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SIR Model Dynamics: Insights into Epidemics and Vaccination

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Abstract This research focuses on the SIR mathematical model, analyzing disease dynamics in populations. The SIR model classifies individuals into Susceptible, Infectives, and Removed categories, guided by differential equations and key assumptions. Addressing questions on disease spread, maximum infectives, total impact, epidemic cessation, and vaccination effects, the study emphasizes the contact ratio's role. A high contact ratio leads to widespread disease, influencing infective numbers and population impact. Epidemic cessation depends on reducing the contact ratio, enhancing recovery rates, and vaccination. The study underscores vaccination coverage's importance, considering effectiveness and population immunization for effective pandemic control, particularly relevant in the context of COVID-19.

Keywords: SIR Model, Epidemic Dynamics, Mathematical Modeling of Infectious Diseases, Vaccination Strategies, Contact Ratio and Disease Spread

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Динамика модели SIR: взгляд на эпидемии и вакцинацию

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Аннотация: В данном исследовании рассматривается математическая модель SIR, анализирующая динамику распространения болезней в населении. Модель SIR классифицирует людей на подверженных инфекции, инфицированных и излеченных, руководствуясь дифференциальными уравнениями и основными предположениями. Исследуя вопросы распространения болезни, максимального числа инфицированных, общего воздействия, прекращения эпидемии и эффектов вакцинации, исследование подчеркивает роль коэффициента контакта. Высокий коэффициент контакта приводит к широкому распространению болезни, влияя на число инфицированных и воздействие на население. Прекращение эпидемии зависит от снижения коэффициента контакта, увеличения скорости выздоровления и вакцинации. Исследование подчеркивает важность охвата вакцинацией, учитывая эффективность и иммунизацию населения для эффективного контроля пандемий, особенно актуально в контексте COVID-19.

Ключевые слова: модель SIR, динамика эпидемий, математическое моделирование инфекционных болезней, стратегии вакцинации, коэффициент контакта и распространение болезни

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Introduction

The power of mathematical models is that they not only tell you things that may seem obvious, but they also tell you how to alter things and control things to get them back under control. The mathematical modeling of infectious diseases, exemplified by the SIR model, offers crucial insights into epidemic dynamics and vaccination strategies. This research navigates through the intricacies of the SIR model, delineating the dynamics of Susceptible, Infective, and Removed populations. As the COVID-19 context underscores, vaccination coverage becomes paramount, demanding an exploration of effectiveness and population immunization to effectively curb pandemics.

Literature Review

The SIR model, which divides the population into susceptible, infected, and recovered compartments, was introduced by Kermack and McKendrick in the 1920s. This model has been refined and expanded upon by various researchers over the years. Flynn-Primrose et al. provide explicit mathematical definitions for model products used in constructing stratified compartmental models [Faris 2021]. The SIR model is a standard model for understanding epidemics, but it assumes that infected patients are identical to symptomatic and infectious patients. However, for COVID-19, it is now known that pre-symptomatic and asymptomatic patients can also be infectious. To address this, a modified version of the SIR model has been proposed, where the population is separated into five compartments: susceptible individuals, pre-symptomatic patients, asymptomatic patients, quarantined patients, and recovered and/or dead patients [Sikder, Hossain, and Islam 2023]. Mathematical models have been widely used to study the spread of infectious diseases. These models provide insights into the dynamics of disease transmission and can help in predicting, assessing, and controlling potential outbreaks [Al-Jebouri 2023]. Contact ratio, which refers to the number of contacts an individual has, plays a significant role in disease transmission. Studies have analyzed the impact of contact ratios on the spread of various infectious diseases. For example, [Sharma et al. n.d., 2021] found that the structure of contact networks, influenced by population-level risk-tolerance regimes and interaction type, affects the spread of the epidemic. Vaccination strategies play a crucial role in controlling and preventing epidemics. Various approaches have been explored in the literature to maximize the effectiveness of vaccination campaigns and their impact on disease dynamics. These strategies include considering network structure centrality measures, disease-spreading parameters, and a combination of both [Chatterjee and Zehmakan 2023].

The basic reproductive number (R0) is a crucial concept in determining epidemic outcomes and influencing disease control measures. It represents the average number of secondary infections caused by a single infected individual in a susceptible population. Studies have explored the importance of R0 in various diseases, including Legionnaires' disease [Ahmad et al. 2023]. The SIR model can be used to understand the dynamics of the COVID-19 pandemic by providing insights into the spread of the virus through populations. The model considers the specific distribution of initially infected individuals and the stochasticity of the transmission process, allowing for more realistic predictions and scenarios [Yao, Jia, and Dai 2023]. Model validation using real-world epidemiological data is crucial for assessing the accuracy and reliability of mathematical models like the SIR model. However, there are challenges and methodologies involved in this process. One challenge is the limited availability of data in the early stages of an epidemic, which can hinder the performance of the model [Nath et al. 2023]. Optimal resource allocation strategies during an epidemic have been discussed in several studies. These studies utilize mathematical models to aid decision-making in resource allocation. [Gupta and Amin 2023] propose a data-driven approach to incorporate parameter uncertainty into resource allocation decisions, improving the efficacy of time-critical allocation decisions by 4-8 %. Vaccination programs have been highly effective in preventing and eradicating infectious diseases, such as

smallpox, polio, measles, and tetanus. These programs have been cost-effective and have had a quick impact on population health by saving lives [Wang, Fekadu, and You 2023]. Numerous lectures, hosted by the Oxford University Department for Continuing Education, have explored the dynamics of the SIR model, which researchers have utilized in this paper [T. Crawford, 2021].

