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Markov chain and queuing theory in nucleic acid tests

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Abstract. This article mainly introduces M/M/1 queue and M/M/S queue applied in nucleic acid tests which are applications of Markov chains in queuing theory. Firstly, it is pointed that in the two kinds of queuing models, the arrival time and the service time have no aftereffect which means the two kinds of time both belong to the Markov chain, and it is also illustrated that the arrival time and the service time obey the Poisson distribution, which reflects the uniqueness and stability of the two types of queuing models. The distribution functions of waiting time, service time queue length and so on could be obtained by solving the models. Therefore, by comparing the advantages and disadvantages of different models, the managers could make better decisions which are helpful to allocate resources reasonably, avoid overcrowding and decrease the risk of virus transmission. Furthermore, some other queuing models which are in the more special cases and the innovations of many queuing models are also presented briefly. In the end, the applications of such queuing models in other fields are shown.

Keywords: Markov chains, queuing theory, M/M/1 queue, M/M/s queue, nucleic acid tests.

1. Introduction

Nowadays, the prevention and control of the epidemic situation is still serious as the novel corona virus spreads quickly and easily, so it's important for the public to finish the nucleic acid tests regularly. As we all know, the nucleic acid tests are usually accompanied by the consumption of human resources, and often need people to wait in line. Therefore, it is inevitable that unreasonable human resource management and people queuing congestion will occur which not only bring economic losses but also hinder the development of work of nucleic acid test. Thence, it is of great importance to predict the queue situation and develop corresponding strategies. There are many public service places in life that are suitable for queuing models, such as supermarkets, banks, hospitals, etc. Therefore, establishing an appropriate queuing model is conducive to helping achieve the above goals.

Norris explains Markov Chains in detail in this book, and introduce the basic principle and models of queues and queueing networks such as M/M/1, M/M/s and some other queuing models briefly in the book, many useful examples which could help strengthen the understanding of readers could also be found in the former exercises [1].

Ai et al. analyzed the queues at outpatient pharmacies by using the M/M/1 queue and M/M/s queue, and the corresponding data which could help put forward a suitable model, meanwhile they also take into account the problem of long-range correlation and raise the importance of obtaining long-term historical data because of the influence of various factors [2]. He creates a new formula which is about the distribution of queue length in the queueing system M/M/1, and gives a new and simple proof of the ergodicity of this system by means of renewal theory. Meanwhile, he also proposed to extend the method to other models like the M/G/1 queue and GI/M/1 queue [3].

Zhou et al. propose to establish the differential equation system of M/M/1 queuing system and use Laplace transform to it. Then the transient distribution of queue length which is in the form of a Laplace transform could be obtained which is helpful to get the information in the queue in time [4]. Xiao introduces and analyses the theoretical method of M/M/1queue and M/M/s queue in detail through probability theory and stochastic process, he not only calculates the parameters, but also listed many examples to illustrate the economic analysis methods for M/M/s decision model and demonstrate the usefulness of the model [5].

Ling et al. take nucleic acid testing in an urban area as an example, and take into account factors such as work intensity. By analyzing the results of M/M/s queue under different conditions, some optimization plans of staff assignments have been developed which ensure the rational use of personnel and avoid waiting too long in queues [6].

Wang explores the problem of queuing for surgery and proposes to use the Markov chain queuing models to make a quantitative analysis and discussion which is helpful to avoid empty service windows or overcrowding. A feasible strategy has been given by analyzing the queuing model M/M/s [7]. Liu et al. propose to use different queuing models in the bank queuing, and come to the conclusion that a large queue is more efficient than some small queues by comparing the efficiency of different models, at the same time, they also remind us that the random arrival law in the real queuing problem mostly obeys the Poisson distribution, meanwhile, the characteristics and conditions of the queuing models should be paid attention to [8].

Yan et al. take into account both the congestion and the vacancy in the queue and present a variable that remains to be resolved, thus establishing a new vector Markov process. Through further analysis of the M/G/1 model, some density evolution equations could be established and solved so that distribution functions of some variables could be derived. At the same time, some conditions that can making queuing more stable can be obtained by applying an embedded renewal process [9]. Yin and Xi embed the Markov chains in the M/G/1 queuing system which is much easier than to describe a semi-Markov process of the state of the system, obtain the steady-state performance sensitivity formula in terms of potential energy and optimize the system by discussing the sensitivity analysis of system performance stability [10].

