, indicating what will occur if current COVID-19 restrictions were followed. Then by using the spatial Markov chain model to study the space distribution dynamics of COVID-19 in Asian countries, it found that linear regression, the normal distribution, and some other constraints were useless to the research on the space effect of COVID-19. Particularly, this model considers the influence of locations to the likelihood of migrating between COVID-19 classes.

3.3.2 Extended Markov chain Model

Sometimes only using Markov chain may cannot attain the expected effect. In order to save the strengths of Markov chain model and avoid the drawbacks, the extension of Markov chain is studied. In the following study, the authors suggested an LSTM-Markov model that employs the Markov model to reduce the LSTM model's prediction error[4]. In order to use historical case data to construct a prediction model for long-term prospective epidemic modes with effect, this research used Markov chain model to make up for the shortcomings of the LSTM models, which usually had low accuracy when making long-term prediction. This is because the Markov chain model supports comprehensive data partitioning, which avoids the error of the LSTM model augmenting over time, allowing the LSTM model's prediction performance to improve. Another work proposed using the Hidden Markov chain to predict COVID-19 evolution in a given country for a period of time[16]. This work is aimed to help Moroccan authorities develop appropriate protocols to contain the progress of the COVID-19 outbreak. It investigate the cumulative number of confirmed, recovered and active cases recorded over a period of time to construct a predictive data matrix for the total number of different kinds of cases.

3.3.3 Markov chain Monte Carlo (MCMC)

Another important application of Markov chain is Markov chain Monte Carlo (MCMC). In this paper, a projective model for repressive strategies was constructed to assist the policy makers in the planning of regulatory measures [17]. The transmission of virus among people is designed as a network model with individuals as nodes and the transmission relationship between individuals as

edges. Individuals were classified according to the number of day-by-day interactions (node degree) and whether they were infected. The Markov chain Monte Carlo method was used to fit the transmission network model with COVID-19 outbreak data published in Wuhan (China), Toronto (Canada), and the Republic of Italy. Another study uses Markov chain Monte Carlo (MCMC) methods to estimate Bayesian parameters for the Susceptible-Infected-Recovered (SIR) and Susceptible-Exposed-Infected-Recovered (SEIR) epidemiological models with time-varying spreading rates for South Africa [18]. Considering some of the observed COVID-19 phenomena, the study modified SEIR and SIR models to fit the epidemic data from South Africa and used MCMC to perform Bayesian inference on the model parameters. Another work used a modified SEIR model to estimate the COVID-19 pandemic transmission across 92 countries and it got enough data in all the countries for modelling [19]. The model monitors people with different health states in each country, including those who are vulnerable, who are pre-symptomatic, who are infected, who have recovered or who have died. It modifies the SEIR model to make explicit statistics of individuals whose cases are detected or not reported, and who are hospitalized or not. In addition to the wide range of data, the model designed three novel features, including infection fatality rate (IFR), symptom severity, and Perceived risk. Then it used the Markov chain Monte Carlo method suitable for high-dimensional parameter space to estimate the parameters.

Table III summarizes the above papers for the model construction and optimization sub-category.

Table 3. Summary: model construction and optimization

Sub-category	Time	Author	Access	Models/Algorithms	Findings
Naïve Markov chain Model	2022	Z. Xu et al.[14]	https://doi.org/10.3390/biology11020190	Continuous Markov-Chain Model	Herd immunity threshold $\gg 1 - 1/R_0$
	2020	Z. D. Shabani et al.[15]	https://doi.org/10.1111/rsp3.12372	Spatial Markov chain approach	1. With the policies at the time, COVID-19 in Asia $\rightarrow 0$. 2. The expansion of COVID-19 was influenced by the neighbors.
Extended Markov chain Model	2021	R. Ma et al.[4]	https://doi.org/10.1038/s41598-021-97037-5	Combining LSTM and Markov method	The modified model's prediction curve is more similar to the real epidemic curve; the mean RMSE is reduced by 40%, the R2 values are all near 1, and the average error is more than 75% lower than LSTM model.
	2020	A. Marfak et al.[16]	https://doi.org/10.1016/j.dib.2020.106067 , (https://www.sciencedirect.com/science/article/pii/S2352340920309616)	hidden Markov chain	Offer both actual and anticipated data matrices for the cumulative to of different types of cases for the time period investigated.
Markov chain Monte Carlo	2020	L. Xue et al.[17]	https://www.sciencedirect.com/science/article/pii/S0025556420300730	data-driven network model	Ways of limiting viral exposure minimize the spread of COVID-19.
	2020	R. Mbuva et al. [18]	https://doi.org/10.1371/journal.pone.0237126	Bayesian inference	The control of imported illnesses, school closures, and stay-at-home orders have all contributed to a 60% fall in the mean spreading rate.
	2021	H. Rahmandad et al. [19]	https://doi.org/10.1002/sdr.1673	Multi-country modified SEIR model	Underreporting is widely severe and varies greatly between countries.

