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Targeted Vaccination for COVID-19 Using Mobile Communication Networks

MohammadMohsen Jadidi
Department of Electrical Engineering
Amirkabir University of Technology
Tehran, Iran
mohsenjadidi@aut.ac.ir

Pegah Moslemi
Department of Electrical Engineering
Amirkabir University of Technology
Tehran, Iran
p.moslemi@aut.ac.ir

Saeed Jamshidiha
Department of Electrical Engineering
Amirkabir University of Technology
Tehran, Iran
s_jamshidiha@aut.ac.ir

Iman Masroori
Department of Electrical Engineering
Amirkabir University of Technology
Tehran, Iran
iman.masruri@aut.ac.ir

Abbas Mohammadi
Department of Electrical Engineering
Amirkabir University of Technology
Tehran, Iran
abm125@aut.ac.ir

Vahid Pourahmadi
Department of Electrical Engineering
Amirkabir University of Technology
Tehran, Iran
v.pourahmadi@aut.ac.ir

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***Abstract*—Vaccination is an effective method for prevention of infectious diseases, but when the number of available vaccines is limited, it is not possible to vaccinate everyone in a society. In this paper, a two-step model is proposed to distribute a limited number of vaccines among the people of a society, in a way that would disrupt the transmission chain of the infectious disease most efficiently. In the first step, the vaccines are allocated to different communities in the society (e.g. cities in a country), and in the second step, the individuals whose vaccination removes the greatest number of transmission routes for the infection are identified in concordance with the regulations of international health organizations. In the second step, contact data is obtained from cellular networks and Bluetooth signals, and a graph-based modeling scheme is utilized in conjunction with a combined susceptibility metric specifically designed for selection of these individuals. The simulations indicate that a 30% drop in infection rate compared to random vaccination could be achieved.**

***Index Terms*—Targeted vaccination, Vaccine allocation, SIR model, COVID-19**

I. Introduction

The COVID-19 pandemic has been a major concern for the international community for a number of months now. This disease was first diagnosed in December 2019 in Wuhan, China, and spread dramatically as a result of its high infection rate. The World Health Organization declared the COVID-19 as a public health emergency of international concern on January, 2020, and a global pandemic on March 2020 [1].

Vaccination can prevent the spread of COVID-19, but due to the limited resources available, public vaccination is not possible in short term. Thus, a limited number of people should be selected in such a way that vaccinating them would be most effective in disrupting the transmission chain of the disease.

Wireless communications infrastructure and smartphone applications could prove useful in gathering information for managing the spread of the disease. Various methods could be employed to collect this information. These including Bluetooth signals to detect proximity and duration of contacts, base station antennas to determine the positions of users, GPS system to track users, network of drones connected to a central unit, and wireless sensor networks to monitor individuals [2].

In order to disrupt the transmission chain of the disease, the authors of [3] prioritize the target group from the community at large by dividing the community into smaller groups and analyzing them, without examining individuals. The method used in [4], [5] is based on the analysis of the eigenvalues of the community graph matrix to vaccinate the nodes that maximize these eigenvalues. The authors of [6] have collected contacts between people using sensors and then modeled them by a graph. Suitable nodes for vaccination are then selected using the centrality metrics. It should be noted that calculating these metrics are not practical for graphs with a large number of nodes. Working on preventing the spread of computer virus and malware in computer networks, the authors of [7] propose a model where users in a network are first divided into clusters, and then either all users in each cluster receive a security software pack to counter the effects of the virus, or none of them does. It is also worth mentioning that in this scenario, a software pack can both prevent a computer from getting infected, and remove infected software from a computer, whereas in the public health case, vaccines cannot cure infected people.

The objective of this paper is to find the target population to achieve the best results in preventing the spread of COVID-19. For this purpose, the problem is divided into two parts: vaccine allocation and targeted vaccination. In the first part, vaccines are distributed among different communities in a society (e.g. different cities), and in the second part, the individuals to vaccinate in each community in order to best disrupt the transmission of the disease are determined and vaccinated.

The rest of this paper is organized as follows: system and epidemiology model are defined in section II, the vaccine allocation problem is discussed in section III. Targeted vaccination is analyzed in section IV. Simulation setup and the results are presented in section V. Section VI concludes the paper.

