# Coronavirus Disease (COVID-19) Identification Time Analysis Using Queueing Model

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## *Abstract*

**Background:** The article presents an application of a model of queues in series queueing system under overloading conditions to estimate the time of detection and identification of coronavirus (COVID-19) infections.

**Objective:** The objective is to present a simplified probabilistic model for assessing the general tendency to estimate the period of time needed to detect and identify already infected citizens before the treatment process really begins.

**Methods:** The law of the iterated logarithm is proved for such a system, which shows that the general identification process corresponds to the law of iterated logarithm.

**Results:** Some numerical examples of a different number of evaluation parameters are provided.

**Conclusions:** The modelling results showed that the sojourn time of the patient in the process of coronavirus investigation/detection/identification and treatment in the case of imbalance in the system as a whole increase in accordance with the law of the iterated logarithm. Even if the process of the treatment phases is well arranged and generally balanced, in case of the rate of investigation/detection/identification is lower than the rate of infection, the total number of already infected and unidentified citizens will increase in accordance with the law of the iterated logarithm.

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# Original Manuscript

# Coronavirus Disease (COVID-19) Identification Time Analysis Using Queueing Model

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## Abstract

The article presents an application of a model of queues in series queueing system under overloading conditions to estimate the time of detection and identification of coronavirus (COVID-19) infections. The objective is to present a simplified probabilistic model for assessing the general tendency to estimate the period of time needed to detect and identify already infected citizens before the treatment process really begins. The law of the iterated logarithm is proved for such a system, which shows that the general identification process corresponds to the law of iterated logarithm. Some numerical examples of the different number of evaluation parameters are provided. The modelling results showed that the sojourn time of the patient in the process of coronavirus investigation/detection/identification and treatment in the case of imbalance in the system as a whole increase in accordance with the law of the iterated logarithm. Even if the process of the treatment phases is well arranged and generally balanced, in case of the rate of investigation/detection/identification is lower than the rate of infection, the total number of already infected and unidentified citizens will increase in accordance with the law of the iterated logarithm.

*Keywords:* Coronovirus identification time, COVID-19, queueing model

## 1 Introduction

The general idea of the major of queueing models is to provide a set of tools aimed at practical arrangement of the process of treatment in a hospital or other medical facility in a proper way. Such models are usually focused on the task of optimizing or minimizing the time that patients spend in queues waiting for treatment, thus raising the effectiveness of the treatment process as the whole. The problems of such queueing models are that: (1) usually, such models are nonlinear, thus making it difficult to develop an analytical model for a wide range of probabilistic distributions of patient arrival and treatment processes, as a result, this requires implementation of a simulation approach to verify and apply such a model to real patient treatment processes; (2) such models are based on the stationary stage of the system, that is, the stage at which the characteristics of the system become stable over time; (3) there is a problem in applying such models to the issue under study, such as the

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spread or treatment of emergency viruses, since the parameters and their probabilistic distributions are not exactly known, and at the same time, the processes are not stationary, which complicates the modelling and analysis of such processes using queueing models; (4) the mathematical apparatus of such models is difficult to understand and analyse, as well as to implement digitalization and further simulation of such models.

The objective of this study is to propose a simple model with an elementary mathematical apparatus for studying the general process of COVID-19 identification and spread and to predict the further number and rate of infection. A queuing in series model is proposed for general modelling of the infection/treatment process. This is a simple model, and it will not give exact numbers or detailed estimates. But this model will show a general trend and will give us a general idea of the quantitative distribution of the number of people infected with the virus over time.

Queuing systems and queuing networks have been extensively studied [1]–[3] . There are classical results that provide analytical results and asymptotic studies of queueing networks. The main difficulty is that such results allow analytic only for a limited number of probability parameters. Usually the main task is to study queuing systems and networks in a stationary mode. The results for asymptotic, heavy traffic and overloading behaviour are presented as well [4]–[8].

