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A simple statistical physics model for the epidemic with incubation period

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ABSTRACT

Based on the classical SIR model, we derive a simple modification for the dynamics of epidemics with a known incubation period of infection. The model is described by a system of integrodifferential equations. Parameters of our model are directly related to epidemiological data. We derive some analytical results, as well as perform numerical simulations. We use the proposed model to analyze COVID-19 epidemic data in Armenia.

1. Introduction

Mathematical modeling for epidemiology has a rather long history, dating back to the studies by D. Bernoulli [1]. Later, Kermack and McKendrick [2] proposed their prominent theory for infectious disease dynamics, which influenced the following SIR and related models. By the end of the last century, significant progress in the field was made (a systematic literature review for this period is presented in Anderson and May’s book [3]). The COVID-19 pandemic has drawn the attention of researchers from all over the world and different areas to epidemic modeling. One of the simplest SIR models for the virus spread in Northern Italy was introduced in [4]. Another research group used the logistic equation to analyze empirical data on the epidemic in different states [5].

Here, we mainly focus on mean-field models that discard the spatial dependence of the epidemic process. Therefore, we avoid network models of epidemics [6]. Moreover, it is crucial to consider the final incubation period of the disease to construct a correct model for the COVID-19 case. Taking into account this distinctive feature, we consider the dynamics of the aged-structured population, which a well-known problem in evolutionary research [7–12]. Generally, epidemic models have a higher order of non-linearity than evolutionary models, although there are some similarities between these two classes.

In this study, we derive a system of integro-differential equations based on the rigorous master equation that adequately describes infection dynamics with an incubation period, e.g., COVID-19. First, we discuss the SIR model. Then, we move on to its modification and apply it to the data on the COVID-19 epidemic in Armenia.

Consider the SIR model where the parameter $S$ stands for the number of susceptible people, $I$ for the number of infected people, and $R$ for the number of people who have recovered and developed immunity to the infection. We assume that $S, I, R$ satisfy the constraint $S + I + R = N$.

$$\begin{align*}
\frac{dS}{dt} &= -aSI, \\
\frac{dI}{dt} &= aSI - bI, \\
\frac{dR}{dt} &= bI,
\end{align*}$$

where $1/b$ is the period when the infected people are contagious.
The parameter \( a \) can be obtained from the empirical data on infection rate:

\[
a = \frac{a}{N},
\]

\[
N = S + I + R.
\] (2)

Thus, we assume that a healthy person is infected with a probability proportional to the fraction of infection in the population. Probability is also proportional to the population density.

One of the most widely discussed and crucial parameters in epidemiological data is the basic reproduction number of the infection:

\[
R_0 = \frac{a}{b}.
\] (3)

For the COVID-19, it has been estimated as [4]:

\[
2 < R_0 < 4
\]

In fact, the real data allows us to measure three main parameters: the exponential growth coefficient at the beginning of the epidemic; the minimum period of time, in which an infected person can transmit the infection; and the maximum period, when an infected person ceases to transmit the infection.

The most important objectives of the investigation are the maximal possible proportion of the infected population, and then the period before the peak of the epidemic.

2. SIR model with incubation period

Consider the spread of infectious diseases with a recovery period up to \( T \) days. At the \( t \)th moment of time, we have \( S(t) \) for the size of the susceptible population, \( R(t) \) for the recovered population. We divide the infected population according to the age of infection, looking at time intervals \( \delta \) and defining \( I_i(t) \) as the number of infected people with the age of infection in \((i\delta,(i+1)\delta)\). We assume that the incubation period for a random infected person is \( L \) and the infection spreads from \( L \) to \( T \) days. Below, we take \( \delta \to 0 \) for the continuous mode of time limit.

