Simulation of Spreading of the Covid-19 Virus: A Generative Approach

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***Abstract*—All national governments and the World Health Organization have heavily relied on modeling to determine the most effective COVID-19 effect mitigation techniques. These have primarily been epidemiological models designed to comprehend the disease's spread and the effects of various therapies. But in addition to issues with disease transmission, a worldwide pandemic raises many other issues and challenges, each of which needs a unique model to determine the best approach. In this paper, I address the difficulties brought on by the COVID-19 pandemic and how simulation modeling might assist in assisting decision-makers in making the best judgments possible.**

***Index Terms*—Covid-19, Data Analytics, Data Visualization, styling, insert**

I. Introduction

By mid-March 2020, 334,000 people had been affected by the novel coronavirus disease (COVID-19), which had spread to 190 nations in just 20 weeks from its epicenter in Wuhan, China. More than 14,500 people died as a result. As of April 6, 2020, there were 1,210,956 sick individuals and 67,594 deaths related to the infection. By the second week of February, several European nations had passed through stage 3 of the epidemic, and India was in the process of moving toward stage 3. It is generally known that the epidemic behaves differently in the same country compared to other countries; mathematical modeling aids in predicting the trajectory of the epidemic to ascertain why the infection is not uniform.

In Bangladesh, the first case was recorded on January 27, 2020, whereas the COVID-19 outbreak was first noted in Wuhan, China, at the end of December 2019. The WHO labeled the Covid-19 outbreak a worldwide pandemic on March 11, 2020. Since then, Covid-19 has spread quickly over the world, resulting in numerous fatalities and devastating socioeconomic effects. The dynamics of mobility and daily activities are key factors in the transmission of COVID-19. Some daily activities that involve close physical contact contribute to the spread of SARS-COV-2. The virus spreads due to the distances required by the spatial distribution of activities. It is crucial to comprehend how daily activities affect COVID-19's dynamics in order to control and restrict its spread [1].

The presented work aims to model the outcome using a dataset of prior covid events and illustrate the dynamics of a covid situation. Additionally, this investigation will simulate COVID cases to test whether the lockdown procedure effectively stops the transmission of this particular virus.

II. Background

Since the Covid-19 epidemic, many compartmental models have been proposed to better understand how this unique illness spreads and to determine the most effective ways to stop its spread. In reality, a renowned mathematician and physicist named Daniel Bernoulli presented the first epidemiological model in 1766. Smallpox was spreading quickly at that time. As healthcare was not as developed as it is now, smallpox is one of the worst diseases in human history. His main goal was to evaluate the effectiveness of the smallpox vaccine. He created a static model in which the ratio of expected time spent in the susceptible condition to expected life expectancy at birth represented the population's division into susceptibles and immune [2].

By creating a straightforward compartmental model for mosquitoes and humans that demonstrated that reducing the mosquito population below a critical level would be sufficient to eradicate malaria, Sir Ronald Ross [3] gave us the idea of the Basic Reproduction Rate that is now used in all the epidemiological models we have. Previously, it was thought that malaria could not be eradicated as long as there are mosquitoes present in the population.

A. Recent Works

The SIR model is an option. The simplest epidemiological model, which serves as the foundation for all others, was first presented in 1927 by scientist William Ogilvy Kermack and physician Anderson Gray McKendrick. [4]. The plan was to divide the population into three compartments: susceptible, infectious, and recovered/removed. They discovered that there is a definite population density threshold that depends on the infectivity rate, recovery rate, and death rate. An epidemic won't occur if population density is below the threshold.

In his article "The SIR model and the Foundations of Public Health," Howard Weiss discussed the herd immunity concept of preventing epidemics by immunizing only a portion of the vulnerable class. He discovered that if the reproduction rate is 1.3, only 23% of the population has to be immunized. This number is 5, meaning 80% vaccination is required for smallpox. Similar to this, it is expected that for covid-19 has a reproduction rate of about 3 and a vaccination rate of 60–70%. As the vaccine rollout is uneven and the virus is mutating, the new strains are more dangerous than the previous ones, we don't know how much the vaccine is effective to them, and even immunity is not permanent—whether it is gained through vaccination or recovery, they could contract COVID-19 again. However, achieving herd immunity only through vaccination seems unlikely to achieve now [5] [6].