Dai et al. explore the optimal stationary policies of a class of controllable M/G/1 queuing systems embedded by the Markov chains conditional on the infinite average-cost criteria, they also introduce the discounted Poisson equation and give the optimality equation. What's more, a value iteration algorithm and a relevant example are illustrated to demonstrate the feasibility and practicality of the optimization [11].

Liu et al. propose to apply the Markov skeleton processes to study the queuing model GI1+GI2/M/1 which is about the situation of two types of customers arriving at the service point in the same period. Besides the probability distributions of the arriving process, waiting time and queue length in this model have also been obtained [12].

Ran et al. compared the status quo of most hospital queuing systems and proposed a new model scheme based on their own needs to help create a good medical environment. Meanwhile, each process in the scheme is introduced in more detail because of service type complexity, and other pending issues related to queuing systems such as automated services in hospital are also raised [13].

Zhang et al. introduce the queuing model G/Ek/c which is relevant to the Erlang distribution, and explain the principle and parameter estimation of the model in detail. Some suggestions about how to reasonably arrange the number of experts are also made for optimizing the queuing system by applying it in hospital ophthalmology [14].

2. Queuing model

In the queue for nucleic acid testing, suppose that there is one staff at each testing site, and let x be the number of testing sites which x is greater or equal to 1, each testing site is independent of each other and serves at the same time.

Due to the time people arrive at the testing sites, the number of people arriving per unit of time and the time it takes to test are random and independent, therefore, it is easy to know that the number of people who arrive at the testing sites for nucleic acid testing at time t obeys the Poisson distribution, and its parameter λ is the arrive rate.

The testing service time follows a negative exponential distribution since it is also independent and random, let μ be the number of people tested per unit time and take it as the average service rate. The average service rate μ will be based on the official description data, as it is difficult to record the service time such as scanning the QR code and taking the throat swab sampling.

Service Guidelines: The service mechanism of the nucleic acid test queuing system is first-come-first-serve (FCFS), and the random variables are independent of each other.

Queuing problems generally involve the number of people at the testing sites which is the sum of the number of people queuing and the number of people being tested and the total time spent on testing which is the sum of queuing time and service time. By building different queuing models, the equilibrium equation of the corresponding system state probability, the waiting time and queue length can be obtained. Meanwhile, it can help to make better strategies through further comparative analysis of the results.

3. Model establishment and analysis

Now take the nucleic acid testing of a community in the past month as an example. First, collect the number of people and related data that the community has undergone nucleic acid testing every day in the past month, and draw it into a frequency histogram. It is easy to know that the connected data follows a normal distribution and is random through the analysis of figure 1.

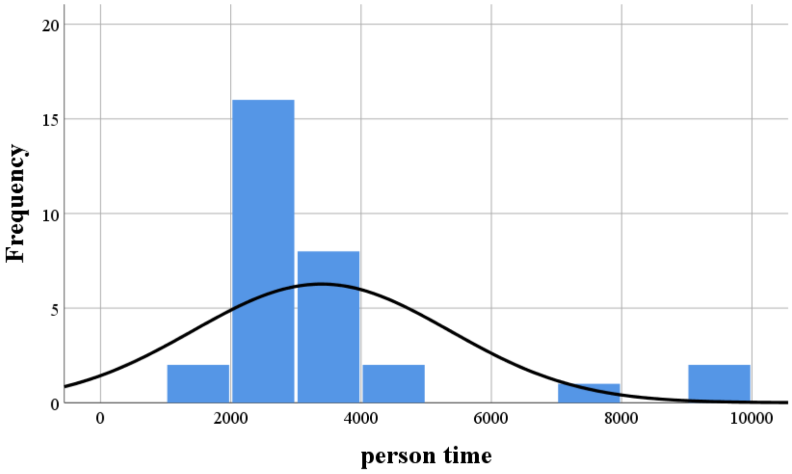

Figure 1. A frequent histogram of daily person time in nucleic acid testing.

By descriptive analysis of the data, the average daily number of nucleic acid tests in the community can be obtained. The working hours of the community nucleic acid testing site have been known that it will start at 8:00 and end at 12:30 in the morning and start at 13:30 and end at 18:00 in the afternoon, which means it will work 9 hours a day. The average service time will be taken from the statement of the medical administrator of the community:7 people can be tested per minute on average.

The way to determine λ: first of all, statistics the number of people who have been tested for nucleic acid every day in a certain area in the past month (31 days), and based on descriptive statistics, the number of people who are tested everyday could be got. Since the time of daily nucleic acid testing has been fixed, the average number of people performing nucleic acid testing per unit time per day can be obtained, and the data also represents the average arrival rate. Thus, it is easy to know that λ=6.28 through Table 1.