Various queueing models are presented for modelling of epidemic and for treatment of patients and other healthcare applications [9]–[12]. For example, Au-Yeung et al. [13] present a model of patient flow in the Accident and Emergency department of a major London hospital. Authors use a real patient timing data for parametrization of the model. Ram Singh et al. [14] provide a comprehensive model for epidemic modelling with alert, infection, vaccination and death phases considered. Authors develop a Markov model by using inflow and outflow transition rates of the model. The queueing models are used for Ebola virus disease transmission and control analysis [15]. The authors promote the queueing technique as an efficient mathematical approach for the study of Ebola virus disease.

## 2 Brief of the model and simulation results

We apply the queues in series queueing system as the model of coronavirus disease (see Figure 1).

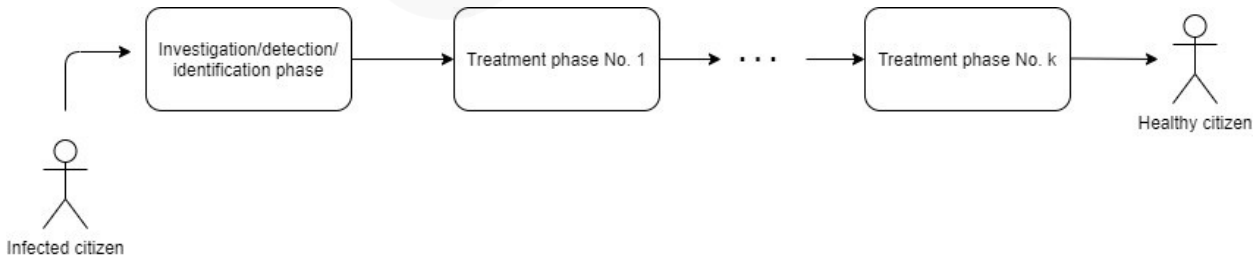


*Figure 1 Queueing systems model for a coronovirus detection/treatment process*

We start from an investigation/detection/identification phase. This phase covers the period from the moment

of infection itself to the time of identification of the virus and consists of (1) the incubation period, then infected citizen (not a patient at this moment of time) actively spreads his or her infection before symptoms become apparent; (2) the investigation phase, then efforts are undertaken to analyse and identify possible risks and identify possibly infected citizens; (3) the detection and further virus identification phase then virus is detected and identified (from that time an infected citizen changes his or her status to become an infected patient). Next, we move on to the treatment phase, which covers all indoor treatment until recovery.

We assume, that the infection process is completely random, and the law of probabilistic distribution is generally unknown. It also means that every healthy person does not know the time and place of their infection, and also that the facts of infection and the time between re-infections will be probabilistically independent. We assume that the investigation/detection/identification process is slower than the infection process as a whole (due to the incubation period and the extra time for virus identification). This obviously means a kind of a bottleneck in the overall treatment process. Even despite a well-balanced treatment process, such an imbalance at the stage of investigation/detection/identification will lead to a logarithmic (in accordance with the law of the iterated logarithm) increase in the time of detection of infection and, accordingly, the subsequent number of infected citizens awaiting identification and further treatment. Moreover, even one unbalanced phase in the entire system will cause such an effect, therefore it is important to consider the investigation/detection/identification and treatment process as a whole. We can compare simulation results with available statistics for a number of identified infections (see Figure 2). We see a similar tendency of the iterated logarithm increase in the number of identified persons.