Model Development

In this model, the total population is divided into three categories or components: S for susceptible, who are individuals who could potentially catch the disease; I for infectives, representing those currently having the disease and capable of infecting others; and lastly, R for removed, encompassing individuals who have already contracted the disease and have now either recovered or died. With all mathematical models, various assumptions are incorporated to simplify real-world phenomena because explaining everything in a set of simple differential equations can be overly complex. The first assumption we make is that the epidemic is sufficiently short, implying that it doesn't last for an extended period, allowing us to assume that the total population remains constant. The second assumption in our model pertains to how the disease is transmitted. We assume that the rate of increase in infectives is proportional to the contact between susceptible and infectives, occurring at a constant rate. Our third assumption pertains to the removal rate, where we also assume a constant rate, encompassing factors such as death or recovery rates, and we maintain that this rate remains constant.

After making our assumptions, we need to formulate the equations governing our model. Concerning the susceptible, the rate of change in the number of susceptible, based on our assumption, indicates an expected decrease as individuals transition to infectives. Consequently, the rate of change in the number of susceptible

$$\frac{\mathrm{dS}}{\mathrm{dt}} = \text{-rSI} \tag{1}$$

The minus sign indicates that the original initial number is decreasing as time progresses, where 'r' is the rate of contact. The rate of susceptibles 'S' is proportional to the number of contacts between infectives and susceptibles. Therefore, 'S' multiplied by 'I' symbolizes the contact between the number of infectives and susceptibles.

For the infectives, we have a similar equation. We aim to understand the rate of change of 'I' over time, and this equation would grow as people move from susceptibles into infectives

$$\frac{dI}{dt} = rSI - aI \tag{2}$$

The first term rSI in equation 2 is the same as in equation 1 but with the opposite sign because susceptibles are moving to become infected. Additionally, based on our assumption that infectives recover or die at a constant rate, if somebody is infective, he would move to the third category, R, or the removal category. The third equation, representing the rate of change of the removed population, must be equal to the gain from equation 2.

$$\frac{dR}{dt} = aI \tag{3}$$

Equations 1, 2, and 3 represent the dynamics of three categories of people within the population. In Equation 1, the number of susceptibles would decrease according to the number of contacts between infectives and susceptibles. In Equation 2, the number of susceptibles would increase due to contact between people and decrease when individuals are dying as a result of the disease or recovering. Finally, in Equation 3, the removed category includes people who no longer catch the disease, either because they have recovered or have died.

Before solving this system of differential equations, we require initial data. Therefore, we need to define the initial number of susceptible people in the population. We can state that the initial number of infectives is denoted as S_o, the initial value of infectives is denoted as I_o, and the initial value of the removed category (R_o) is set to zero, as no one has yet recovered or died as a result of the disease.

$$S = S_o\ , I = I_o, R = R_o = 0 \quad initially$$

We assumed that the population must be constant due to the epidemic. What this means is that the rate of change of susceptibles plus the rate of change of infectives plus the rate of change of removed must always be zero because the total population is given by $S + I + R = I_o + R_o$.

$$\frac{d}{dt}(S + I + R) = 0 \quad (4)$$

We can solve 1,2 and 3 equations because we know the initial condition of the population, so the total population doesn't change over time. So, we can take the initial value, which is the starting point representing the population value, as time cannot change it; it always has a constant value.

Results and Discussion

According to our built system, we should answer these questions

Q1 Will the disease spread?

We have an initial number of infected people given by I_o at the beginning of the epidemic, and what we want to know is whether that would grow. If the infected start to grow, then the disease would spread through the population, so what we are interested in is the rate of change of the number of infectives in equation 2. But before we do that, we want to start with equation 1, as it would always be a negative number since all of its parameters are positive numbers and it contains a minus sign. So, the change of S would always be negative; this tells us that S at any given time must be smaller than or equal to the initial value S_o.

$$S \leq S_o \quad (5)$$

Now we can take this value S_o and plug it into equation 2

$$\frac{dI}{dt} < I(rS_o - a) \quad (6)$$

So, the epidemic would occur if the size of I increases from its initial value I_o, so the answer to our first question would be related to the sign of this term $(rS_o - a)$ equation 6. If this term is positive, so there will be a spread of the disease. This means if $S_o > a/r$ the disease indeed will spread.

The value of r/a is called q which is called the contact ratio, which is a fraction of the population that comes into contact with an infected individual during the period when they are infectious. We can also re-arrange $S_o > a/r$ to be $S_o q > 1$ or $R_o > 1$. Condition $R_o > 1$ determines whether or not the epidemic will occur. Where R_o is the reproductive number which represents the number of secondary infections in the population caused by initial primary infection. R_o value will tell how many infections in the average one infected person will give the disease to within susceptibles. The value of R_o in COVID-19 is estimated to be 3 to 4, which is why it is spread so rapidly all around the world.