Table 1. Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation	Skewness	Kurtosis
person time	31	1811	9819	3389.84	1972.556	2.421	5.388

3.1. Model establishment

It is easy to know that the queuing model turns to be a continuous-time Markov chain from the analysis of the Markov chains and the queuing model, and a certain discrete-time Markov chains could be embedded in the queue by applying the memoryless of the Poisson process of arrivals. Thus, the equilibrium equation of the system state probability can be obtained by using the method of literature.

$$\begin{cases} \mu P_1 = \lambda P_0 \\ (y+1)\mu P_{y+1} + \lambda P_{y-1} = (\lambda + y\mu)P_y, (y = 1,2,3,\cdots, x-1) \\ \lambda P_{y-1} + x\mu P_{y+1} = (\lambda + x\mu)P_y, (y = x, x+1, \cdots) \end{cases} \tag{1}$$

In the above formula: $\sum_{y=1}^{\infty} P_y = 1$, the system reaches steady state if and only if $\rho = \frac{\lambda}{x\mu} < 1$.

stability index：

$$P_0 = [\sum_{y=1}^{x-1} \frac{1}{y!}(\frac{\lambda}{\mu})^y + \frac{1}{x!} * \frac{1}{1-\rho} * (\frac{\lambda}{\mu})^x]^{-1} \tag{2}$$

$$P_y = \begin{cases} \frac{1}{y!}(\frac{\lambda}{\mu})^y P_0, y \le x \\ \frac{1}{x! x^{y-x}} * \left(\frac{\lambda}{\mu}\right)^y P_0, y > x \end{cases} \tag{3}$$

$$L_q = \frac{(x\rho)^x \rho}{x!(1-\rho)^2} P_0; L_s = L_q + \frac{\lambda}{\mu} \tag{4}$$

$$W_q = \frac{L_q}{\lambda}; W_s = W_q + \frac{1}{\mu} \tag{5}$$

In the above formula: L_q represents the average waiting queue length of the system; L_s represents the average queue length of the system; W_q represents the average waiting time of residents in the system; W_s represents the average length of stay of residents in the system; P_0 represents the probability that the system is idle; P_y represents the probability that there are y residents in the system.

3.2. Model solution

M/M/1 queue is the simplest queue of all, and it is a case when x is equal to 1, the number of residents in the queue evolves as a Markov chain.

The queuing model M/M/1 evolves like a random walk and it has some Markov properties such as recurrent, transient, equilibrium and so on, which correspond to the problems to be solved.

As it has already been known that λ=6.28 and μ=4, various indexes of the system can be obtained from the formula (1-5), and the results are shown in the following Table 2.

Table 2. M/M/1 model system stability index.

x	ρ	P_0	L_q	L_s	W_q	W_s
1	0.897	0.103	7.825	8.722	1.246	1.389

M/M/s queue is a variation on the last queue model, and it often has more than 1 servers. As each server is μ, it can be easily known that this queue model performs a Markov chain which is similar to the preceding example.

What's more, a birth-and-death chain can be obtained, and by analyzing the related Markov chains properties and using the above data, the relevant index tables when x=2 and x=3 could also be obtained in Table 3.

Table 3. M/M/s model system stability index

x	ρ	P_0	L_q	L_s	W_q	W_s
2	0.449	0.381	0.226	1.123	0.036	0.178
3	0.299	0.405	0.030	0.927	0.005	0.148

3.3. *Model analysis*

Through the above data analysis, it will be found that different results brought about by using different queuing models when nucleic acid testing is carried out in this area. Notice first the data indexes obtained in Table 2 when using the M/M/1 queue model, the value of ρ is close to 1 and the value of P_0 is close to 0 which means the work intensity of the staff is high and there is almost no time for rest, at the same time,L_s=8.722 means that the average team length is about 9 people, and the people are more crowded, which is not conducive to epidemic prevention and control. W_s=1.389 means that the average queuing time exceeds one minute and has a certain impact on the normal life and work of the residents.

When the M/M/s queue model is used, by analyzing the situation of arranging three testing points in first, it will be found that the probability of the queue being idle is much higher than that of arranging one testing point, meanwhile, the overall work intensity in not high which means that it is easy to see that the staff are idle for a long time. L_s=0.927 shows the average queue length is less than 1 person and there is almost on need for people to queue resulting in a waste of space resources such as venues. Many of the above problems reflect the problem that there are too many testing points arranged at this time. However, if two testing points are arranged, it will be found that the work intensity of the staff is moderate, and there will be no overwork or too much leisure. At the same time, the average queuing length will not be too long or too short showing there will be no overcrowding or almost no queues, and it also meets the requirements of epidemic prevention and control. In the two cases of the testing points arrangement of the M/M/s queue model, the average time of queuing is approximately equal to 10 seconds, which takes less time and has almost no impact on the normal life and work of the residents.