Recent modeling papers on COVID-19 primarily focus on epidemiology, making an effort to estimate the disease's basic reproductive number as well as to provide estimates of the effectiveness of various interventions in flattening the epidemic's growth curve to lessen the burden on the healthcare system. The well-known SEIR model (Susceptible - Exposed - Infectious - Recovered) is the most widely used model for defining epidemiology. It is typically used at the population level to express the percentage of the population in each state at any particular time. The SEIR model is employed by Lin et al. (2020), Fang et al. (2020), and Tang et al. (2020) to both explain the pandemic and evaluate the effects of mass social isolation regulations using data from China [7].

The Systems Dynamics approach has been used to develop a mathematical model. It is based on a SIR model, with the addition of state and auxiliary variables for hospital capacity, contacts, contacts with sick people, and fatalities, resulting in a model with four stock variables. Similarly, it was able to model "quarantines" or lockdowns and the efficiency of contact reduction using piecewise functions. The results demonstrate the reduction in infected individuals brought on by the quarantines. The model was run using a 100,000-person population. The simulations display possible infection trends in three different circumstances [8].

According to current studies, the incubation period for coronavirus infections is between 2 to 14 days, and the greatest amount of time before hospitalization is 10 days [9]. The World Health Organization (WHO) estimates that there are between 2 to 8 weeks between the onset of clinical symptoms and death. According to another study, viral shedding lasts between 8 to 37 days. Furthermore, a new paper suggests determining the best times to apply each intervention because the efficacy of the interventions varies on a variety of conditions. However, to stop the infection from spreading further, the majority of nations have instituted a 14-day self-quarantine. Because individual contact patterns are very dynamic and nonhomogeneous throughout each population, it is crucial to mathematically estimate the lockdown duration needed to stop the spread of COVID-19 infection with respect to each country [10]. For 4-5 days at room temperature, SARS-CoV can live on inanimate items such as metal, wood, paper, glass, and linen. As the peak viral load in the respiratory tract happens roughly ten days after the onset of symptoms, it has been demonstrated that clinically unwell people are crucial to the spread of the SARS-CoV [11].

In March 2020, the National Provider Identifier (NPIs) expanded across 80% of OECD countries in a 2-week timeframe. Prior adoptions of a policy among geographically close countries, or the number of earlier adopters in the same region, was a key predictor of a country implementing NPIs. The number of incidents or fatalities, the proportion of people over 65, or the nation's hospital beds per person were all factors that did not predict the adoption of NPIs. We all appeared to be "locked in this emotional elevation of COVID-19 deaths and misery above anything else that could possibly matter," according to the report. The uncontested belief was that "there were and are no alternatives to severe methods used on entire populations with little regard for cost and consequences." [12] [13]

The "Corona Dilemma," which is based on the so-called "Trolley Problem" in philosophy, has been put out by economist Paul Frijters for our consideration. Imagine that you are the person who can "pull the lever on the train tracks to prevent the approaching train from running straight," he tells us. We have the choice of diverting the train or not. If the train is not diverted, the virus will rage unrestrained, resulting in COVID-19 deaths. However, "if you pull the lever - the diverted train will put whole countries into isolation, destroying many global industries and thereby affecting the livelihood of billions, which through reduced governmental services and general prosperity will cost tens of millions of lives [i.e., COVID-19 reaction]". The globe pulled the trigger, and neither modeling nor policy took into account the unforeseen health effects of these actions. [14]

III. Methodology

The most helpful metric is the infection-fatality rate (IFR), which response to the query "What are the odds that I will pass away if I get sick?" The IFR is determined by dividing the number of COVID infections by COVID deaths:

$$IFR = (COVID\ Deaths\ /\ COVID\ Infections)$$

Although it looks simple, this is not the case. The causes are twofold: (1) It's not always clear what qualifies a "COVID death." If a person with high blood pressure contracts COVID and dies from a stroke, which caused his death—the virus or his preexisting medical condition? (2) The high incidence of asymptomatic carriers and persons who only experience minor infections and forego testing make it challenging to estimate the number of COVID infections. Despite these