Real data was collected and organized by the World Health Organization (WHO). Some data points were missing, and therefore, we employed interpolation techniques to fill in these gaps. Figure 1 displays the basic reproduction number calculated by the WHO, with the interpolated graph overlaid. The dataset spans from May 2020 to January 2023.

As mentioned earlier, when the condition $R_o > 1$ satisfies ? the answer determines whether the number of infected people will increase or decrease. Therefore, it is essential to identify when the value of R_o is below or above 1. Figure 2 illustrates the distinct values of R_o, indicating whether it is above or below 1.

In Figure 3, When plotting the daily count of infected individuals alongside the corresponding values of the basic reproduction number R_o, we observed a clear pattern: as R_o exceeds 1, the number of cases, scaled up to a maximum of 2.5, increases, while it decreases as R_o falls below 1. The intersection of the Ro curve with the vertical line at 1 manifest as a turning point in the graph representing new cases.

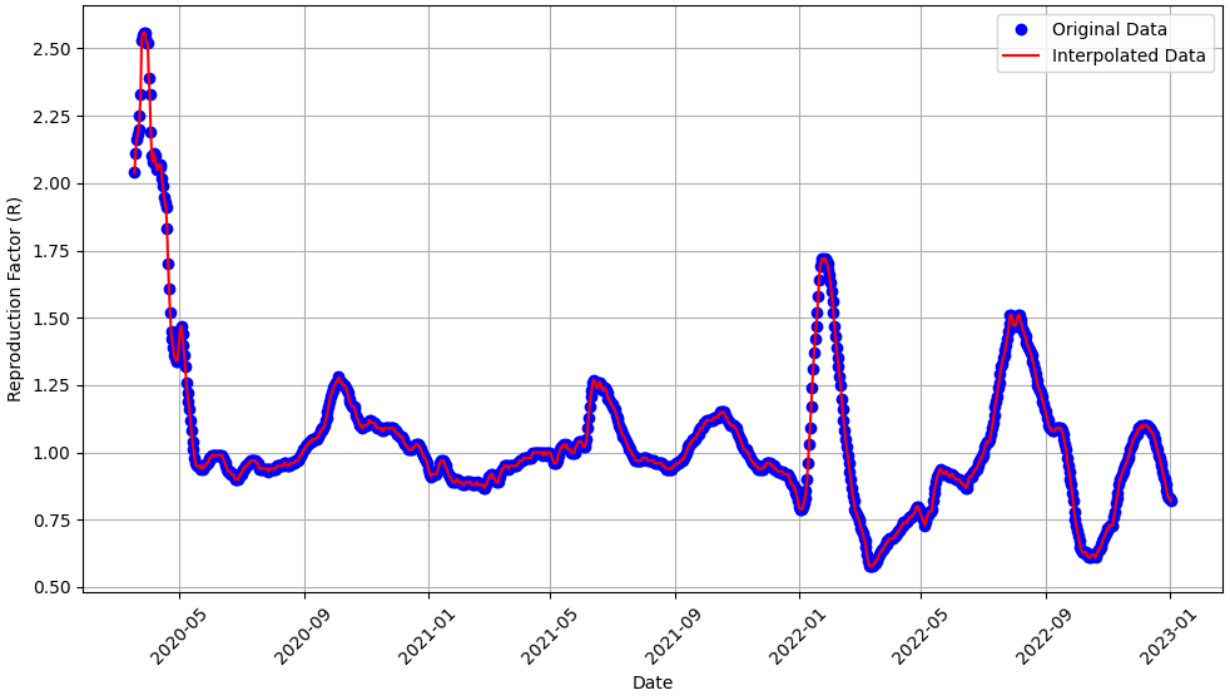


Fig.1. Real data of R_o for Russia over time (Our Data explorer website)
Рис.1. Реальные данные R_o по России с течением времени