By analyzing and comparing the results of the above three kinds of testing points arrangements, it can be seen that setting the correct number of nucleic acid testing points that meet the actual situation can not only reduce the consumption of human resources, decrease the impact on people's normal life, but also be beneficial to the implementation of the epidemic prevention and control policy.

In addition to applying and solving the above two types of queuing models, other models which can match various situations in reality could also be introduced, such as GI/M/1 model which apply the theory of life-death process and embed Markov skeleton process, GI1+GI2/M/1 model which divide customers into two groups based on arrival time, M/G/1 model which generalizes the service time, G/Ek/1 model which generalizes the arrival time and use the service time obeying to the Erlang distribution.

4. Conclusion

The queuing has always been a relatively frequent problem in people's life. In the current time, people often need to queue up to complete the nucleic acid test in order to fight the novel coronavirus, and queuing is often limited by human resources and place. About the above problems, the article has discussed and analyzed two kinds of simple queueing models the M/M/1 model and M/M/s model in detail, reflecting that the correct use of queuing models could not only reduce people's queuing time, improve testing efficiency, but also avoid crowds gathering which is beneficial to epidemic prevention and control.

In reality, people's selection of testing points, different types of testing services and many other issues involved in queuing are often complicated and diverse. In this regard, many models have been optimized and improved, and many novel queuing models that consider more factors have also been proposed. However, the current research on the probability distribution of arrival time and service time of such queuing models is still insufficient, thus, the further exploration of more specific queuing models is still required. Furthermore, the number of people undergoing nucleic acid testing is also affected by many factors such as community requirements, weather, and their own needs, so it is also necessary to collect long-term relevant data.

References

[1] Norris J R 1997 Markov Chains. *Cambridge University Press, New York.*
[2] Ai Y H, Liu Y Q and Yan J D 2009 Research on Markov Chain Queuing Model in Hospital Outpatient Pharmacy. *China Digital Medicine,* (11): 47-49.
[3] He Q M 1992 A Note on Queueing System M/M/1, *Journal of Mathematical Research & Exposition,* (12): 2.
[4] Zhou Y W, Fan H H and Yang X X 2006 The New Method to Calculate the Transient Distribution of the Length of Queuing System. *Journal of East China Jiao Tong University,* (23): 1.
[5] Xiao W P 1985 Analysis Method of Queuing System M/M/S. *Construction Mechanization,* (4): 2.
[6] Ling T T, Ding B L and Duan S S 2022 Optimal Setting of Testing Sites for Nucleic Acid Tests of Entire People Based on Queuing Theory. *Journal of Taiyuan University (Natural Science Edition),* (40): 1.
[7] Wang L Z 2007 The Use of Markov's Queue Model in Hospital Management. *Chinese Journal of Hospital,* (14): 2.
[8] Liu H W 2006 Investigation on the Efficiency of Bank Queuing. *MIEM,* (74): 342 - 345.
[9] Yan Q Q, Shi D H and Guo X G 2005 A New Vector Markov Process for M/G/1 Queue. *Journal of Shanghai University,* (2): 120 -123.
[10] Yin B Q and Xi H S 2001 Performance Sensitivity Analysis of M/G/1 Queue System. *Applied Mathematics a Journal of Chinese Universities,* (2): 38 - 42.
[11] Dai G P, Yin B Q, Xi H S and Zhou Y P 2003 Performance Optimization of a Class of Controllable M/G/1 Queuing Systems. *In: The 22th Chinese Control Conference. Hubei.* 432 - 435.
[12] Liu Z M, Xu X H and Hou Z T 2001 Queuing Model of GI1+GI2/M/1. *Journal of Changsha Railway University,* (19): 4.
[13] Ran J H, et al. 2006 Design of queue system based on hospital information system for medical examination and laboratory diagnostic service in out-patient department. *HOSPITAL DIGITALLIZATION,* (27): 50-51.
[14] Zhang S Y, et al. 2011 Queuing theory model G/Ek/c and application of it in hospital eye specialist treatment. *In: China Annual Conference on Health Statistics in 2011. Xian.* 380-386.