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II. System and Epidemiology Model

A. System Model

The proposed system model is shown in Fig. 1. It is assumed that the supply of available vaccines is limited. Social contacts are first extracted by triangulating the positions of the people using wireless networks. Then a disease propagation graph is formed using this data. The available vaccines are then allocated among different communities according to the spreading model of the disease. Finally, in each community, the vaccines are assigned to the people in such a way that would cut the greatest number of links between people.

B. SIR Model

The SIR model is a simple mathematical model where the population is divided into three groups: Susceptible, Infected, and Recovered. The recovered group contains people who recover from the disease, are vaccinated, or die [8], [9].

Suppose that P is a set of populations, and $s_j(t)$, $i_j(t)$ and $r_j(t)$ represent the fractions of the susceptible, infected, and recovered people in population $j \in P$ at time t, respectively. Denoting the number of people in population j by N_j and the number of susceptible, infected and recovered people at time t by $N_{s_j}(t)$, $N_{i_j}(t)$ and $N_{r_j}(t)$ respectively, we have: $s_j(t) = \frac{N_{s_j}(t)}{N_j}, i_j(t) = \frac{N_{t_j}(t)}{N_j}, r_j(t) = \frac{N_{r_j}(t)}{N_j}$. Since $N_{s_j}(t) + N_{i_j}(t) + N_{r_j}(t) = N_j$ is valid for every t,

$$s_j(t) + i_j(t) + r_j(t) = 1 \qquad \forall t \geq 0, \forall j \in P. \tag{1}$$

The SIR model is described by the system of differential equations in (2), where β_j and γ_j represent the disease transmission rate and recovery rate, respectively [10].

$$\begin{aligned} \frac{ds_j(t)}{dt} &= -\beta_j s_j(t) i_j(t) \\ \frac{di_j(t)}{dt} &= \beta_j s_j(t) i_j(t) - \gamma_j i_j(t) \\ \frac{dr_j(t)}{dt} &= \gamma_j i_j(t) \end{aligned} \tag{2}$$

In this system of equations, the first equation states that the change of susceptible people is related to the population of the susceptible group and the number of infected people. The third equation expresses the relationship between changes in recovered and infected people. The second equation can be obtained from the first equations, third equation and (1).

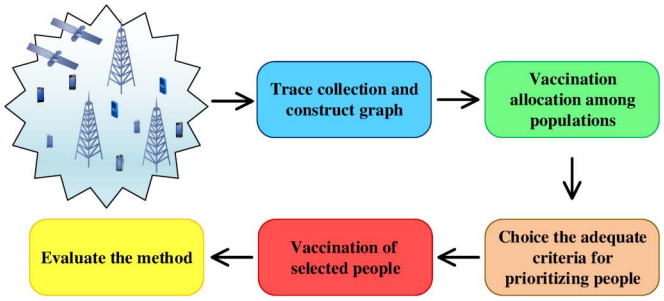


Fig. 1: The Proposed System Model

III. Vaccine Allocation

The problem of distributing a limited number of vaccines among different populations is formulated as an optimization problem in this section.

A. Vaccination, Immunity and Herd Effect

Vaccination decreases the number of susceptible people and thus reduces the number of people who will eventually be infected. In this problem, the objective function is defined as the total number of people who do not get infected. Vaccination increases these people in two ways. The first way is for people who have been vaccinated, which is called the direct method, and the second way is for people who are not vaccinated but will be less exposed to the disease when other people are vaccinated, which is called the indirect method.

Suppose a fraction of the population j is vaccinated at time τ. This fraction is denoted by f_j that $0 \leq f_j \leq s_j(\tau)$. It is also assumed that everyone is immune immediately after vaccination. So at time τ, the $(s_j(\tau), i_j(\tau), r_j(\tau))$ situation changes to the $(s_j(\tau) - f_j, i_j(\tau), r_j(\tau) + f_j)$ situation, that is, at the time of vaccination, f_j is subtracted from the susceptible people fraction and added to the recovered people fraction [9]. Fig. 2 shows the solution of the SIR model with vaccination. In this figure, the dashed lines are for the unvaccinated case and the solid lines are for the vaccinated case. It is observed that with vaccination, the $i_j(t)$ curve is lower than in the case without vaccination and has a smaller maximum.

