Markov chains as a simulation technique for epidemic growth

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***Abstract*—Modeling various phenomena occurring in nature allows us to predict future effects in reality. One of such example is modeling the growth of infection in a given population depending on various parameters. In this article, we show the use of discrete Markov chains in order to model the epidemic with distinction into four states in which individuals in the population may be. More accurately – healthy, infected, sick and recovered. The article presents a mathematical model describing the phenomenon together with a calculation example and simulations. The obtained results were described and discussed.**

Keywords: discrete Markov chains, epidemic growth, mathematical model, simulation

I. Introduction

Stochastic processes are a family of random variables defined in a certain probabilistic space. It is the field of the probability theory, which in today's science has become one of the most dynamically developed fields due to the numerous applications in optimization techniques or artificial intelligence. Such processes enable defining various phenomena based on a certain probability of its occurrence, as well as its components.

The field of stochastics found its place in the theory of optimization, where Lévy and Poisson processes were used in modeling various types of phenomena occurring in nature. Optimization theory has gained the most, where techniques inspired by nature have been created to this day. An example is the cuckoo algorithm intended originally to search for extremes of function. The movement of these birds was modeled using the Lévy flights. In [1]–[3], the author presented the idea of searching key-points on images which can be used for feature extractions. Proposed idea is important in security because using stochastic algorithms almost guarantees finding other features due to the random placement of individuals in the population at the beginning of the algorithm. With similar motives in [4], [5], the author showed the use of these algorithms in two-dimensional games, where such an algorithm can be used to model the opponent's movement. Additionally, in [6]–[8], heuristic approach was used in different games. Similar algorithms are genetic ones based on chromosomes. Their use is visible in route planning programs [9]–[11], whether the deployment of service stations in some area due to existing roads and their traffic [12].

Another application is artificial neural networks, where there is a specific variation thereof with a stochastic note. In [13], [14], the authors model such networks and analyze the flow of information. Hybrids are also created, such as the connection of heuristics with neural networks [15]. Not only neural networks, but other artificial intelligence algorithms are used in practical terms, an example of which is optimization green computing awareness [16]. Another interesting idea is modeling of contaminant transport in porous media and monitoring of water quality [17], [18].

In this paper, we describe one of the classic stochastic tools such as Markov chains. We show their use in modeling the epidemic phenomenon and pay attention to their use in forecasting future phenomena.

II. Markov chains

The process $\{X_n, n \geq 0\}$ of state space S is called the discrete Markov chain, if for each $n \in \{0, 1, \dots\}$, the following equation occurs

$$\begin{aligned} P\{X_{n+1} = i_{n+1} | X_n = i_n, \dots, X_0 = i_0\} \\ = P\{X_{n+1} = i_{n+1} | X_n = i_n\} \end{aligned} \tag{1}$$

for all possible states $i_0, \dots, i_{n+1} \in S$.

It is a mathematical model of a random phenomenon evolving over time in such a way that the past affects the future only through the present. This model has state space S, where we can give the following properties

1) S it is a finite or at most a countable set of states,
2) $S = \{0, 1, 2, 3, \dots\}$,
3) $X_n = i$, what means, that at time n, the process is in the state of i.

Let us define the initial distribution of states, i.e. the distribution of the variable X_0. A probability vector as $\pi = [p_0, p_1, \dots]$. For each state $i \in S$, we have

$$p_i = P\{X_0 = i\}. \tag{2}$$

In addition, we define the probability of transition between two specific states. It is determined using a matrix $\mathbf{P} = (p_{ij})$. If S is a set defined as $(1, 2, \dots, m)$, than a matrix $\mathbf{P}$ has dimension equal $m \times m$. As p_{ij}, we can define the probability

of going from one state i to another j in one step. Generalizing this, we have

$$p_{ij} = P\{X_{n+1} = j | X_n = i\}. \tag{3}$$

Using the initial vector π and the probability matrix $\mathbf{P}$, we define the Markov chain. And its behavior is defined using a stochastic matrix $\mathbf{P} = (p_{ij})$.

We assume that every element of such a matrix must be greater than 0 and the sum of elements of each row must be 1. This matrix has the following form

$$\mathbf{P} = \begin{pmatrix} p_{11} & p_{12} & \cdots & p_{1m} \\ p_{21} & p_{22} & \cdots & p_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ p_{m1} & p_{m2} & \cdots & p_{mm} \end{pmatrix} \tag{4}$$

If the Markov chain is in the state i at n, then the probability of being in the state j after k periods is defined as follows

$$P(X_{n+k} = j | X_n = i) = P(X_k = j | X_0 = i) = p_{ij}(k), \tag{5}$$

where probabilities are independent of n, $p_{ij}(k)$ is an element at position (i, j) in $\mathbf{P}^k$.