Assuming that the spread of infection has a rate \( a \), we obtain the following system of equations:

\[
\frac{dS}{dt} = -aS(t)\int_L^T d\tau I(\tau, t)
\]

\[
\frac{dI}{dt} = -dI/dx,
\]

\[
\frac{dR}{dt} = I(T, t).
\] (4)

where the coefficient \( a \) is expressed via the infection rate coefficient \( A \),

\[
a = \frac{A}{N}.
\] (5)

We suggested that after \( T \) days a person recovers and the patients are not isolated from the rest of the population between days \( L \) and \( T \). Eq. (4) describes the dynamics of the population over discrete time, which is the right choice for numerical simulation.

Consider now the continuous-time version of the model. In the limit of small \( \delta \), we introduce the continuous function \( I_i(x, t) \) as the size of the infected population with age \( x \), \( x+\delta \). The continuous time versions for the first three equations are:

\[
dS/dt = -aS(t)\int_L^T dx I(x, t)
\]

\[
dI/dt = -dI/dx,
\]

\[
dR/dt = I(T, t).
\] (6)

The solution of the second equation in Eq. (6) is

\[
I(x, t) = J(t-x),
\] (7)

where we denote \( J(x) = I(0, t) \)

Then we get

\[
J(t+\delta) = aS(t)\int_L^T dx J(t-x), \text{ or}
\]

\[
J(t) = aS(t-\delta)\int_L^T dx J(t-x-\delta).
\] (8)

Using the latter expressions, we get the following full system of equations:

\[
dS/dt = -aS(t)\int_L^T dx J(t-x),
\]

\[
dI/dt = -dI/dx,
\]

\[
dR/dt = I(T, t).
\]
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Fig. 1. The infected population size \( I(t) \) in Armenia with respect to time in days. The count of days starts at March 24. The total population size is 3 million. Here, \( k = 0.0887, L = 5, T = 15, a = 0.235 \). At the start, we have 250 infected people.

\[
\frac{dJ(t)}{dt} = a \frac{dS}{dt} \int_{L}^{T} dx J(t-x) + aS(t) [J(t-L) - J(t-T)],
\]
\[
dR/dt = J(t-T). \tag{9}
\]

At the start, when \( S' \ll S \)
\[
\frac{dJ(t)}{dt} = aS(0) [J(t-L) - J(t-T)].
\]

Substituting an ansatz \( J(t) = e^{kt} \), we get:
\[
1 = aS(0) \frac{e^{-kL} - e^{-kT}}{k}. \tag{10}
\]

At \( k \rightarrow 0 \), we get:
\[
1 = aS(0)(T - L).
\]

For increasing \( a \), we get an increasing value of \( k \) as well. In the SIR model the epidemic threshold is at \( R = 1 \) or \( a = b \), so our model is similar to SIR with \( b = 1/(T - L) \).

In Fig. 1, we analyze the epidemiological data for COVID-19 in Armenia using our model. We examine the dynamics of infected population in Armenia from March 25, when the quarantine in the country has been introduced by the government, until April 5.

In Fig. 2 we have another regime of epidemics, since April 5 till May 31. We have done our calculations April 15, in the first submission of the article we gave the data till May 2.

In Fig. 3 we give the long period prediction — the peak of epidemics is August 20, later there is a 72\% infection of population, using the empiric data till April 15 for the calibration of our model. Fortunately the exponential growth phase has been changed, and since June 2 there is a linear growth for \( I(t) \).
3. The generalization of our model

3.1. The main equations

Let us consider the case, when the infectivity (the ability to transfer the infection to susceptible individuals) of infected individuals depends on the age of infection (via a kernel \( f(x) \)), also the population with the age \( x \) is diluted with the rate \( g(x) \). The latter seems to be a reasonable assumption, since an infected individual with a large age reveals some symptoms of infection, therefore, has chances to be isolated. Now Eq. (4) is modified:

\[
\begin{align*}
\frac{(S(t + \delta) - S(t))}{\delta} &= -aS(t) \sum_L T I_l(t) f(l\delta), \\
I_j(t + \delta) &= I_{j-1}(t) - I_j(2g(t)), \\
R(t + \delta) &= R(t) + \delta I/T \delta, \\
I_0(t + \delta) &= a\delta S(t) \sum_L I_l(t) f(l\delta).
\end{align*}
\]  