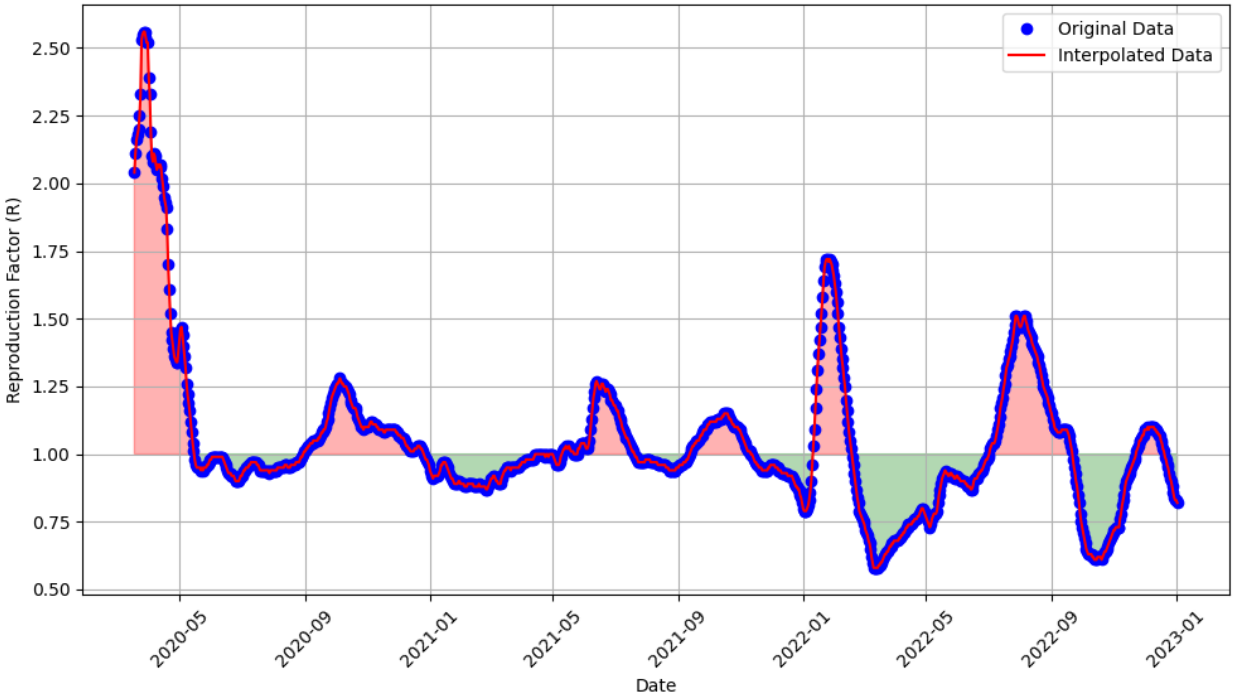


Fig.2. Discriminating R_o values
Рис.2. Различающиеся значения R_o

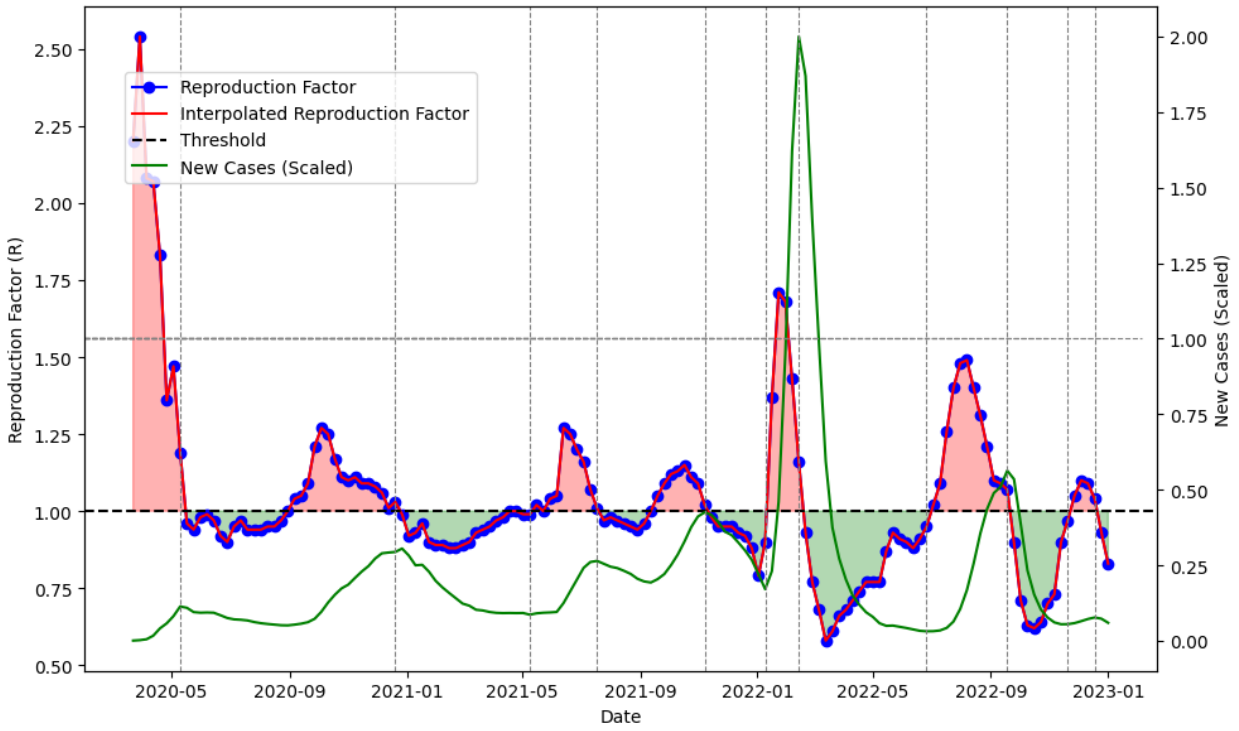


Fig.3. Relation between R_o and new cases
Рис.3. Связь между R_o и новыми случаями

Q2 What would be the maximum number of infectives?

