Information feedback provokes multi-peak dynamics in the modern world epidemic spreads

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Research Article

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Information feedback provokes multi-peak dynamics in the modern world epidemic spreads

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Abstract

We propose simple agent-based mathematical model of epidemic development capable to generate various multi-peak dynamics typical to COVID-19 pandemic. Agents are supplied with very simple kind behavior moving in a homogeneous interaction space with a constant speed. There is a probability of infection transmission if the agents meet with at certain distance. Next we assume that our agents get three features of intelligences called here: (i) information induced feedback, (ii) delay reaction on danger and (iii) danger adaptation. All these features are accounted in the model by the infection probability that becomes dynamic variable driven by additional differential equation. The information feedback means that this probability decreases with growing number of infected cases. It reflects facts that in modern world information media monitor the pandemic situation and with progressing infection around people start to protect them carefully that finally leads to the decrease of infected cases. Characteristic timings accounted in our model by delay reaction on the information feedback and danger adaptation time are also important in the probability dynamics. Surprisingly, but within these simple assumptions that did not touch any molecular specificity of COVID-19, except quite long exposure time, we immediately get a multi-peak dynamics of the pandemic development. Here, we show different conceptual cases of how such rhythmicity evolves under different parametric conditions.

Introduction

It has become evident that the spread COVID-19 pandemic in the world represents global challenge in all spheres of life including science and technology. Obviously, that the development of vaccines and drugs against COVID-19 made the most significant contribution in fight with virus. On the other side, modeling spread of the infection and epidemic predictions became crucially important during the pandemic. These issues were critical also for authorities to organize life and economics playing with mobility restrictions and isolations. Mathematical models proposed to describe infection dynamics were mostly based on classical SIR approach accounting also different factors specific for COVID-19 such relatively long incubation period and the possibility of the virus to survive without carrier. Most of mathematical models capable to fit initial data were generally unable to make reliable rather long-term predictions. Of course, there were a lot of biological factors of COVID-19 that was difficult to account such as intensive mutations that led to different parameters of virus contagiousness, different time scales in the incubation and infection period, etc.

Existing models employed two basic concepts in mathematical modeling. The first one is the extension of classical SIR models proposed by Kermack and McKendrick [1]. Different modifications divided basic S (Susceptible), I (Infectious), R (Recovered) classes on groups with
different ages, some models differentiated classes on geographical locations and others [2, 3]. Compartmentalization is one way to introduce spatial heterogeneity into the basic SIR model [4, 5]. A number of works have been published using SIR and its modifications to predict and evaluate the impact of quarantine measures on the epidemic dynamics of COVID-19 [6, 7]. [8] showed that strict government regulation improves the epidemiological situation, but as the number of infected people increases, the effectiveness decreases somewhat. In general, modeling shows that early detection, early isolation, early treatment, and a comprehensive treatment strategy are needed to slow the spread of a pandemic [8, 9].

Another approach employed agent based models simulating the dynamics of a large number of interacting agents [10, 11]. At variance with population approach such models can take into account heterogeneity of evolution space [12, 13]. Moreover, the agent-based approach makes it possible to implement adaptive behavior through "local intelligence". In turn, adaptive behavior, which consists in the ability of an agent to change its state following a change in its environment, can lead to non-linear causality. Behavioral reactions of agents determine additional changes in the environment, which in turn affect the behavior of agents, etc. [14].

One of the characteristic feature of the COVID-19 dynamics was the appearance multiple peaks in the infection cases [15–18]. Several consequent peaks may differ in the amplitude and duration depending on particular country. Dynamical origin of such multi-peaks dynamics is still a discursive issue. In the framework of SIR concept a possible origin of the oscillation is finite immunity period with consecutive transfer from R to I classes [19, 20]. However, one can note the first two year COVID-19 statistics that the peaks are repeated much faster than estimated length of immunity period after the decease. A number of studies have shown the possibility of repeated peaks when restrictive measures are canceled [6, 15, 21–23]. On the other hand, [24] show that a change in the structure of the social network during the development of an epidemic peak or its decline can lead to repeated peaks.

An interesting concept in the framework of SIR approach was recently proposed in [25] incorporating social component. In particular, based on general adaptation syndrome (GAS) theory by Hans Selye [26] SIR model was supplied by three behavioral stages of the human being prompted by a stressor should be accounted. The susceptible class was split on three subgroups including ignorant, resistance and exhaustion types. In the result the model demonstrated two consequent peaks due to interplay between these subclasses with different effective infection rates.