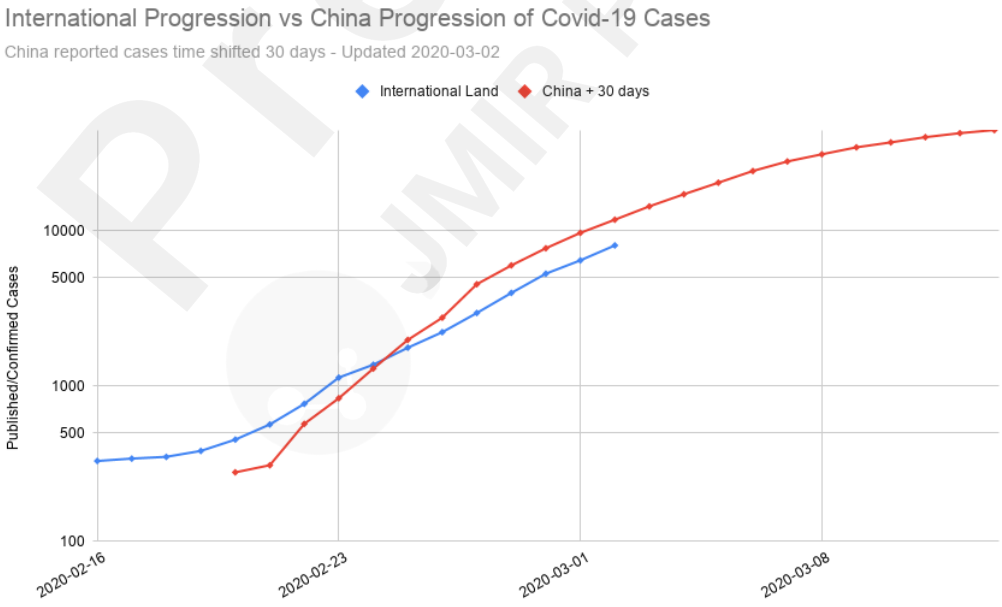


*Figure 2 International/China progression of Covid-19 cases. Retrieved from* [16].

# 3 Mathematical model

## 3.1 Statement of the problem

We investigate here a $k$-phase system of queues in series $\{GI/GI/1\}_{\{k\}}$ (i.e., a patient arrives to the first node and, after the patient has been served in the $j$-th servicing node, he or she goes to the node $j+1$ and, after the patient has been served in the $k$-th node, he or she leaves the queue) which consists of a number of consistently connected nodes of $GI/GI/1$ type for the first node and each other node of $G/GI/1$ type. Service times in each node are i.d.r.v.

Let us denote by $r_n^j$ the time of arrival of the $n$-th patient to the node number $j$; by $\tau_n^j = r_{n+1}^j - r_n^j$ – an interarrival time to the node number $j, j \geq 1$ (if $j=1, \tau_n^1 = \tau_n$ means interarrival time to the system, and let assume $\tau_n$ be mutually independent identically distributed random variables); by $s_n^j$ – service time of the $n$-th patient in the $j$-th phase; let service times $\{s_n^j\}$ in each phase of the queue for $j=1,2,\cdots,k$ be mutually independent identically distributed random variables. Let denote by $E$ and $D$ the first and second moments for any random variable.

Next, denote by $v_n^j$ the waiting time of the $n$-th patient in the $j$-th phase of the queue; $w_n^j = \sum_{i=1}^{j} (¿ v_n^i + s_n^i) ¿$ stands for the sojourn time of the $n$-th patient (time, which the $n$-th patient spent in the queueing system until the $j$-th phase), $j=1,2,\ldots,k$. By $T(n)$ we denote the sojourn time of the $n$-th patient in the whole system, that is $T(n) = w_n^k$ for the k-phase queues in series system. By $t_n^j$ we denote the sojourn time of the patient in the node number $j$, that is $t_n^j = v_n^j + s_n^j$. Let denote $\delta_{j,n} = s_n^j - \tau_n$. Let also denote $\alpha_j = E\,\delta_{j,n}, \alpha_0 \equiv 0, D\,\tau_n = \sigma_0^2, D\,s_n^j = \sigma_j^2, \tilde{\sigma}_j^2 = \sigma_0^2 + \sigma_j^2, j=1,2,\ldots,k;$

## 3.2 Mathematical results

**Proposition 3.2.1** [The lineal form of a recurrence equation for the sojourn time of a patient for a system of queues in series of type $\{GI/GI/1\}_{\{k\}}$ under overloading conditions]

If there is a permanent queue in the phase $j$, the following recurrence equation for the sojourn time $w_{n+1}^j$ of the $n+1$-th patient is valid

$$w_{n+1}^j = s_{n+1}^j + w_n^j - \tau_n;$$
$$n=1,2,\cdots.$$

*Proof.* The is a classical result of the following recurrence equation for the sojourn time $w_n^j$ of the $n$-th patient in the $j$-th phase [17]:

$$w_n^j = w_n^{j-1} + s_n^j + \max\left(w_{n-1}^j - w_n^{j-1} - \tau_n, 0\right);$$
$$j = 1,2,\cdots,k; n = 1,2,\cdots;$$
$$w_0^j = 0, \forall j; w_n^0 = 0, \forall n.$$