Age group	Male	Female	Mean
0-4	0.003	0.003	0.003
5-9	0.001	0.001	0.001
10-14	0.001	0.001	0.001
15-19	0.003	0.002	0.003
20-24	0.008	0.005	0.006
25-29	0.017	0.009	0.013
30-34	0.033	0.015	0.024
35-39	0.056	0.025	0.04
40-44	0.106	0.044	0.075
45-49	0.168	0.073	0.121
50-54	0.291	0.123	0.207
55-59	0.448	0.197	0.323
60-64	0.595	0.318	0.456
65-69	1.452	0.698	1.075
70-74	2.307	1.042	1.674
75-79	4.26	2.145	3.203
80+	10.825	5.759	8.292

TABLE I
AGE-WISE DISTRIBUTION OF DEATH PER 100 PERSON.

difficulties, it's crucial to calculate precise IFRs. A group of researchers led by Megan O'Driscoll and Henrik Salje gathered information on COVID-19 mortality in 45 countries and almost two dozen seroprevalence investigations to get the most accurate estimates available (which determine the percentage of a population that has antibodies against the coronavirus and, hence, the percentage likely to have been infected). They identified sex- and age-specific IFRs using this data [15].

A. Data Analysis

Several observations are important to note. First, as we have long known, young adults (those in college or younger) are extremely unlikely to pass away. The age ranges of 5 to 9 and 10 to 14 have the lowest mortality rates. (It is understood that an IFR of 0.001% means that one person in that age group will perish away for every 100,000 infected.) The risk of death is three times higher in the 0–4 and 15–19 age groups than it is in the 5–9 and 10–14 age groups, but it is still incredibly low at 0.003%. (or 3 deaths for every 100,000 infected).

Second, across the 60–64 age range, the IFR gradually rises with age. However, the IFR climbs significantly thereafter, starting with the 65–69 age group. IFR for this group as a whole is just over 1%. (or 1 death for every 100 infected). There is a significant risk of mortality there. (The "1% threshold" is indicated by the red line in the chart.) The IFR then significantly increases and is extremely frightening for persons in their 70s and older. If infected with the coronavirus, those aged 75 to 79 have a greater than 3% probability of dying,

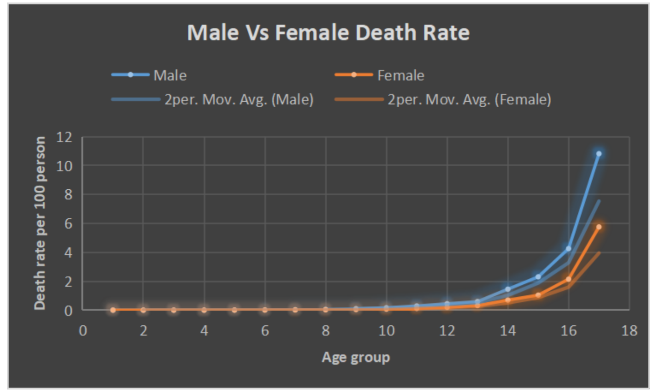

Fig. 1. Male Vs Female Death Ratio over age group

while those 80 and older have a more than 8% likelihood. That has about the same probability as rolling two dice and getting a four.

IV. IMPLEMENTATION

The implementation has been done in three parts $nolockdowncase$, $self-quarantinecase$, and $fulllockdowncase$. Each of the implementations has been discussed in this section part by part starting with $nolockdowncase$.

A. No Lockdown Case

The $matplotlib$ library has been utilized for the implementation. The initial population was estimated at 350 people. When the data are analyzed, the statistical distribution yields a value of 0.04, and the infection probabilities are set at 0.07. The dataset gives a death chance of 0.04, and adding 0.1 shows how likely it is for elderly people to die. According to the data set, the infected per unit time for no lockdown process is 70. This study implements the population setup function, which assumes that age is a $random\ normal$ range between 45 and 90 years old and that population is an empty array. A $random\ uniform$ approach has been adopted for the x and y data. The population of the array will then have the added parameters of covid status, age, x, y, infection rate, and infected since. Then, utilizing the positions, directions, and speeds, the $movement\ adjustment\ function$ was put into practice. A check for infection was then performed using the parameters $population$ and $currentframe$. This process goes through each infected person to see whether anyone is nearby. Then, to determine if someone has passed the $TIMEINFECTED$ frames, the $live\ or\ die$ has been calculated using loops per frame. The age of 65 was chosen for this implementation because the dataset suggests that after 65, the risk of dying increases noticeably. After appending the right updated arrays, the array was updated and the padding was modified so that it could be plotted on a graph.