3.4. Evaluation

In the references of our study, most of the literature is evaluated based on the model built and the graphs provided by the data, as shown in Table IV. This approach takes full advantage of the results of the modeling. Some evaluation approaches compare the study's own proposed model curves with the actual curves: comparing the LSTM-Markov model with the LSTM model reveals that the LSTM-

Markov model has a lower average error rate. In terms of prediction, the model also accurately predicts the subsequent trend[4]. Another approach to the analysis emphasizes the importance of choosing the appropriate data to calibrate the model and to do so precisely. Because of the large number of parameters that inevitably enter the epidemiological model, calibration requires parameter inference in a high-dimensional space, which is likely to be improperly fitted due to failure to achieve global optimality. Since there will be uncertainty in many variables in the prediction, then the model prediction must systematically take into account this variable uncertainty and finally complete the evaluation of the model by giving a model that takes into account the synthetic data[14]. The analysis of important components provides a forecast of the broader trend. For example, we selected key cities in mainland China and analyzed the number of exported cases and infections in these cities and combined them with graphs to predict future epidemiological trends. In addition, as flights from mainland China, mainly from Beijing, Shanghai, Shenzhen and Guangzhou, are predicted to deliver infected cases to other countries, other countries are predicted to face epidemic attacks in the future as well[20]. The PMCMC method was used to conduct the analysis by integrating data from Ethiopia, Nigeria, Tanzania and Zambia, as these four countries provided good estimates of the model parameters. Moreover, in most cases, the fitted bands generated by the PMCMC algorithm can cover the time series of cumulative cases well. Finally, the predicted data were adjusted in the context of reality, because although the fitted curves could cover the cumulative number of reported cases well, the underlying reproduction number in Tanzania might be underestimated, while the same similar situation occurred in Ethiopia[21]. The evaluation method is the processing and analysis of the data modeling, refining and correcting the data drawn from the model built.

Table 4. Summary: Model Evaluation

Time	Author	Access	Models/Algorithms	Findings
2019	Joseph T Wu, et al.	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7159271/	Markov chain	Outbreak in major Chinese city grows exponentially, but lags Wuhan by 1-2 weeks [20].
2021	Benyu Shi, et al.	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7788178/	Markov chain, SEIR Model	The earlier the intervention is implemented, the better the epidemic will be controlled [21].
2020	Wong George, et al.	https://www.osti.gov/pages/biblio/1714406	Markov chain, MCMC Model	report the median and the 68.4% and 95.6% confidence intervals of several dynamical outputs of our model [13].
2022	Zhaobin Xu, et al.	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8869237/	Markov chain, SIR Model	herd immunity thresholds do not provide protection against infection [14].
2021	Amit K Chattopadhyay, et al.	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8173017/	Markov chain, SIRV Structure, ML Prediction, PHIRVD Model	Detailed temporal distribution of future reproduction numbers verified by real data [23].
2021	Zahrte El Oula Frihi, et al.	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7891107/	Markov chain, SIR Model	presented a user-friendly toolbox for the simulation of the propagation throughout multiple regions [22].

4. Dicussion

Although hundreds of studies have been published and numerous models have been constructed on the forecast of the COVID-19 epidemic, their models still have flaws. The following is three problems that exist in most of the models. First is that most studies of the epidemic's transmission pattern employ the reproductive number R_0 as a measurement index. The herd immunity threshold, on the other hand, does not have a straightforward relationship with its R_0 . The actual herd immunity threshold could be substantially greater than the R_0 -derived one. As a result, the conclusions are less

effective. Another is that, despite the fact that those models offer a lot of promise for stimulating more realistic statistical data, they haven't used them in real life because the data isn't available. Finally, the influencing elements only take into account the surface factors that are directly related to the epidemic, such as the number of confirmed cases, rather than other influencing factors like gender, age, occupation, or geography.

By understanding the limitations we begin to analyze the previous research unfolding. We first optimize the models, including the naive Markov chain model, extended Markov chain model, and Markov chain Monte Carlo (MCMC), and then analyze the data sources and data processing, such as the different objectives and domains involved in the different directions of the study, and the overlap rate and utilization rate after using multiple data. The process of data processing also needs to be re-examined, such as the method of classifying data into categories, and the accuracy of the categories, as many studies simply classify data into yes and no, which often requires further study. Finally there is also a need to analyze the evaluation methods. Most of the assessments incorporate graphs and the models built, but they still need to be corroborated by the actual situation. In many cases, actual conditions can help reduce errors and lead to more accurate predictions.

5. Conclusion

In conclusion, Markov chain models are used to forecast stationary random events quantitatively using the autoregressive process approach. It is a forecasting method for predicting the changes of events at various moments (or periods) in the future based on the current state of the event. Due to the magnitude of the damage produced by COVID-19, it is vital to employ Markov chains to create models of infectious illnesses in order to forecast epidemics and execute preventative measures. Recent research use Naïve Markov chain model, or combine Markov chain model with LSTM model to predict the evolution of Covid-19, confirm the morbidity and fatality of Covid-19, and analyze factors that influence the spread of the Covid-19. Researchers also apply Markov chain to Monte Carlo optimization algorithm to find effective ways to control imported illnesses, limit and minimize the spread of Covid-19. It is undeniable that some current studies have certain limitations. To illustrate, many research employ the reproductive number R_0 as a measurement index, which does not have a direct relationship with the herd immunity threshold. Also, the selection of data and the impact of other influencing factors on the experimental results still need to be more carefully considered. Re-examining the data, such as the method of classifying data into categories, and the accuracy of the categories, and corroborating the model and assessment to the actual situation should be taken in consideration in the future studies.

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