It is true, that if the time $\tau_n + w_n^{j-1} \geq w_{n-1}^j$, the waiting time in the $j$-th phase of the $n$-th patient is $0$. In the case $\tau_n + w_n^{j-1} < w_{n-1}^j$, the waiting time in the $j$-th phase of the $n$-th patient is $v_n^j = w_{n-1}^j - w_n^{j-1} - \tau_n$ and $w_n^j = w_n^{j-1} + v_n^j + s_n^j$. Taking into account the above two cases, we finally have the result. The proposition result follows.

■

**Theorem 3.2.1** [The law of the iterated logarithm (LIL) for the sojourn time of a patient for queues in series type $\{GI/GI/1\}_k$ system in a quasi-stationary state] In a quasi-stationary state, when there is always a queue in at least one node of the system with a maximum number equal to $j$ (that is $\exists j \geq 1 \vee \forall n > 1, v_n^j > 0$ and if $\exists j' \vee \forall n > 1, v_n^{j'} > 0$, then $j' \leq j$) then

P¿

$$a(n) = \sqrt{2n\ln\ln n};$$

$$K = 0, k = 1, j = 1; K = \sum_{i=1}^{j-1} s_1^i + \sum_{i=j+1}^{k} t_n^i, j > 1, k > j; K = \sum_{i=1}^{j-1} s_1^i, j > 1, k = j; K = \sum_{i=j+1}^{k} t_n^i, j = 1, k > j.$$

*Proof.*

1. Let assume, that $j$ is the biggest number of the node with a permanent queue, that is if $\exists j' \vee \forall n > 1, v_n^{j'} > 0$, then $j' \leq j$. As there is a permanent queue in node $j$ of the queueing system, therefore we could write
   $w_1^j = \sum_{i=1}^{j} s_1^i = K' + s_1^j$ (there is no queue for the first patient in any node) and further
   $w_2^j = w_1^j + s_2^j - \tau_2^j = K' + s_1^j + s_2^j - \tau_2^j;$ $w_3^j = w_2^j + s_3^j - \tau_3^j = K' + s_1^j + s_2^j + s_3^j - (\tau_2^j + \tau_3^j); \ldots;$
   $w_n^j = K' + \sum_{i=1}^{n} s_i^j - \sum_{i=1}^{n} \tau_i^j = K' + \sum_{i=1}^{n} (s_i^j - \tau_i^j)$, where $\tau_1^j = 0$ and $K' = \sum_{i=1}^{j-1} s_1^i$.
2. If $k > j$, then in all nodes with bigger numbers than $j$, that is $\forall j'' \vee j < j'' \leq k$ there will be a limit stationary distribution of the sojourn time of the patient $n$, that means that $\forall n > 1, K'' = \sum_{i=j+1}^{k} t_n^i \in R$ is a finite number. That is $\forall n > 1, w_n^k = w_n^j + \sum_{i=j+1}^{k} t_n^i = K + \sum_{i=1}^{n} (s_i^j - \tau_i^j)$ where $K = K' + K'' \in R$.
3. The classic results (LIL for the sum $S_n$ of independent and i.d.r.v. with means zero and unit variances) [18], [19] states that

$$P\left(\lim_{n\to\infty}\frac{S_n}{a(n)}=1\right)=P\left(\lim_{n\to\infty}\frac{S_n}{a(n)}=1\right)=1.$$

where $a(n)=\sqrt{2n\ln\ln n}$.

4. Let denote the random variable $m_n^j=s_n^j-\tau_n, \forall j,n$. For this we have $\sum_{i=1}^{n} m_i^j=\sum_{i=1}^{n}(s_i^j-\tau_i)=w_n^j-K$ and $\sum_{i=1}^{n} E(m_i^j)=\sum_{i=1}^{n} E(s_i^j-\tau_i)=\sum_{i=1}^{n}\alpha_j=n\cdot\alpha_j$.