To compare the performance of different methods of vaccine allocation, the final state of the system is considered. Function $H_j(f_j, \tau)$ is defined as the final fraction of susceptible people in the population j while an f_j fraction of susceptible people is vaccinated at time τ [9]. Formally,

$$H_j(f_j, \tau) = \lim_{t \to \infty} s_j(t, f_j, \tau), \tag{3}$$

where $f_j \in [0, s_j(\tau)]$ and $\tau \geq 0$.

The people in the susceptible group can achieve immunity in several ways. Those who receive the vaccine or recover from the disease will be immune. Those with contacts confined to

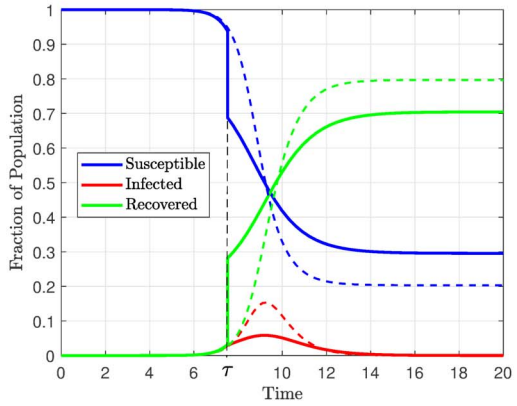


Fig. 2: The three compartments of the SIR model, with vaccination occuring at time τ for population j. Solid lines represent the vaccinated case and dashed lines represent the unvaccinated case. It is assumed that $\beta_j = 4$, $\gamma_j = 2$, $s_j(0) = 1 - 10^{-8}$, $i_j(0) = 10^{-8}$, $r_j(0) = 0$, $f_j = 0.25$ and vaccination occurs when 2.5% of the population is infected.

vaccinated and/or recovered people are also immune to the disease. This type of immunity is called herd immunity. The portion of the population that not get the disease due to herd immunity is called herd effect. $H_j(f_j, \tau)$ measures the herd effect on the population j, according to (3).

There is no explicit expression for the $H_j(f_j, \tau)$ and the general structure of this function is examined. To investigate the structure of this function, the cases of fixed vaccination time and fixed vaccination fraction are denoted by $H_j(f_j)$ and $H_j(\tau)$ respectively.

Fig. 3 presents $H_j(f_j)$ and $H_j(\tau)$. As shown in Fig. 3a and proven in [9], $H_j(f_j)$ has one maximum point and an inflection point. By evaluating the function $H_j(f_j)$ in terms of different β_j and γ_j, it can be concluded that the overall structure of the $H_j(f_j)$ does not depend on these variables and has a specific shape. In Fig. 3b, τ_{max} is the time when the fraction of vaccinated people equals the fraction of susceptible people, in other words $s(\tau_{max}) = f_j$. The maximum value of $H_j(\tau)$ occurs at $\tau = 0$, and it is monotonically decreasing with respect to τ. In fact, the best time for vaccination is at the beginning of the outbreak, and if there is no vaccine available at the beginning of the outbreak, vaccination should be performed as soon as possible. Like $H_j(f_j)$, The overall structure of $H_j(\tau)$ is not dependent on β_j and γ_j values.

B. Vaccine Allocation Problem Formulation

Assuming that V is the number of available vaccines, the goal is to maximize the total number of people in different populations who are never infected. The optimization problem can be formulated as follows [9]

$$\underset{\mathbf{f}=[f_1,f_2,\cdots,f_{|P|}]}{\text{maximize}} \quad \sum_{j\in P} N_j f_j + \sum_{j\in P} N_j H_j(f_j) \tag{4a}$$

$$\text{subject to} \quad \sum_{j\in P} N_j f_j \le V, \tag{4b}$$

$$0 \le f_j \le s_j(\tau), \quad \forall j \in P. \tag{4c}$$

The first and second terms in (4a) represent the direct and indirect (herd) effects of vaccination, respectively. (4b) represents the constraint on the number of vaccines available. It is also assumed in (4c) that the vaccinated fraction cannot be negative or greater than the fraction of susceptible people at the time of vaccination. It is noteworthy that constraint (4b) must be active since if f_j is chosen in such a way that $N_j f_j < V_j$, increasing f_j increases both the number of vaccinated people and the herd immunity, which corresponds to an increase in the objective function, i.e. objective function is monotonically increasing with respect to f_j.