B. Full Lockdown Case

Similar to the $no\ lockdown\ case$ instance, the parameters have remained the same with the addition of the

$self\ quarantine$ time new parameter. Being in the asymptomatic stage of covid, this is the amount of time it takes for an infected person to quit moving. There are now four final statuses available, including healthy, ill, immune, and dead. For this implementation, a $self\_quarantine$ function has been proposed. This function distinguishes this file from $no\ lockdown\ case$ by causing afflicted individuals to cease moving after a predetermined number of frames (to take the asymptomatic stage of the virus into account). The $matplotlib$ package is then used to plot the array.

C. Self Quarantine Case

This section resembles the $full\ lockdown\ case$ that takes into account all circumstances. The population setup function is updated to use a normal distribution for age because age isn't a uniform distribution in real life. The population size, distribution, and death probabilities are all the same as in the previous two implementations. Everybody who was infected stopped moving, however, a unique function has been added to the $live\ or\ die$ function, forcing them to move once more. The axes were automatically scaled after receiving the updated array, and the graphs were then drawn.

V. Result

This simulation of virus transmission has been created using $matplotlib$, with 3 cases has been evaluated: without lockdown effects, no lockdown case This is merely a safeguard. In the self-quarantine case file, sick individuals will cease moving and a Full lockdown Case slows everyone down while yet having the same self-quarantining effect as a self-quarantine Case. Green denotes health, red indicates infection, blue denotes immunity, and grey denotes death in the diagrams below. Each case will be presented as it is below.

A. No Lockdown Case

In this instance, the infection spreads uncontrollably. This example demonstrates how quickly a virus can spread and serves just as a control. At some moment, about half of the population is present. Since hospitals can only care for half the population at once, having this in real life would increase the risk that many people would die. However, hospital capacity is not programmed in, therefore the simulation does not account for this.

Figure 2 states the initial stage of the simulation. It is visible that, at the initial stage, everyone is in healthy condition.

Next, after 50 time frame, it is visible that the covid cases are increasing which started after the 10th time frame. Figure 3 illustrates the situation.

After that, we can see a rapid increase in covid cases where some of the previous cases got immunity whereas after the 40th time frame the growth of covid is going exponentially high and most of the people either are in an immunity state or affected. In figure 4 it is clearly visible.

Finally, after the 300th time frame, it is observable that new covid cases have not been found anymore. In the 150th epoch

Fig. 2. Initial State

Fig. 3. Covid Cases

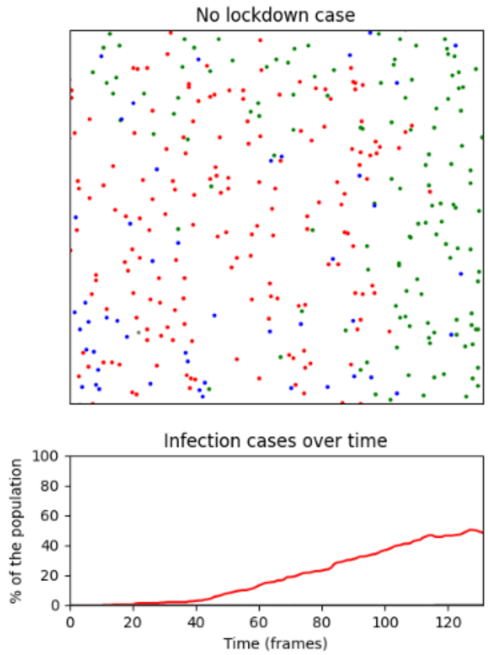

Fig. 4. Rapid Covid Cases

death cases have been found and after the 250th epoch, the number of death cases went high than the newly affected. We can see a bell-shaped curve has been generated from the 50th to 250th epoch for no lockdown case illustrated in figure 5.

B. Full Lockdown Case

The version in which everyone is slowed down is the toughest. This one takes the longest to clear the virus more than 700 frames but only a few people are affected at once. Initially, we can see no impact of covid yet in figure 6.

Then, after a very long time as illustrated in figure 7, at the 200th epoch, the affected rate is very minimal than the no lockdown case. The impact started from the 25th epoch and after a long time, plenty of people is not affected.