The number of maximum infections is very helpful when we trying to distribute health resources. So, we want to create an equation for I that's in terms of various parameters we know within our system of equations. we would divide equation 2 by equation 1 to end up with equation $\frac{dI}{dS}$

$$\frac{dI}{dS} = \frac{rIS - aI}{-rIS} = -1 + \frac{a}{rS} = -1 + \frac{1}{qS} \tag{7}$$

We can solve this equation directly by integrating both sides of the differential equation and as we would have initial conditions,

$$I + S + \frac{1}{q} lnS = I_o S_o + \frac{1}{q} lnS_o \tag{8}$$

Equation 8 for I in terms of S and other parameters of our model, we haven't yet found I_{max} which is the maximum number of infectives at any given time, which is what we want to answer our second question. To obtain the maximum I in equation 8 we need to differentiate it and equal it to zero. As we saw the derivative of equation 8 is equation 7. So, we conclude that the maximum value of I in equation 8 occurs when substituting $S = 1/q$ in equation 8 and re-arranging for I. We get

$$I_{max} = I_o + S_o - \frac{1}{q}(1 + \ln(qS_o)) \tag{9}$$

Equation 9 says that the maximum number of infectives equal to the total population $I_o + S_o$ minus a function of q .We denoted looks$(1 + \ln(qS_o)$ as $f(q)$, we are interested how it is looks like.

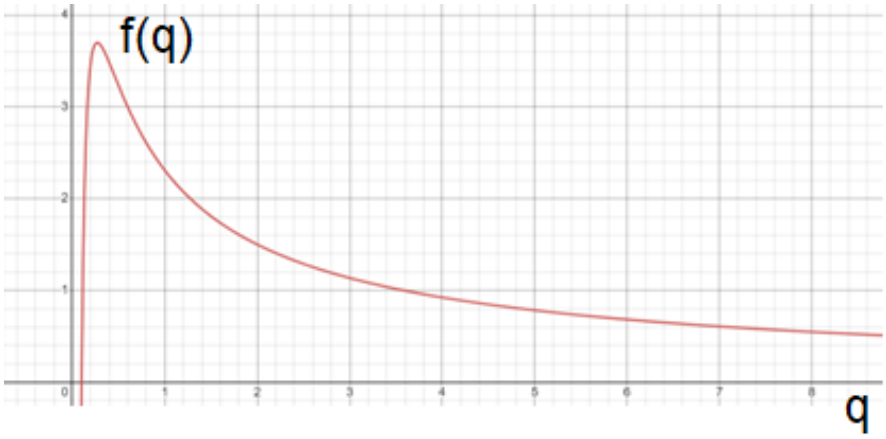
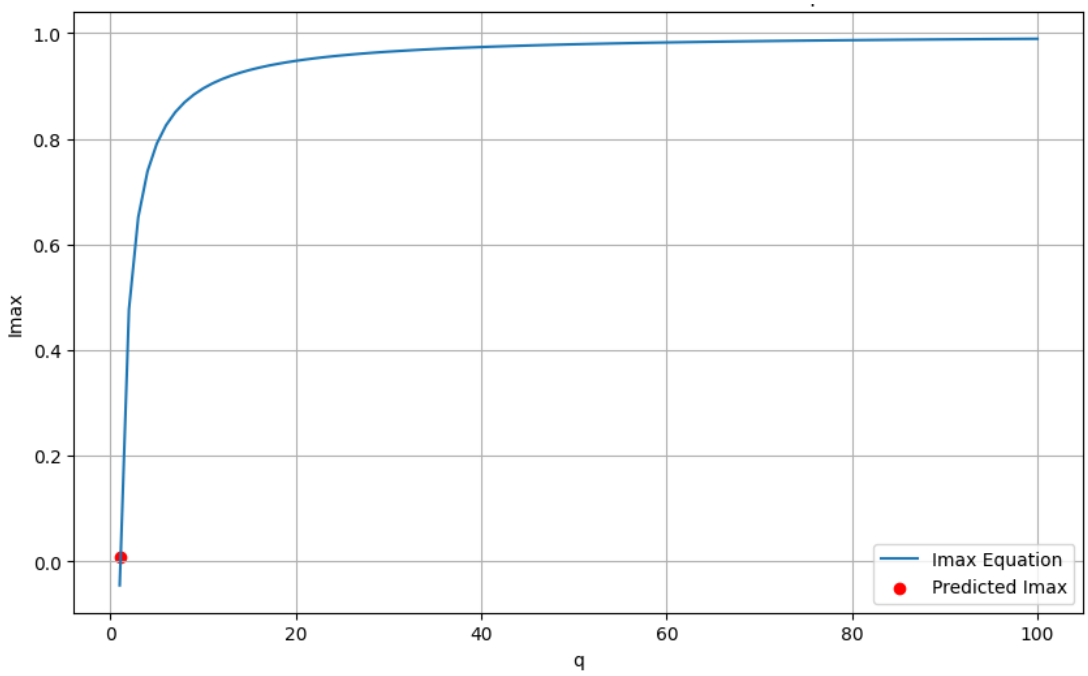