Focusing on conceptual origin of the multi-peak dynamics in our study we made a step back from average population SIR type modeling to population of agents evolving in a homogeneous medium with certain type of intelligence. The agent’s intelligence is a conceptual feature of modern technological world. Communication and information technologies involving TV, mass media and internet provided fast integration of information and their delivery to almost all individuals in the world. This information inevitably corrects the behavior of the agents. Even without introduction subclasses like it was done in [25] we assume that information about the decease cases provides a negative feedback on the agent behavior. The feedback rule may be formulated in a quite general and simple form. Significant increase of infected cases delivered by information media provokes more careful behavior of the agents and, in turn, the its decrease leads to careless behavior. These information induced behavioral changes can be accounted by variable probability, \( p \), that we in our model. This variable depends on the number of agents in state “Infectious”, and in time, \( p(t) \), exponentially decays to its stationary value with a characteristic time reflecting inertia in the individual reactions on the information content. In
addition, agent behavior was also supplied with "habituation to danger" characterized by a decrease in the level of caution of individuals with time.

**Model**

Concept of the model is illustrated schematically in Fig.1A. Agents evolve in a twodimensional world. Information about epidemic dynamics is continuously collected and integrated, specifically by mass media and internet with rather fast time scale, and then delivered to each agent in the agent world. The states of the agents are described in terms of SEIR models: Susceptible (S), Exposed (E), Infectious (I), Recovered (R). For simplicity, we assumed that each agent is an independent unit moving at its own constant speed \( v_i \). The direction of movement changes only when an agent reaches the boundary of the modeled space. Figure 1B illustrates the simulation agent space with agent’s states shown by colors. The transition from S to E occurs with probability \( p \) when an S-agent appears within the radius of infection \( R_i \) of I-agent. The transition of an agent from state E to I is carried out through the latency period \( \Delta t_{li} \). In turn, the agent's recovery period \( \Delta t_{ri} \) determines the duration of the agent's stay in state I (Fig. 1C).

Fig. 1. A. Concept of the multi-agent model in the information field. A) Conceptual diagram of the interaction of agents between themselves and the information field. B) An overall view of model scene and scaled fragment (the insert). Green, yellow, red and grey colors illustrates susceptible, exposed, infected and recovered states of the agents, respectively. C) A scheme of state transition: S – susceptible, E – exposed, I – infectious, R – recovered. \( R_i \) – the infection radius of agent \( i \); \( \Delta t_{li} \) – the latency period; \( \Delta t_{ri} \) – the recovery period.

In numerical simulations we developed computational framework which was implemented in the QT cross-platform (Windows, Linux, Mac OS) development environment in the C++. The application can be found in Supplementary material. The application has an advanced graphical user interface (GUI) for setting model parameters including the number of agents in the population \( N \), the size of the simulated space \( S \) and the probability \( p \). We use \( N = 10000, S = 2800 \times 2800 \) pixels. Such parameters as \( \|v\| \), \( R \), \( \Delta t_{li} \) and \( \Delta t_{ri} \) are set in the GUI as mean and standard deviation of sets obeying the Gaussian distribution. In particular \( \|v\| = 0.5 \pm 0.2 \) pixels/hour, \( R = 3 \pm 1 \) pixels, \( \Delta t_{li} = 5 \pm 1 \) days and \( \Delta t_{ri} = 14 \pm 2 \) days. The step of the model is 1 hour, the initial conditions include 100 I-agents (1%), uniformly distributed in the model space.

For our purpose, here we neglected many specific features of COVID-19 infection including changing infection probability due to mutations, possibility of reinfection, vaccination, changing states due to therapy and others. As one may expect, in this form with no intelligence,
agent’s dynamics will lead to statistics very much similar to population models. The use of a constant infection probability $p$ in the absence of spatial heterogeneity in our model results in the dynamics typical for population models of the S(E)IR type. In particular, we observe an exponential increase in the number of infected agents at the initial stage of the epidemic. Then there is a decrease in the rate of infection, reaching an epidemic peak, and finally, a decline in the number of infected.

Next, we supply agents in our model by very simple type of “intelligence”. We introduced a global information field in the following form. The information represents the number of overall infected agents constantly monitored in time. Furthermore, agents change their behavior according to simple rules. If we see large number of infected individuals we choose more careful modes of behavior due to natural fear of illness and death, and/or due to authority restrictions. Otherwise, if one note from the information field that the number of infected persons goes down, then individuals become less restricted in their modes of behavior. In terms of the agent’s behavior these rules can be accounted by the information-dependent infection probability, $p$. For our purpose of qualitative simulations we chose the feedback function in the form of sigmoidal curve illustrated in Fig. 2. The infection probability $p$ depends on the number of infected $I$-agents, $N_i$. Specifically, we introduce the function in the following form:

$$p(N_j) = p_{\text{max}} - \frac{p_{\text{max}} - p_{\text{min}}}{1 + e^{-\frac{12N_j}{N_{i,\text{max}}}}}.$$  

Here $p_{\text{max}}$ is the maximal value of the infection probability $p$ (the base line for $p$). The value $p_{\text{max}}$ can be interpreted as the probability of infection in case of minimal caution in the agent society. Minimum probability of infection, $p_{\text{min}}$, corresponds to the case of maximum alert state in the limit of increasingly large number of infected cases. Furthermore, we can use coefficient $C_F = \frac{p_{\text{max}}}{p_{\text{min}}}$ as strength of the negative feedback.