At the next stage in figure 8, we can see in the 350th step the covid cases are getting higher. It is unusual and can not be determined the trend of this as it is going high for sometimes and again going low for example after the 300th step it is increasing but from 200 to 250 it is decreasing. However, the infected population is very less and some immunity is visible.

After the 550th iteration, the number of the infected case has not increased but the death rate is visible which is the same as the infection rate. However, the healthy population is still in great numbers,s and the death rate is very lower than in the no-lockdown state. Figure 9 shows this result.

Finally, after the 700th iteration, it is visible that no new covid cases have arrived. There is still a death toll but the all-over situation is good. It is visible in figure 10.

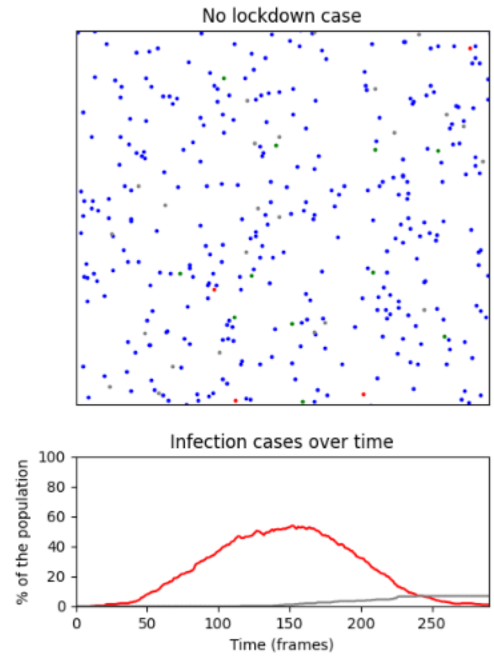

Fig. 5. Death Cases

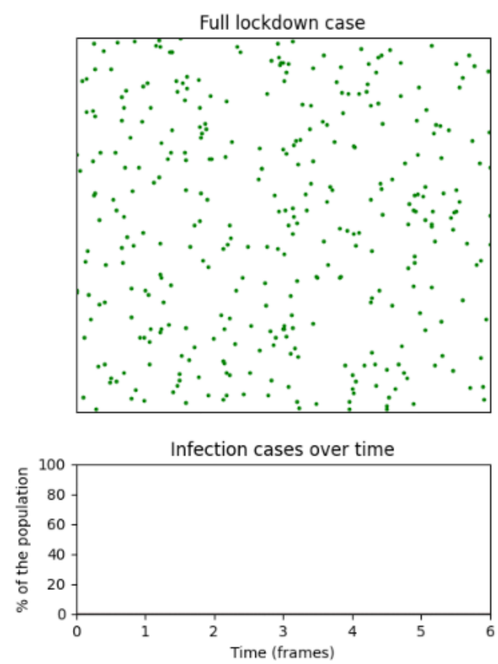

Fig. 6. Initial State

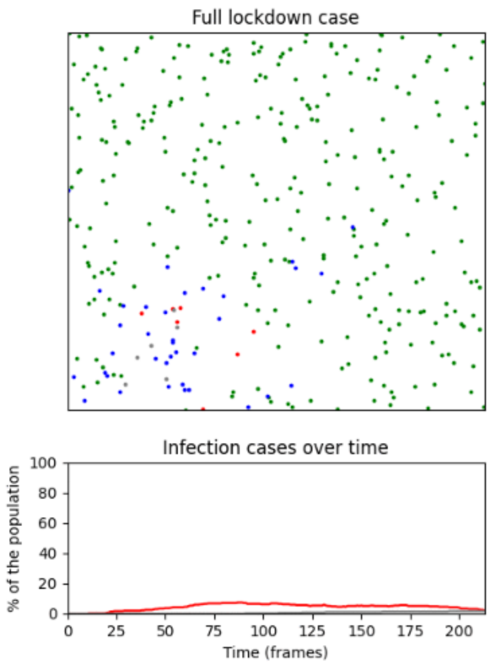

Fig. 7. Covid Cases

Fig. 8. Unusual Cases

Fig. 9. Death Cases

Fig. 10. No Covid Cases

C. Self Quarantine Case

This version prevents infected individuals from moving. Due to the asymptomatic nature of COVID's spread, this occurs with some delay. The initial stage is clear in covid cases as illustrated in figure 11.