Fig.4. Plot of function $\frac{1}{q}(1+\ln(qS_o))$

Рис.4. График функции $\frac{1}{q}(1+\ln(qS_o))$

The key parameter is the value of q which is the contact ratio which is the fraction of the population that comes into contact with an infected individual. In the recent COVID-19, the value of q is high because the disease is very easy to transmit, with lots of people getting it, and lots of people getting into contact with those that have it, especially during long incubation periods where the symptoms do not show. Ultimately for our model, q is very big for the COVID-19 outbreak. Looking at Figure 4 , if q is big, so $f(q)$ would be small, and then I max would be big. What this means for the maximum number of infectives is that the maximum number of people that can have the disease at any given time is equal to the total population minus the function in Figure 1 ($f(q)$ where in this case quite small (when q is big) which is very bad news in the outbreak when have large q value.



Predicted q value: 1.054

Predicted Imax value: 0.009 = 0.9 % of the population

Fig.5. Maximum infected cases as a function of q

Рис.5. Максимальное количество инфицированных случаев в зависимости от q

With considering that $I_{max} = I_o + S_o - \frac{1}{q}(1 + \ln(qS_o))$ from equation 9 , and $I_o + S_o$ is 1 for the whole population , and qS_o is R_o , we can calculate R_o by taking average of all the recorded values in the dataset, in Figure 5 we drew the value of Imax as a function of q , then by using our recoded data in (Our Data explorer website) , we calculated the mean value of q for the whole period of study .

The red point in indicate the real q from the dataset after taking the average of all R_o within the dataset (Our Data explorer website). the substitute R_o and the Imax taken from given dataset to find the average real q for the last pandemic.

Q3 How many people will catch the disease?

In our assumption, we assumed that the total population was constant. We first need to think about what it means for diseases to "end", because if we want to know the total number of people that caught the diseases, we need the actual spread of the disease to end, this means that the number of infectives must go down to zero. So, we can call it the end of the outbreak. We have to look at our assumption that the total population doesn't change

$$R + I + S = I_o + S_o \tag{10}$$

We have to find the size of R in equation 10 when the number of I goes to zero, so we have to re-write equation 10 at the end of the epidemic

$$R_{end} = I_o + S_o - S_{end} \tag{11}$$

In equation 11 we noticed that the sum of people infected and recovered or died is the total population $I_o + S_o$ minus the susceptibles left after the end of the pandemic. The only unknown value in equation 11 is S_{end} . We can find S_{end} by substituting $I = 0$ in equation 8.

$$S_{end} + \frac{1}{q} lnS_{end} = I_o + S_o + \frac{1}{q} lnS_o \tag{12}$$

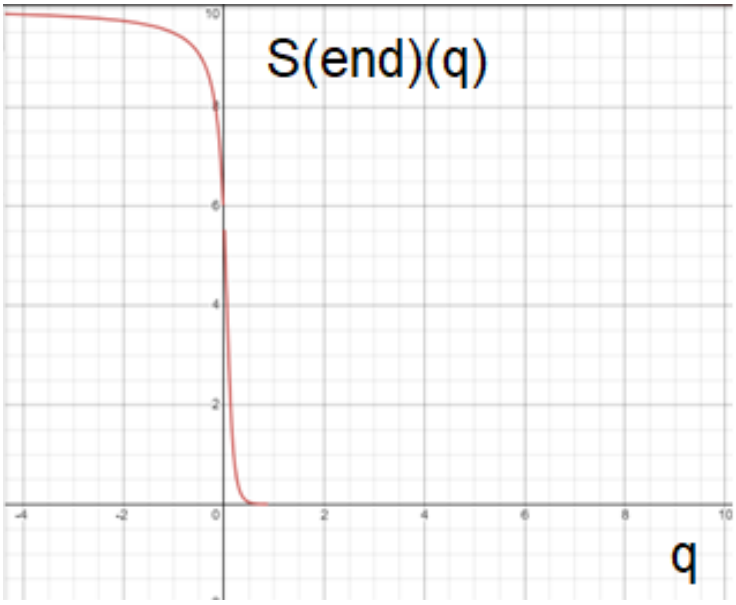


Fig.6. The plot of the equation 12
Рис.6. График функции 12

We have to solve equation 12 to find the number of susceptibles left after the end of the disease, then we have to substitute the value of S_{end} from equation 12 into equation 11 to find the value of R_{end} which is the answer to question 3. so, we would plot S_{end} versus q.

As we noticed from Figure 6 the large value of q the S_{end} is small and therefore according to equation 11, the value of R_{end} is large which is of course bad news. In summary, quite a lot if not the vast majority of the population will catch the disease if the value of q is sufficiently large.

Q4 What is the condition for an epidemic to stop, and how it would be affected by a vaccine?

In Equation 2 ($\frac{dI}{dt} = I(rS - a)$) we saw that the term $(rS - a)$ has to be negative for the pandemic to stop. So, the number of people with the disease must be decreasing, so they would get down to zero and stop.