![Fig. 2. Epidemic feedback as the dependence of infection probability $p$ on relative number of infectious agents $N_j$. $p_{\text{max}}$ – base line of probability, $C_F$ – coefficient of the feedback, $N_{i,\text{max}}$ – the relative number of infected, causing maximum vigilance. We defined it using the following expression: $p(N_{i,\text{max}}) = (0.0025C_F + 0.9975)p_{\text{min}}$, that fixed 2.25% from the asymptotic value $p_{\text{min}}$. Results](image)

Information supplied, e.g. “intellectual” agents, immediately started to demonstrate much more complicated dynamics relative to traditional a “blind” homogeneous models. Figure 3 illustrates the first simulation results. One can observe noticeable peaks in the dynamics of infected cases. Following Eq. (1), infected probability, $p$, follows the infection peaks (Fig. 3). Each such drop of $p$ provides an opportunity for a quick completion of the current peak, a decrease in the number of infectious and, as a consequence, an increase $p$ in the future. Obviously, because we neglected reinfection transition the number of peaks was always limited and the epidemic eventually ends.
Fig. 3. An example of two-peak epidemic dynamics with the negative feedback. The blue marker indicates the beginning of maximum alert state with the smallest value of $p$. Parameters used: $p^{\text{max}} = 0.1$, $\mathcal{C}_F = 100$, $N_{t_{\text{max}}} = 0.35$.

Next, we analyzed what parameters control the number of peaks, their amplitudes and the inter-peak interval. Figure 4 summarizes simulation results for different values of $N_{t_{\text{max}}}$ and $\mathcal{C}_F$. In the absence of the feedback ($\mathcal{C}_F = 1$), the epidemic dynamics is standard displaying single peak. When increasing the feedback, e.g. for larger values of $\mathcal{C}_F$ additional multiple peaks appeared. Note, that $\mathcal{C}_F$ is shown in the logarithmic scale. At the same time increasing number of peaks is associated with lower amplitude (Fig. 4, the right panel). Parameter $N_{t_{\text{max}}}$ characterizing the threshold of feedback activation also influenced the multi-peak dynamics. The greater $N_{t_{\text{max}}}$ was, the fewer peaks with greater amplitude were observed. In turn, the inter-peak interval was not dependent on the parameters of the feedback and was defined by characteristic time scales of infection, incubation and recovering. Its average value for chosen parameter set was approximately 26 days. In simulations we also noticed that the inter-peak interval depended linearly on both the latency and recovery periods $\Delta t_l$ and $\Delta t_r$ (not shown here).

Next, we noticed that even qualitative comparison of the value of inter-peak interval obtained in simulations and data of COVID-19 dynamics showed that they differed significantly. Intervals between neighboring peaks may last several months or even more [27]. It means that something significant was missed in our original model formulations. Indeed, Eq. (1) implied immediate reaction of agents on the information about infected cases. Obviously, that in reality there is delay between the information feedback and agent response, e.g. changing the probability. This delay may be defined by many reasons including a lag between the moment when a person becomes infectious until the PCR positive test; time to make decision by the authorities on restriction level; a delay in media integrating the epidemic situation and, probably, a delay in agent response on the information, e.g. “inertia of mind”. This additional time scale can be accounted in the simple form of the following linear differential equation:

$$\frac{dp}{dt} = \frac{p_{\infty} - p}{\tau},$$  

(2)
where $p_\infty$ denotes equilibrium level $p$ defined by Eq. (2) and $\tau$ is the characteristic time of agent reaction on the feedback information.

Fig. 4. Characteristics of epidemic dynamics depending on parameters of negative feedback: $N_i^{\text{max}}$ and $C_F$. Note that there is no feedback when $C_F = 1$.