   It is obvious that $\forall j=j'$ the variable $\widetilde{m}_n^{j'}=\frac{m_n^{j'}-E(m_n^{j'})}{\widetilde{\sigma}_{j'}}$ has the first moment equal to $0$ and the second moment equal to $1$. It is clear, that $\forall n$ variables $\{\widetilde{m}_n^j\}$ are independent and identically distributed. The result of the Theorem obviously follows from the classic LIL result (3) for $\sum_{i=1}^{n}\widetilde{m}_i^j, \forall j$, that is

$$\sum_{i=1}^{n}\widetilde{m}_i^j=\sum_{i=1}^{n}\frac{m_i^j-E(m_i^j)}{\widetilde{\sigma}_j}=\frac{\sum_{i=1}^{n}(m_i^j-E(m_i^j))}{\widetilde{\sigma}_j}=$$

$$\frac{\sum_{i=1}^{n} m_i^j-\sum_{i=1}^{n} E(m_i^j)}{\widetilde{\sigma}_j}=\frac{w_n^j-(K+n\cdot\alpha_j)}{\widetilde{\sigma}_j}.$$

■

Figure 3 presents an example of a Monte-Carlo simulation results. It can be seen that the sojourn time of the infected person is within the limits of the iterated logarithm.

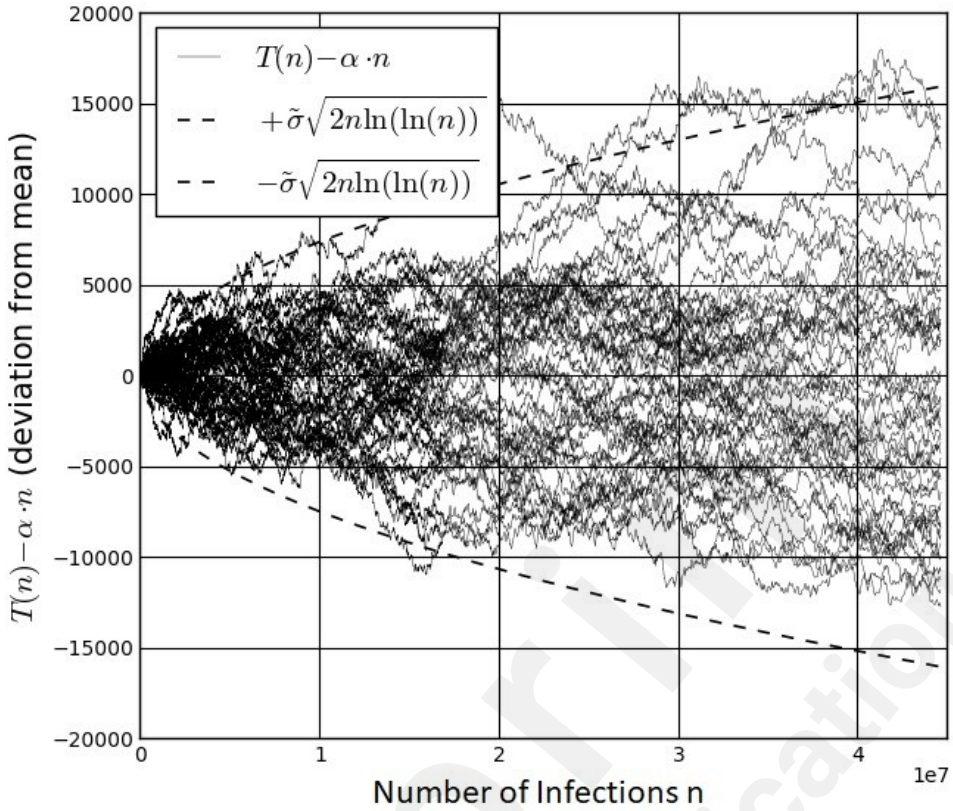


*Figure 3 Sample simulation results for the system of queues in series. Exponential distribution. Retrieved from* [20].