III. Markov chains for epidemic simulations

The spread of infection can be represented using a mathematical model – a discrete Markov chain. In this model, we divide the population into four groups marked as states S=$\{0, 1, 2, 3\}$, i.e.

- 0 – susceptible sus,
- 1 – infected inf,
- 2 – sick $sick$,
- 3 – recovered rec.

Unfortunately, there is no way to create a perfect model, that is why we create several assumptions that simplify this model

- a healthy person can become infected with an infection,
- an individual in the infected group may go only to the disease state,
- a sick subject can leave a group of patients only through complete recovery,
- recovery guarantees immunity,
- immunity is not inherited
- age, sex and social status do not affect the probability of infection,
- climate or demographic changes do not affect the epidemic.

For such assumptions, the stochastic matrix can be defined as

$$\begin{pmatrix} p_{sus,sus} & p_{sus,inf} & p_{sus,sick} & p_{sus,rec} \\ p_{inf,sus} & p_{inf,inf} & p_{inf,sick} & p_{inf,rec} \\ p_{sick,sus} & p_{sick,inf} & p_{sic,sick} & p_{sick,rec} \\ p_{rec,sus} & p_{rec,inf} & p_{rec,sick} & p_{rec,rec} \end{pmatrix} \tag{6}$$

where p is the probability of changing states at t to $t+1$. An initial vector can be represented as

$$\mathbf{P}_0 = \begin{pmatrix} n_{sus} & n_{inf} & n_{sick} & n_{rec} \end{pmatrix}, \tag{7}$$

where n is the number of individuals in specific group at the initial stage.

IV. Experiments

A. Numerical example

Let us assume that at the beginning of our experiment, the population is made up of a thousand people, where 495 people are healthy, 3 are infected and 2 are sick. Hence, the initial vector is

$$\mathbf{P}_0 = \begin{pmatrix} 495 & 3 & 2 & 0 \end{pmatrix}. \tag{8}$$

The stochastic matrix is defined as follows

$$\mathbf{P} = \begin{pmatrix} 0.8 & 0.1 & 0.1 & 0 \\ 0 & 0.35 & 0.4 & 0.25 \\ 0 & 0 & 0.85 & 0.15 \\ 0 & 0.05 & 0.02 & 0.93 \end{pmatrix}. \tag{9}$$

After the first iteration, there is

$$\mathbf{P}_0\mathbf{P} = \begin{pmatrix} 495 & 3 & 2 & 0 \end{pmatrix} \begin{pmatrix} 0.8 & 0.1 & 0.1 & 0 \\ 0 & 0.35 & 0.4 & 0.25 \\ 0 & 0 & 0.85 & 0.15 \\ 0 & 0.05 & 0.02 & 0.93 \end{pmatrix} = \\ = \begin{pmatrix} 396 & 51 & 52 & 1 \end{pmatrix}. \tag{10}$$

After the second iteration, there is

$$\begin{pmatrix} 396 & 51 & 52 & 1 \end{pmatrix} \begin{pmatrix} 0.8 & 0.1 & 0.1 & 0 \\ 0 & 0.35 & 0.4 & 0.25 \\ 0 & 0 & 0.85 & 0.15 \\ 0 & 0.05 & 0.02 & 0.93 \end{pmatrix} = \\ = \begin{pmatrix} 317 & 57 & 104 & 21 \end{pmatrix}. \tag{11}$$

B. Simulation experiments

Simulations were conducted for two stochastic matrices. The first of these was described by the Eq. (9) and the second one has the following form

$$\mathbf{P} = \begin{pmatrix} 0.8 & 0.1 & 0.1 & 0 \\ 0 & 0.59 & 0.4 & 0.01 \\ 0 & 0 & 0.99 & 0.01 \\ 0 & 0.05 & 0.02 & 0.93 \end{pmatrix}. \tag{12}$$

Both matrices are similar but differ in the selected values. In the second matrix, the probability of transition from the infected to recovered and sick to the recovered state drastically changed, which means minimal chance of recovery. In all simulations, we assumed that the population is composed of 500 individuals. The effect of the difference in people needed for the spread of the disease on the entire population was examined. Tests were performed for the population composed of 1000000 individuals in population and 1 sick for two different step (time) values – $\{25, 150\}$. The results are shown in the form of diagrams in the Fig. 1–4. It is easy to see that the charts are identical regardless of the initial vector parameters (for the same probability matrix). Hence, the simple conclusion that Markov models allow simulation of the epidemic phenomenon, but the initial vector has little effect. Mainly stochastic matrices play a role, thus estimating the probability of transition between selected states.