The function $F_j(f_j)$ is defined as the total effect of vaccinating a fraction f_j of the population j. This effect consists of the direct and indirect (herd effect) immunities discussed earlier, and can be written as follows:

$$F_j(f_j) = H_j(f_j) + f_j. \tag{5}$$

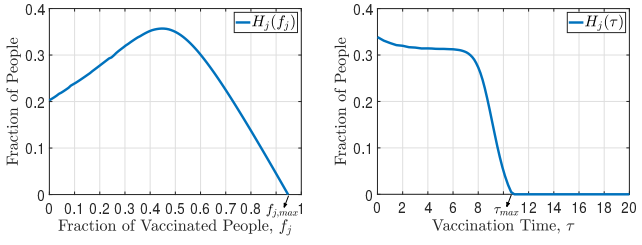
It should be noted that the objective function in (4) is equal to $\sum_{j\in P} N_j F_j(f_j)$. Fig. 4 shows the function $F_j(f_j)$. The maximum value of the fraction of vaccinated people is equal to the fraction of susceptible people at vaccination time, i.e. $f_{j,max} = s(\tau)$. As observed, $F_j(f_j)$ is monotonically increasing and reaches its peak at $f_j = f_{j,max}$, i.e. it is better to administer as many vaccines as possible to the population.

C. Solution of the Vaccine Allocation Problem

So far, we have only examined the objective function, and concluded that the objective function is monotonically increasing with respect to f_1 and f_2. In this subsection, we focus on the constraints of the optimization problem.

By assuming the existence of two populations, constraint (4b) represents the half-plane at the bottom of $N_1 f_1 + N_2 f_2 = V$ line. This line intersects the axes f_1 and f_2 at points $\frac{V}{N_1}$ and $\frac{V}{N_2}$, respectively. Also, constraint (4c) represents a rectangle with two vertices $(0,0)$ and $(s_1(\tau), s_2(\tau))$. By assuming $s_1(\tau) > \frac{V}{N_1}$ and $s_2(\tau) > \frac{V}{N_2}$ (if any of these two relations does not hold, the feasible set will be smaller) The contour plots of the objective function and the feasible set are plotted in Fig. 5 for $N_1 = N_2 = 100$. β, γ, and the initial values of the two populations are assumed to be the identical.

As already mentioned, constraint (4b) must be active, hence in Fig. 5 the feasible points must reside on the line passing through the points $(\frac{V}{N_1}, 0)$ and $(0, \frac{V}{N_2})$, in fact the two-dimensional feasible set is reduced to a line segment (to a $|P|-1$ dimensional hyperplane in general). To solve the optimization problem with regard to the concave structure of the objective function, an algorithm inspired by the gradient



(a) $i(\tau) = 0.025$ (b) $f_j = 0.25$.

Fig. 3: Herd effect function. (a) constant τ, $H(f)$. (b) constant f_j, $H(\tau)$.