Figure 5 illustrates model dynamics with the inertial response on the information feedback. Due to the delay the alerts points corresponding to minima of $p$ values (Fig. 5A, blue markers) took place on the decay of each peak comparing to instantaneous dynamics (Fig. 3). There was also an increase in time of both peak values and the inter-peak interval. The larger the value of $\tau$, the greater the peak-to-peak interval. Figure 5B illustrates the dependence of the inter-peak interval on the reaction time in several simulation series and corresponding linear and power-law fits. So that, the inter-peak interval can reach values of several months similarly to observed COVID-19 data.

Fig. 5. Dynamics of the multi-agent model with feedback reaction delay. A) Example of simulation with longer inter-peak period (up to 89 days). Blue markers indicate the alert points where $p(t)$ reaches its minima. Parameters values: $\tau = 30$ days, $p^{\text{max}} = 0.03$, $C_F = 30$, $N_i^{\text{max}} = 0.01$. B) The inter-peak interval obtained in a series of simulations vs. characteristic time of the process of relaxation $p$ to $p_\infty$.

We also noticed that in all simulations consequent peaks had lower amplitudes than the first one. It should not be, however, general limitation of the model. Another qualitative
correction of the model was the account for effect of risk habituation [28]. Obviously, over time, people tend to pay less attention to repetitive signals of danger. At the same time, negative information feedback may persist, but its activation requires higher values of infected cases. In our model it can be accounted by simple linear trend:

$$N^\text{max}_t(t) = N^\text{max}_t \left(1 + c_a \tau\right)$$  \hspace{1cm} (3)

Figure 6A illustrates the dependence of equilibrium information feedback function, $p_\infty(N_t)$, dependences for different habituation times. For illustration, epidemic dynamics was calculated for $c_a = 9 \text{ year}^{-1}$ (Fig. 6B). In this case, each year $N^\text{max}_t$ was increased by $9N^\text{max}_t$ and our model demonstrated repetitive peaks with increasing amplitude. Variable $N^\text{max}_t$ increased linearly (Fig.6B, dashed line), corresponding to shift of the alert population state to larger values of $p$ (Fig.6B, blue markers) where the epidemic was more and more pronounced.

![Fig.6](image)

**Fig.6.** An example of multi-peak epidemic dynamics with feedback reaction and risk habituation. A) Dependences $p_\infty(N_t)$ taken at different times. B) The epidemic dynamics with increase in the amplitude of repeated peaks. Blue markers indicates the alert points with minimums in the dynamics of $p$. Parameters used: $c_a = 9$, $\tau = 30 \text{ days}$, $p^{\text{max}} = 0.03$, $C_p = 100$, $N^\text{max}_t \left(1 + c_a \tau\right) = 0.001$.

**Discussion**

Being a global challenge COVID-19 pandemic stimulated research in many areas of science including mathematical modeling and statistics. Technologies of modern world permitted collecting data and monitoring of epidemic situation in most of the world countries in real time. Of course, it stimulated attempts to construct different predictive statistical and dynamical models targeting long term predictions. To our knowledge, most of models designed on actual data failed to make even qualitative forthcoming predictions albeit were quite successful in fitting data post-factum exploring different epidemic features. If one looks at the epidemic curves in different countries [27] there are drastically different qualitatively and cannot be integrated in one statistical or functional law. The reasons of that may be different. Indeed, there was complex virus dynamics with strong ability to survive, intensive mutations, different stamps, specificities to particular groups populations and many other. In this case, it looks hardly possibly to construct a universal predictive model.

In our research we tried to address conceptually basic features of COVID-19 qualitative dynamics and identify possible dynamical mechanisms responsible for so variable epidemic statistics in different countries. At the moment of beginning of 2022 we can safely approve the following basic features of COVID-19 dynamics including multi-peak character comprising 2, 3 or more humps in the infected cases and variable magnitude, duration and inter-peak intervals.
Surprisingly, that our model constructed on the assumption of “intellectual agents” interacting with global information media successfully demonstrated all these qualitative features of the COVID-19 dynamics. Because of the reasons explained above we did not target to fit quantitatively statistics of particular countries. We neglected obvious detailing of the model, e.g. heterogeneity of the agent space, differentiations in agent behavior, virus details, vaccinations, therapy, etc, to verify that agent interaction with modern world information field, that never existed in the past epidemics, represents universal robust mechanisms of the multi-peak dynamics with different statistics of peak magnitudes and characteristic timings that can be found in the COVID-19 statistics.

Finally, this information field effect may have a kind of “quantum interpretation” in the sense that any measurement changes the state of a quantum system. In the current pandemic case measurement of the epidemic changes its spread in a quit sensitive hardly predictable way.

Statements and Declarations

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Conflict of interest
The authors declare that they have no conflict of interest.

Data Availability Statement
Data sharing is not applicable to this article as no datasets were generated or analysed during the current study.

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