# 4 Discussion and Conclusions

Firstly, the modelling results showed that the sojourn time of the patient in the process of coronavirus investigation/detection/identification and treatment in the case of imbalance in the system as a whole is increased in accordance with the law of the iterated logarithm. Even if the process of the treatment phases is well arranged and runs smoothly, in case of the rate of investigation/detection/identification is even slightly lower than the rate of infection, the total number of already infected and unidentified citizens will increase in accordance with the law of the iterated logarithm. Let's continue with some examples.

We are considering a system with a well-balanced phase of treatment, resulting the possibility of reliable estimation of various probabilistic parameters for such a phase. For example, an estimate of the sojourn time of infected patients in the phase of stationary treatment. This is assumed to be a finite and relatively short period of time. At the same time, suppose the case of imbalance in the first phase (investigation/detection/identification) of the model. The main question is: when will a certain number of infected citizens be finally identified as infected?

As an example, we give a sample of calculations. Let assume that the total period of COVID-19 infection (from the first case detected to the present) is just over 3 months (aprxmt. 141,000 minutes). Assume that inter investigation/detection/identification time (the time period needed to identify the case of infection) is

exponentially distributed with the probabilistic parameter of the exponential distribution equal to $1/2.4$. This means that on average it takes about two and a half minutes to identify the case of infection. Simple calculation for the number of infected citizens which is equal to $100{,}000$ shows approximately $a(n)=\sqrt{2n\ln\ln n}=\sqrt{2\cdot 100{,}000(\ln\ln 100{,}000)}\approx 700$ and using the Theorem 3.2.1 results we have $141{,}000\approx\widetilde{\sigma}_1\cdot 700+\alpha_1\cdot 100{,}000$ and from that we have approximately $\alpha_1=1.4$. This means (as $\alpha_1$ is the difference in means between virus identification time and interpersonal contact which leads to infection time) that the process of interpersonal contact, which leads to infection, is about $1$ minute on average. Thus, if the contact of citizens, which leads to infection, occurs every $1$ minute, even though the virus investigation/detection/identification time is on average about $2$ minutes, and the further inpatient treatment process is well balanced, this ultimately leads to the mathematically unlimited number of infected citizens (in the mathematically unlimited period of time). In practice, this ultimately leads to a sufficiently long time to identify infection and a corresponding increase in the number of infected citizens.

The positive results of this modelling is that such an increase in the number of infected patients is almost linear. This due to the relatively slow rate of increase of the iterated logarithm part compared to the rest part of the Theorem 3.2.1 result. Let provide a numerical example. Let calculate the period $T(500{,}000)$ (with the same identification rate as in the previous example) for identification of let's say half a million citizens, that is, when will $500{,}000$ citizens be identified as infected? Assuming the same conditions as in the previous example, we have: $a(n)=\sqrt{2n\ln\ln n}=\sqrt{2\cdot 500{,}000(\ln\ln 500{,}000)}\approx 1{,}600$. $T(500{,}000)\approx\sigma_1\cdot 1{,}600+\alpha_1\cdot 500{,}000=704{,}160$, that is, keeping the same infection/identification rate, half the million infected patients will probably be identified within $704{,}160$ minutes or approximately $16$ months after the start of the infection process in December 2019, i.e. in March $2021$.

The solution to this problem would be to balance the investigation/detection/identification and treatment processes as a whole with a reduction in the time required for the investigation/detection/identification phase, which would lead to a sufficient reduction in the identification time and the corresponding number of infections. Let provide a numerical example. Let calculate the period $T(500{,}000)$ for infection of, let say, half a million citizens, that is: when $500{,}000$ citizens are detected as infected, if the investigation/detection/identification rate is $1/1.4$ (or $1.4$ minutes on average) and at the same time, the rate of contacts leading to infection is on average of $1$ per minute, as it was in the previous examples? We have $a(n)=\sqrt{2n\ln\ln n}=\sqrt{2\cdot 500{,}000(\ln\ln 500{,}000)}\approx 1{,}600$.

$T(500{,}000)\approx\sigma_1\cdot 1{,}600+\alpha_1\cdot 500{,}000=202{,}757$, that is, keeping the same infection rate, we may have a half the million infected patients already identified as infected within $202{,}757$ minutes, or approximately $4.7$ months from the start of the infection process in December 2019.