(11)

The continuous time limit gives the following system of equations:

\[
\begin{align*}
\frac{dS}{dt} &= -aS(t) \int_L^T dx I(x, t) f(x), \\
\frac{dI(0, t)}{dt} &= a \frac{dS}{dt} \int_L^T dx I(x, t) + aS(t) \int_L^T dx I'(x, t) f(x), \\
\frac{dR}{dt} &= I(T, t) + \int_L^T dx I(x, t) g(x), \\
\frac{dI(x, t)}{dt} &= -\frac{dI(x, t)}{dx} - g(x)I(x, t).
\end{align*}
\]  

(12)

Consider now the asymptotic solution:

\[
I(x, t) = q(x)e^{kt}.
\]  

(13)

Then, we get the following equations:

\[
q(x) = e^{-\int_0^t (k+g(y))dy},
\]  

(14)

and

\[
1 = a \int_L^T dx f(x)e^{-\int_0^t (k+g(y))dy}.
\]  

(15)

Thus, we derive for the epidemics threshold:

\[
1 = a \int_L^T dx f(x)e^{-\int_0^t g(y)dy}.
\]  

(16)
3.2. The specific functions $g(x)$

Let us analyze our Eq. (16). If we are trying to reduce the growth rate $k$, it can be done in two ways:

1. reducing the number of contacts, $A$,
2. increasing the $g(x)$ via containment activities.

Let us introduce non-zero reduction, just after 7 days, $g(x) = g$. Hence, we get the following result:

$$1 = a \left[ \int_{L}^{T_1} dxe^{-kx} + \int_{T_1}^{T_2} dxe^{-(k+g)x} \right].$$

We should estimate the value of $g$ that stops the epidemics.

4. Conclusion

In this paper, we introduced a version of SIR model for infection spreading with known incubation period. This model was applied to analyze the COVID-19 epidemic data in Armenia. We constructed the simplest version of population dynamics of age-structured population. Close work has been done in [13], which is related to SIR model, see also [14,15]. In [13], a temporal kernel $F(t)$ has been introduced that modulates the infectivity of each infected individual. Compared to such model, we introduced the distribution of infected population at given moment of time via an age of infection, instead of looking just long history of focus populations. In other works related to the population dynamics of age-structured population, the differential equations with time delay usually have been considered. Instead, we use integro-differential system of equations, which seems to be an adequate approach to the current situation with COVID-19 epidemic.

From our perspective, the proposed approach significantly changes the epidemiological picture (compare to classical SIR models), since the virus is active for about two weeks. Next, we introduced two functions: $f(x)$, which describes the distribution of infectivity by age, and $g(x)$, which describes the content measures. In the normal SIR model, we have two parameters for the rate of infection and the removal of infections. In our integro-differential model, mapping to elementary processes is straightforward: we just need the velocity parameter $a$ and two periods: the incubation period $L$ and recovery period $T$ with symptoms after the carrier is separated from society. We derive an analytical result for exponential growth in the early stages of epidemics, as well as for the epidemic threshold. It will be very interesting to investigate the transitional situation near the threshold. We suggest simply making numbers and choosing a parameter value to match the correct exponential growth.

We applied our model to understand the situation with epidemics in Armenia. both the simple version of the model and the generalized version. What is advantageous in the second version of our model, that we can clearly separate two aspects of the epidemic: contact strength (through coefficient $A$) and deterrence measures through parameter $g$. Our model with few degrees rather accurately described the exponential growth phase of the epidemics. For the linear growth phase (the case in Armenia since June 2) we need to use the many degree model using some network for the human contacts. The geometry of the network should be essentially 1-dimensional to support the constant growth of infected population. Such are small world networks. In [16] has been investigated an epidemics model using small world network, mapping to SIR. It will be interesting to look the generalization of our model for such a geometry.

Here we give a statistical physics description of the epidemics. For the qualitative physics description from the perspectives of complex systems, see [17].

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