Fig. 11. Initial State

In the next stage, we can see the virus spread started from the 10th epoch and it is increasing rapidly like the no lockdown stage. After the 70th epoch, there are a lot of covid cases that are visible in the respected figure 12.

After the 350th epoch, we can see most of the population is immune and the increase is going low. From the 10th to 300th we can observe a bell-shaped curve that represents a certain increase and decrease in a particular time frame. However, death cases started from the 100th epoch and went equal with new cases at 350th from figure 13.

Finally, after the 400th iteration, all the newly affected cases went zero. The death toll is still there but most of them are immune and no new case has been discovered. Figure 14 illustrates the situation.

VI. Conclusion and Future Work

The scientific viewpoint on what may be improved is also present. In this simulation, one can acquire immunity if one managed to survive the infection. Real life doesn't operate in that way. The majority of values are pretty arbitrary and don't accurately reflect how COVID actually functions. This implementation didn't factor in population density when choosing the number of people, but some were purposefully chosen.

Fig. 12. Rapid Covid Cases

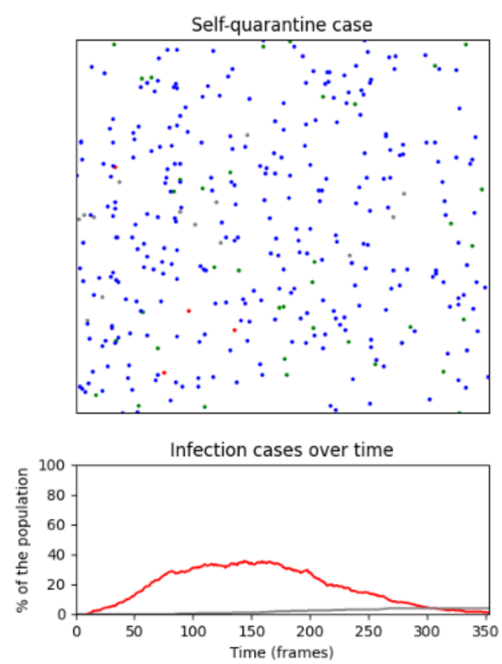

Fig. 13. Covid Decreases

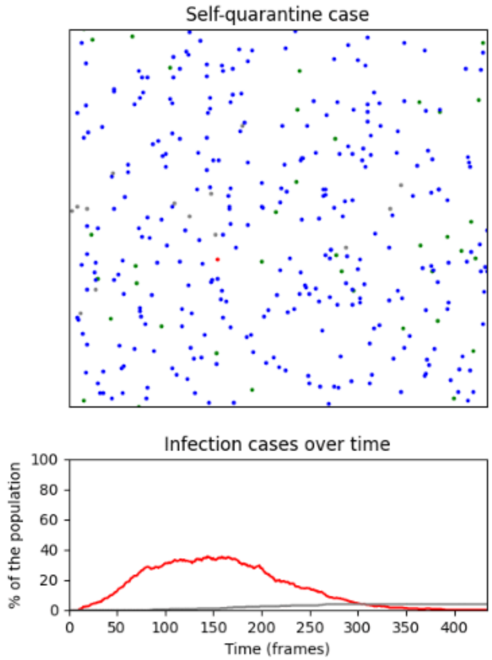

Fig. 14. Final Situation

Due to the lifting of the lockdown and the end of social isolation, the second wave is particularly bad. The virus was also made more contagious by the mutation. Despite a large number of instances, there are fewer fatalities now than there were in the past. To combat this virus, we must take precautions and immunize the majority of people. When developing algorithms to tackle the COVID-19 pandemic, which are shed light on in this work, several challenges may prevent the beneficial effect of the deployment of big data analytics mechanisms in the medical sector. Understanding big data enables the construction of proactive supply administration, such as the health sector staff allocation algorithm and the prediction of ICU demand, which is based on the anticipated needs of patients and the cases in each city. Big data models like machine learning make it easier to identify the many illness models, symptoms, and condition advancement as well as the dissemination agents connected to the pandemic. Benefits in formulating policies and taking proactive measures, as well as coming to conclusions about the distribution of medical supplies.

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