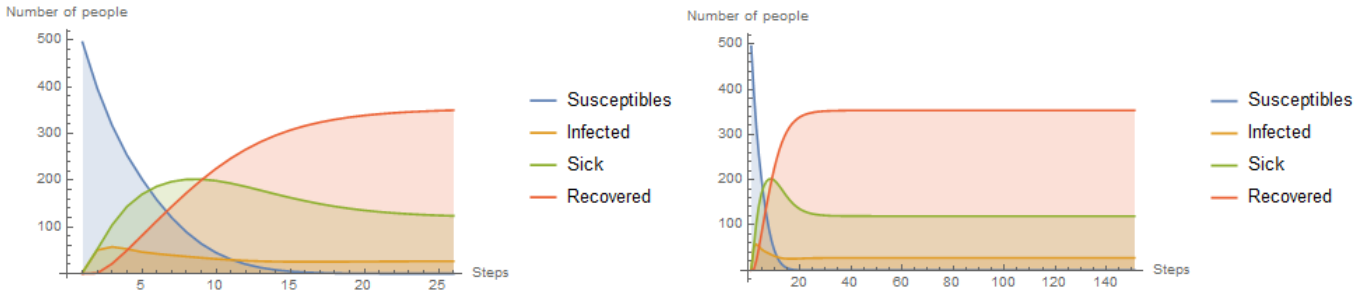

Figure 1: Measurements for the first matrix and population $\{495, 3, 2, 0\}$.

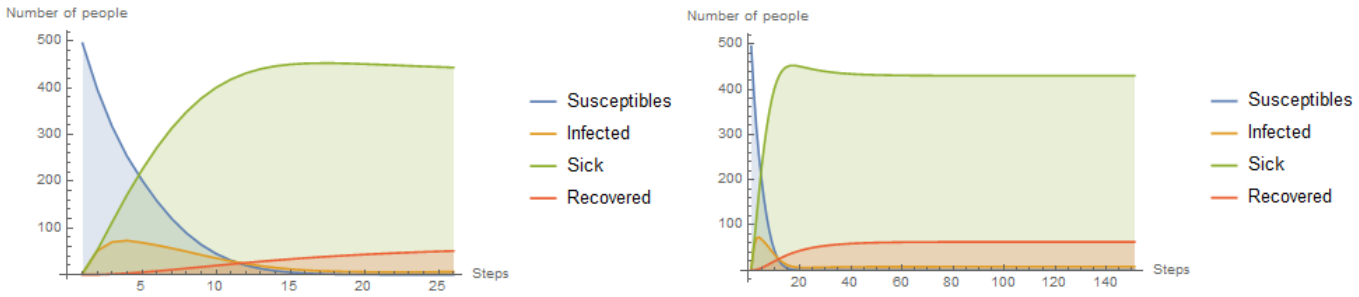

Figure 2: Measurements for the second matrix and population $\{495, 3, 2, 0\}$.

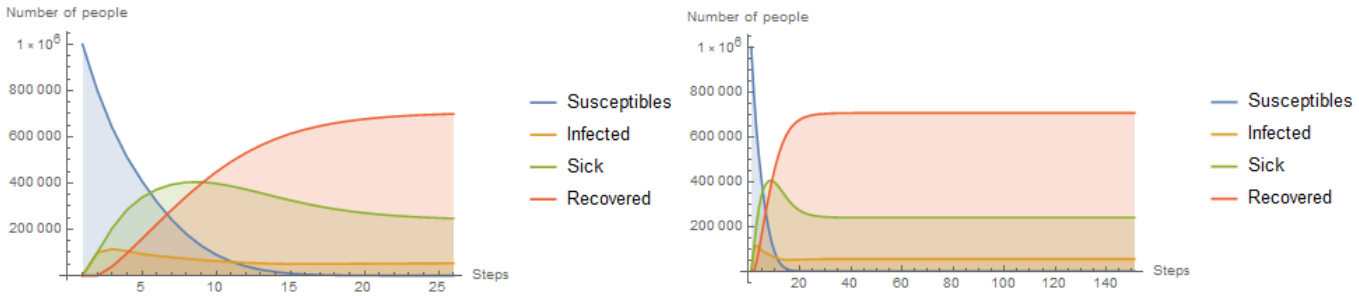

Figure 3: Measurements for the first matrix and population $\{1000000, 0, 1, 0\}$.