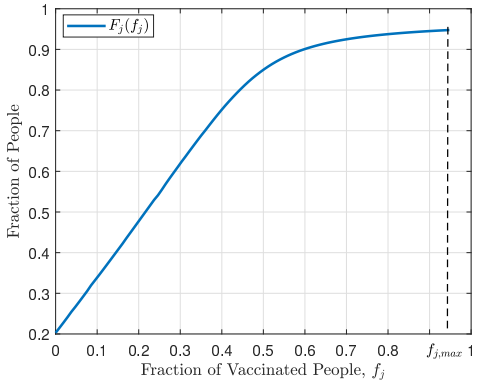


Fig. 4: The Total Effect of Vaccination

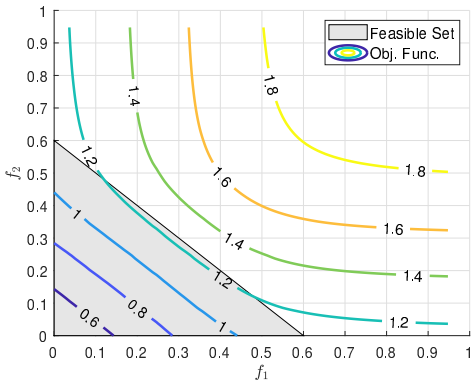


Fig. 5: Contour Plots of the Objective Function and the Feasible Set

descent method can be utilized. An arbitrary point on the $N_1 f_1 + N_2 f_2 = V$ line is selected, and is iteratively moved on the $N_1 f_1 + N_2 f_2 = V$ line in the direction that the value of the objective function increases to reach the maximum point. To solve a problem with larger dimensions, could proceed like a two-variable problem, except that the feasible points have higher dimensions (one less than the dimensions of the problem variable). The alternative method is to find the vaccination fraction ratio for each two populations and finally distribute the vaccines based on these ratios.

IV. Targeted Vaccination

In this section, we first introduce the disease propagation graph and its parameters, and then present a targeted vaccination algorithm to control the pandemic.

A. Disease Propagation Graph

Since the disease can spread via physical contact between infected and susceptible people, we could utilize a graph to model the transmission of the disease, where nodes represent individuals and the edges represent the existence of contact between two people. This graph is called the disease propagation graph [6], and it is defined as $G = (V, E, W)$ where $V = \{v_1, v_2, \ldots, v_{N_V}\}$ is the set of nodes (individuals) in the graph, and $E = \{e_1, e_2, \ldots, e_{N_E}\} \subseteq \binom{V}{2}$ is the set of the edges of the graph, with weights $W : E \to \mathbb{R}^+$ assigned to the edges. N_V and N_E represent the number of individuals in the study population and the number of contacts between them, respectively. The elements of set E are ordered pairs; In other words, for $u, v \in V$, there exists an edge $e = (u, v) \in E$ if and only if there is a contact between u and v. Since the disease can be transmitted in both directions, this graph is undirected. The weight of each edge in the disease propagation graph indicates the disease transmission probability between the two individuals. These weights depend on the duration and frequency of contacts between the people, the distance between them, and their locations.

B. Centrality Metrics

The importance of each node in the spread of the disease can be measured by standard centrality metrics [6], [11], [12]. A new metric called connectivity centrality that measures how much an infected node can infect the rest of the nodes and is defined as follows [6]:

$$C_{con} = \sum_{v=u, v \in V} c(u, v), \tag{6}$$

where $c(u, v)$ is equal to $\frac{w(u,v)}{h(u,v)}$ if u and v are connected and zero if u and v are not connected, $w(u, v)$ is weight of the edge between u and v; and $h(u; v)$ represents the number of paths from u to v. It should be noted that after calculating the values of each centrality metric for nodes in the graph, the nodes that have the highest value for each metric are not necessarily candidates for vaccination, since some nodes might be infected and it is pointless to vaccinate infected people.

C. Infecting Ability and Infection Susceptibility

To find the best vaccination candidates, the susceptibility of nodes to infection by other nodes should be considered. For this, two metrics should be defined for each node: infecting ability, and infection susceptibility. Infecting ability is defined as the ability of each individual to infect other people in the community, and infection susceptibility is defined as the probability of getting infected for each node.

The set of all infected nodes is denoted by I. To calculate the infecting ability metric, it should be noted that, no one can infect a node that is already infected , and the impact of any given node on other nodes that are close to infected nodes is negligible [6]. Infecting ability is then defined as:

$$\varphi(u, v) = \sum_{v \neq u, v \in V} c(u, v). \tag{7}$$

Infection susceptibility is defined as follows:

$$\psi(u, I) = \begin{cases} 1 & \text{if } u \in I \\ \sum\limits_{v \in N(u)} \psi(v, I) \cdot \frac{w(u,v)}{\max\limits_{w \in V} C_d(w)} & \text{if } u \notin I \end{cases} \tag{8}$$

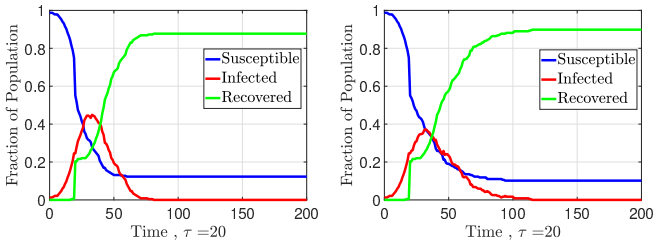
where C_d is degree centrality. (8) is a recursive model, and the linear equations system should be solved in order to obtain infection susceptibilities.