## 5 Declaration of Conflicting Interests

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

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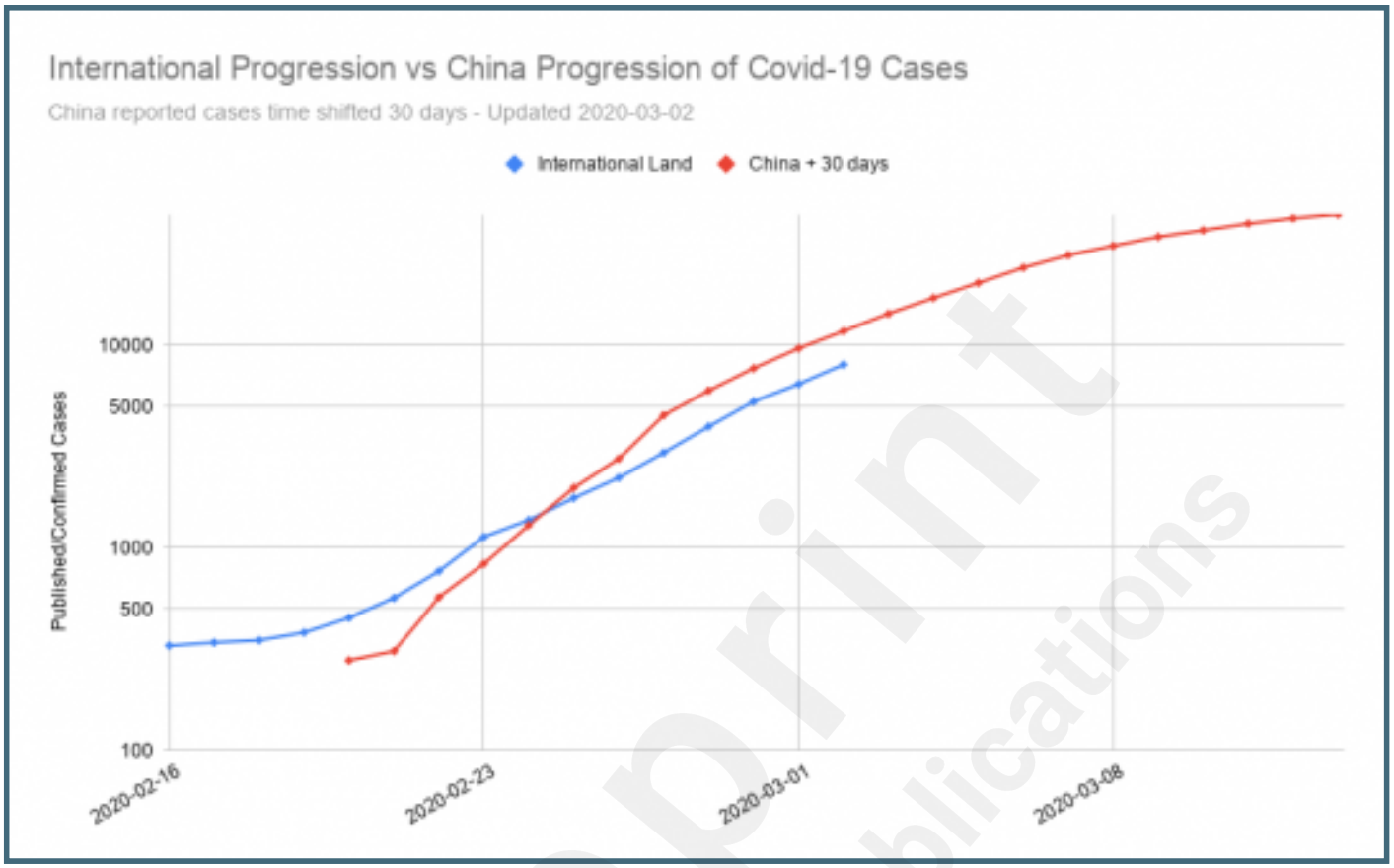
# Supplementary Files

# Figures

Queueing systems model for a coronovirus detection/treatment process.

International/China progression of Covid-19 cases. Retrieved from [16].



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