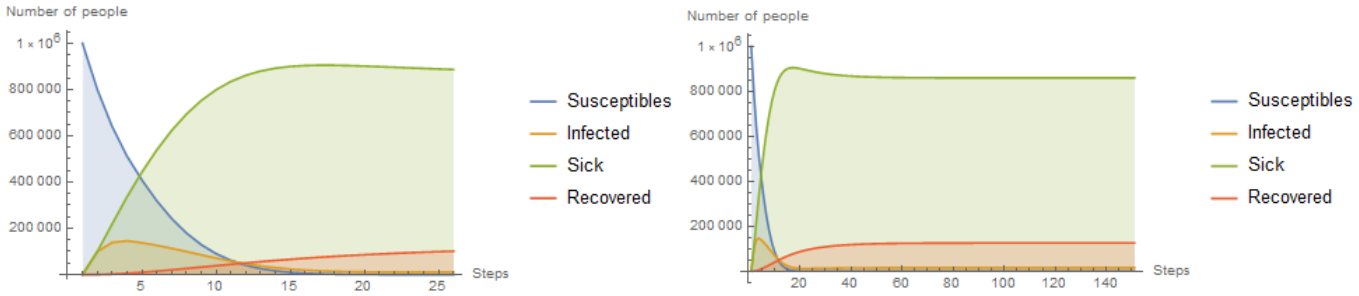

Figure 4: Measurements for the second matrix and population $\{1000000, 0, 1, 0\}$.

Note that in the probability of transition from infected and sick to healed state are 25% and 15%. In the population the average number of healthy is around 80% people and it stays independent of the step. Large differences in jumps between the population can be seen in the first 20 steps, where the population is infected and gets ill. The further step, the more stable the chart is, which may be due to the lack of changes in the stochastic matrix. From a practical point of view, the infection can evolve, and then these matrices can change. Unfortunately, the classic approach to Markov's chains does not modify the matrix during operation, although there are models that can do it. Impact on these matrices will result in a much better realignment of the model.

For the experiments we have carried out, we have performed statistical tests. On the significance level $\alpha = 0.1$, we also verify the hypothesis about the compatibility of the data distri-

Table I: Statistical tests for susceptible table

	Statistic	p-value
Anderson-darling	12173.87	0
Cramer-von Mises	34.27	0
Kolmogorov-Smirnov	0.84	$1.59 \cdot 10^{-95}$
Kuiper	0.92	$6.11 \cdot 10^{-114}$
Pearson χ^2	1573.91	$5.65 \cdot 10^{-328}$
Watson U^2	11.52	0

Table II: Statistical tests for infected table

	Statistic	p-value
Anderson-darling	406.59	0
Cramer-von Mises	45.77	$1.22 \cdot 10^{-15}$
Kolmogorov-Smirnov	0.93	$8.45 \cdot 10^{-117}$
Kuiper	0.93	$3.19 \cdot 10^{-115}$
Pearson χ^2	2084.21	$4.73 \cdot 10^{-438}$
Watson U^2	11.69	0

bution with the Gamma distribution with the shape parameter equal to 1 and the scale parameter equal to 2, which results are presented in Tab. I–IV. According to the tests carried out, in the case of each table presenting the process of healthy, infected, sick, recovered, at the significance level $\alpha = 0.1$, we can reject the hypothesis about the compatibility of the distribution of data with the Gamma distribution with the parameter equal to 1 and scale parameter 2.

V. Conclusion

Discrete Markov chains allow us to model phenomena occurring in nature. Each step depends on the previous one, although there is no change in probabilities during operation. This is a quite serious shortcoming in predicting the future effects of the model. In the analyzed case of epidemic spread, such action resulted in the absence of a possible mutation of the disease. However, it is worth noting that if the disease started to be fatal after a certain amount of time, in the case of the second matrix, it could kill almost the entire population, as opposed to the first one.

This type of modeling of phenomena may allow us to improve the predictions of some phenomena that depend only on selected states and the table of probabilities. The number of states can be huge, but then the problem arises to create such a matrix and find its coefficients. The simulations showed that there is a large impact of even a small change in the main matrix.

Table III: Statistical tests for sick table

	Statistic	p-value
Anderson-darling	22104.23	0
Cramer-von Mises	49.74	0
Kolmogorov-Smirnov	0.99	$3.04 \cdot 10^{-132}$
Kuiper	0.99	$9.11 \cdot 10^{-131}$
Pearson χ^2	147.19	$2.61 \cdot 10^{-24}$
Watson U^2	12.35	0

Table IV: Statistical tests for recovered table

	Statistic	p-value
Anderson-darling	3601.29	0
Cramer-von Mises	46.94	$6.66 \cdot 10^{-16}$
Kolmogorov-Smirnov	0.95	$3.19 \cdot 10^{-122}$
Kuiper	0.95	$2.19 \cdot 10^{-122}$
Pearson χ^2	1967.18	$8.61 \cdot 10^{-413}$
Watson U^2	12.04	0

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