To more accurately assess the eligibility of the nodes for vaccination, both infecting ability and infection susceptibility should be taken into account. To do this, we define combined susceptibility as follows:

$$\zeta(u, I) = \frac{\varphi(u, I)}{\max\limits_{v \in V \setminus I} \varphi(v, I)} \cdot \frac{\psi(u, I)}{\max\limits_{v \in V \setminus I} \psi(v, I)}, \tag{9}$$

where $V \setminus I = \{v | v \in V, v \notin I\}$.

In the targeted vaccination algorithm, the candidate nodes for vaccination are selected and vaccinated based on an appropriate metric. After calculating the appropriate metric for all nodes, the node with the highest value is vaccinated if it is susceptible to the disease. The selected node is then removed from the graph, and the graph is updated. This process is then repeated until all available vaccines are administered.



(a) Random (b) Degree metric

Fig. 6: Fraction of susceptible, infected and recovered people, with $\alpha = 0.2$ and $f = 0.2$.

V. Simulation And Numerical Results

The proposed method has been simulated using the Primary school - cumulated networks dataset [13], which is a contact tracing network in an elementary school, representing a weighted graph of daily face-to-face contacts among 236 individuals. The SIR model has been utilized in simulating the spread of the disease. On the first day, 1% of the nodes are randomly infected, and the rest of the nodes are considered susceptible to infection, and the infection spreads among the population. After the number of infected nodes exceeds αN_V, (where α controls the vaccination time), fN_V vaccines are administered to the nodes obtained from the proposed method (where f is the fraction of the population that is vaccinated). The disease continues to spread after vaccination, until no infected nodes remain, and the disease is eradicated.

The fractions of susceptible, infected, and recovered people are plotted in Fig. 6. It can be seen that the overall structure of the figure is similar to that of Fig. 2 but the susceptible and infected fractions suddenly change by a value equal to the vaccination fraction. Vaccination is performed randomly in Fig. 6a, whereas the degree centrality metric is used in Fig. 6b. It is evident that targeted vaccination reduces the maximum number of infected people.

Fig. 7 represents the infection rate over time. It is observed that targeted vaccination using each metric can reduce the infection rate after vaccination and bring it down to zero. However, as the figure suggests, using the combined metric results in an immediate reduction in the rate of infection after vaccination, and keeping the slope of the contamination curve lower (more negative) in comparison to other metrics.

VI. Conclusion

In this paper, a targeted vaccination method was presented to allocate a limited number of vaccines among different populations, and to vaccinate the candidates whose removal would be most effective in inhibiting the ability of the disease to spread in each population. To facilitate the prioritization of the individuals, population modeling and vaccine allocation problems have been formulated using graph-based methods and contact tracing data obtained from cellular networks and Bluetooth signals. By examining different metrics, such as centrality, degree, and connectivity, a combination of metrics was proposed to model infecting and infection susceptibility.

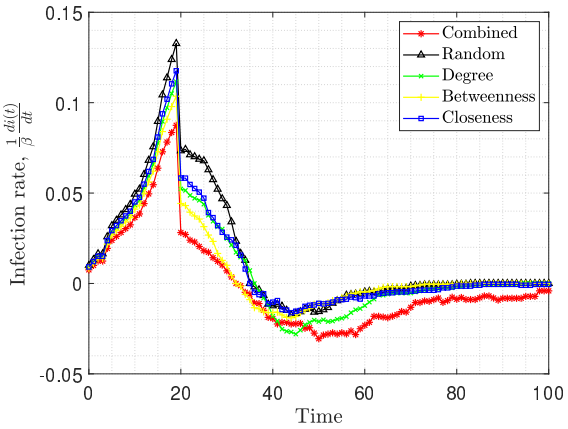


Fig. 7: Infection rates respect to time for different metrics. $\alpha = 0.2$ and $f = 0.25$ is assumed.

The simulations indicate that this combined metric for infecting and infection susceptibility can control the spread of the disease faster than any other metric on its own, and achieve a 30% drop in infection rate compared to random vaccination.

Acknowledgment

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