If the term $(rS - a)$ would be negative then

$$R := \frac{rS}{a} < 1 \quad \text{for disease to stop} \tag{13}$$

From inequality 13 we see that there are three parameters to make this inequality right, which are reducing r, S or increasing a which means how long people are sick, the longer the one is sick, the larger opportunity to infect other people. We will control that with better medication to get people healthier sooner. Where r is the rate that infected people pass the disease on to susceptibles people, we can keep this parameter down by lockdown and social distancing or keep them quarantined. As vaccines became available, we need to pay attention to how the availability of vaccines effect the conclusion we draw from our model.

With vaccine we try to get the S which is the number of susceptibles people down, Vaccines can effectively reduce S such that R stays below one even if we go back to normal life.

Q5 How many people do we need to vaccinate to stop the pandemic?

At the start of pandemic, Ro equal $Ro{=}rSoa$ because it is a new disease, nobody had it before and nobody has immunity, so $So{=}1$ which means everybody is susceptible everybody could get the disease, so $Ro{=}ra$.

After vaccination, the people stay susceptibles, and if we denote the proportion of susceptibles people vaccinated by v then

$$S^* + v = 1 \;\rightarrow\; v = 1 - S^* \tag{15}$$

For pandemic to stop, this inequality has to be true

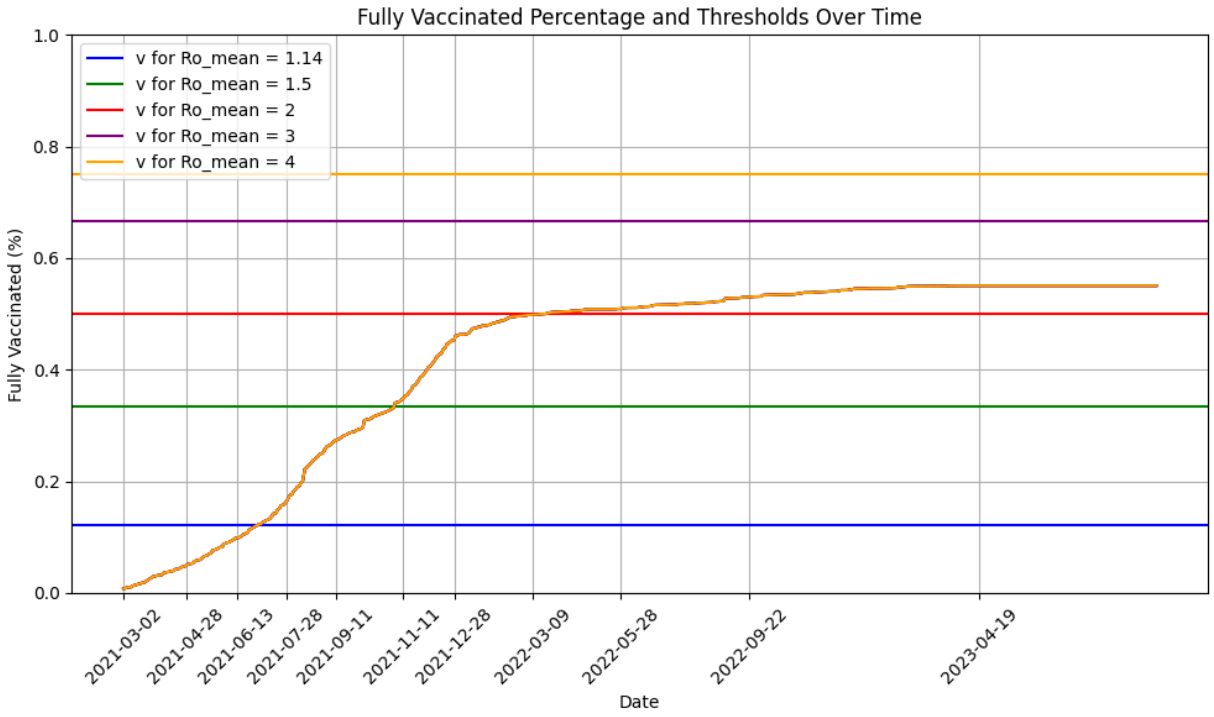
$$\frac{rS^*}{a} < 1 \rightarrow\; S^* < \frac{a}{r} \rightarrow\; S^* < \frac{1}{R_o} \tag{16}$$

According to equation 15, If $\frac{a}{r} = \frac{1}{R_o}$ of the people or less still susptables because they are not vaccinated, then the disease will stop, which means if $R_o = 3$, then 2/3 of people need to be vaccinated before the disease stops.

According to the equation 15, for the pandemic to stop, portion of people vaccinated should be

$$v > 1 - \frac{1}{R_o} \tag{17}$$

In Figure 7, the percentage of fully vaccinated individuals in Russia over time is depicted on the horizontal axis. After calculating the mean of the reproduction factor from the onset of the disease until the first person was fully vaccinated, the resulting value was 1.14. Therefore, the value of v needed to satisfy the inequality 17 is 0.122 of the population, indicating that at least 12.2 % of the Russian population needs to be vaccinated for the disease to stop. Allowing people to return to normal life implies that $R_o$would increase since the contact rate will rise. So, we assumed various values of Ro and determined the corresponding minimum v needed to halt the disease. The minimum threshold of v is depicted with different colors.



For Ro_mean = 1.14, v > 0.122
For Ro_mean = 1.5, v > 0.333
For Ro_mean = 2, v > 0.5
For Ro_mean = 3, v > 0.666
For Ro_mean = 4, v > 0.75

Fig.7. Fully vaccinated percentage overtime in Russia

Рис.7. Процент полностью вакцинированных пациентов в России в различные периоды времени

Q6 What happen if the vaccine isn't 100 % effective?

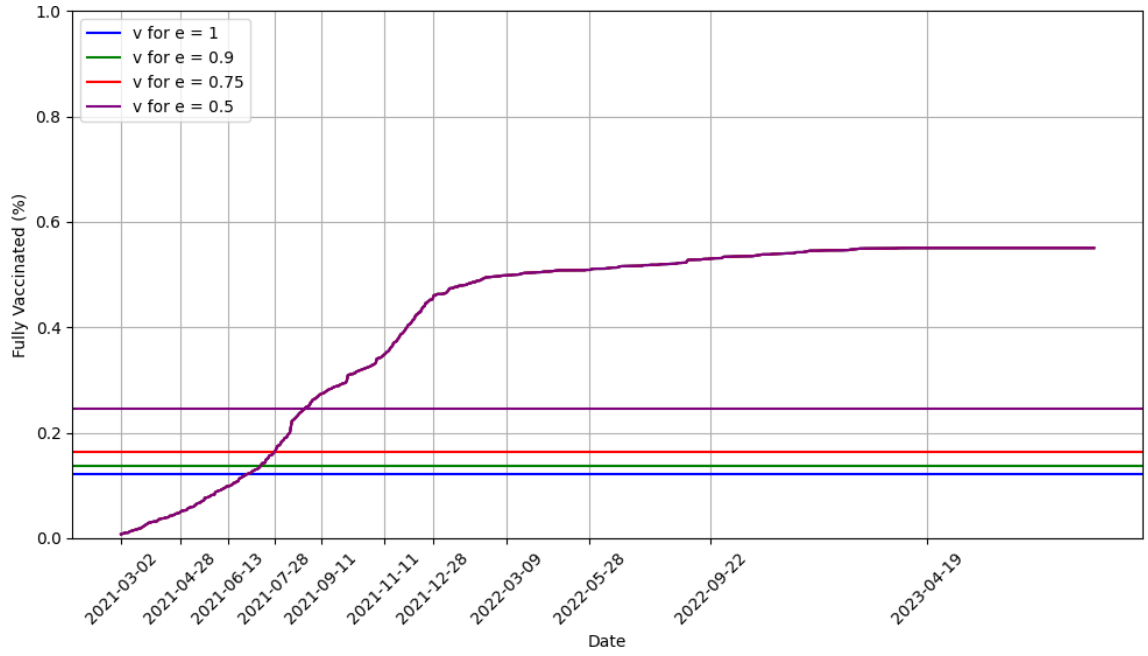
If the vaccine is not 100 % effective, this changes the inequality in 17, where not all vaccinated persons have an immunity against the disease, lets denote the effectiveness of the vaccine by e and the part of vaccinated population that has a full immunity against the disease by v_{eff} ,were

$$v_{eff} = e.v \tag{18}$$

So, if we have 100 people vaccinated and a 95 % effective vaccine, so 95 of those people would be immune against the disease. considering equation 18 and plugging it in inequality 17, we conclude that for the disease to stop the number of vaccinated should be

$$v > \frac{1}{e}(1 - \frac{1}{R_o}) \tag{19}$$

In Figure 8, we present the same graph as in Figure 7, depicting the scenario for the fully vaccinated population. However, we now incorporate the effect of vaccination according to Equation 19. As the efficacy of the vaccine diminishes, there is a corresponding increase in the percentage of the population that needs to be vaccinated.



For e = 1, v = 0.122 For e = 0.9, v = 0.136
For e = 0.75, v = 0.163 For e = 0.5, v = 0.245

Fig.8. Fully Vaccinated Population vs. Time with Vaccine Efficacy

Рис.8. Полностью вакцинированное население в сравнении с временем действия вакцины

Conclusion

For COVID-19, contact ratio q is the main key to determining the behavior of the disease. We can see that if q is large, the disease will spread and epidemic will occur. In the answer of question two we had known that the maximum number of infectives is equal to everybody minus some function of q (Figure 1), which is high for small values of q, which means as q goes high this function in Figure 1 would be low and therefore the I_{max} would be low. In question 3 the total people who catch the disease is which tell us that basically again that most majority of population will catch the disease if the value of q is large.

Equation 16 indicated, the value of susptables people (non-vaccinee) should be lower than $1/R_o$ for the pandemic to stop. in equation 17 we saw that the proportion of people need to be vaccinated should be at least $1\text{-}1/R_o$ for the pandemic to stop. If the vaccine is not 100 % effective, as mentioned in inequality 19, at least $1/e(1\text{-}1/R_o)$ need to be vaccinated for the pandemic to stop.

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