Utrametric diffusion equation on energy landscape to model disease spread in hierarchic socially clustered population

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Abstract

We present a new mathematical model of disease spread reflecting some specialties of the covid-19 epidemic by elevating the role of hierarchic social clustering of population. The model can be used to explain slower approaching herd immunity, e.g., in Sweden, than it was predicted by a variety of other mathematical models and was expected by epidemiologists; see graphs Fig. 1,2. The hierarchic structure of social clusters is mathematically modeled with ultrametric spaces having treelike geometry. To simplify mathematics, we consider trees with the constant number $p > 1$ of branches leaving each vertex. Such trees are endowed with an algebraic structure, these are p-adic number fields. We apply theory of the p-adic diffusion equation to describe a virus spread in hierarchically clustered population. This equation has applications to statistical physics and microbiology for modeling *dynamics on energy landscapes.* To move from one social cluster (valley) to another, a virus (its carrier) should cross a social barrier between them. The magnitude of a barrier depends on the number of social hierarchy's levels composing this barrier. We consider *linearly increasing barriers.* A virus spreads rather easily inside a social cluster (say working collective), but jumps to other clusters are constrained by social barriers. This behavior matches with the covid-19 epidemic, with its cluster spreading structure. Our model differs crucially from the standard mathematical models of spread of disease, such as the SIR-model; in particular, by notion of the probability to be infected (at time t in a social cluster C). We present socio-medical specialties of the covid-19 epidemic supporting our model.

keywords: energy landscapes; ultrametric spaces; p-adic numbers; ultrametric diffusion equation;social barriers; linear growing barriers covid-19; epidemic; disease spread; herd immunity; hierarchy of social clusters; superspreaders, asymptomatic individuals; rigid vs. mild social restrictions.

1 Introduction

The covid-19 epidemic has many unusual features (see appendix 1). One of them plays the crucial role in disease (say a virus) spread. We formulate it as the basic assumption of this paper (see also [1]):

AS0 *Virus' spread in population is constrained by the hierarchic social cluster structure.*

How can one model mathematically hierarchic social clustering of population? In a series of works [2]-[7], we constructed *ultrametric clustering* of population by using the system of hierarchically ordered social coordinates and this approach was applied in cognition, psychology, sociology, information theory (see also [8]-[12]). In this paper, we shall use ultrametric diffusion equation [13]-[21] to describe dynamics of covid-19 spread in socially clustered population. It is important to note that ultrametric spaces have treelike geometry and we study virus' dynamics on social trees. To simplify mathematics, consideration is restricted to homogeneous trees with p-branches leaving each vertex. Such trees are endowed with an algebraic structure, these are p-adic number fields $\mathbf{Q}_p$. We remark that p-adic numbers are widely used in number theory and algebraic geometry. Their applications to natural phenomena started with string theory and quantum physics [22]-[24].

The specialties of covid-19 epidemic[1] are not reflected in the standard mathematical models [25]-[27], such as, e.g., the canonical SIR model [28] and its diffusion-type generalizations, e.g., [29]. Consequently, in spite of the tremendous efforts [30]-[36], mathematical modeling of covid-19 spread cannot be considered as successful. Therefore, we have to search for new mathematical models reflecting better the covid-19 specialties. The recent paper [1] based on **AS0** can be considered as a step in this direction. In it, we studied the problem of *approaching herd immunity in heterogeneous socially clustered population.* A virus does not spread throughout population homogeneously

[1]See appendix 1, "covid on surface", "covid in air", "asymptomatic individuals", "no mass-events", "superspreaders"; in this paper we are interested in mild restrictions, as say in Sweden, i.e., without lock-down.

as it is described by the standard models of disease spread. Its spread has the clear social cluster character (cf. with disease spread modeling in articles [37]-[40], especially with the last paper as referring to epidemic in Sweden). The virus spreads relatively easy in a social cluster that was infected by somebody, but approaching other clusters is constrained by social barriers.

Such virus spread is described very well by *dynamics on energy landscapes.* The latter is well developed theory with numerous applications to statistical physics (e.g., spin glasses) and microbiology [41]-[47]. An energy landscape is a system of (energy) valleys separated by barriers of different heights having a hierarchic structure. A system (physical, biological) can move inside a valley or jump over a barrier to another valley, with some probability. Thus, the simplest mathematical model is given by *random walks on energy landscapes* (see, e.g., [48]). Behavior of random walking depends crucially of grows of barriers coupled to the hierarchic structure of an energy landscape.

Geometrically the hierarchy of valleys (clusters) of an energy landscape has the treelike structure. As is well known, trees also give the geometric representation for ultrametric spaces and vice verse. Thus, dynamics on energy landscapes, collection of clusters separated by hierarchically ordered barriers, can be represented as dynamics in ultrametric spaces.

In the first paper [1] on ultrametric approach to disease spread, we explored the random walk in ultrametric spaces, see, e.g., [48] for simple mathematical theory. Such random walk is the discrete version of *ultrametric diffusion.* Theory of diffusion equations in ultrametric space is well developed [13]-[21]. In the present paper, we apply its powerful mathematical apparatus for modeling disease spread in hierarchically structured social clusters. The problem of approaching herd immunity is reformulated in terms of ultrametric diffusion equation. This reformulation makes the model mathematically rigorous (studies [41]-[47], [48] were at the physical level of rigorousness) and opens the door for development of a variety of new mathematical models of disease spread taking into account the hierarchic social cluster structure of population.

We consider a country relatively mild preventing measures[2] and model this situation with linearly increasing barriers; context of rigid preventing measures as say lock-down can be modeled with exponentially increasing barriers.

For Sweden, this problem of approaching herd immunity is of the big value. The country did not impose the lock-down and the system

[2]See [1], appendix 2 for compact description of situation in Sweden, March-June 2020, from the viewpoint of imposing social barriers.

of measures presented by the state epidemiologist Anders Tegnell and his team was aimed to approach herd immunity and, in this way, to make essentially weaker or escape at all the second wave of covid-19 epidemic and may be proceed without vaccination. However, the dynamics of population's immunity against coronavirus is very slow, essentially slower than it was predicted by Swedish epidemiologists and by mathematical models of disease spread [3] (see, e.g., [49]-[51] for reports from Public Health Institute of Sweden, [32]-[34] for attempts of mathematical modeling and [52]-[56] for reports from massmedia).

As we have seen [1], ultrametric random walk (with jumps over mild barriers linearly growing with levels of social hierarchy) generates dynamics with asymptotic behavior of the power type; herd immunity in a social cluster C grows as

$$p_{\mathrm{Im}}(C,t) = 1 - t^{-q}, q > 0. \tag{1}$$

Generally (but, of course, depending on the parameter q) this function increases slowly. This asymptotic can explain unexpectedly slow approaching herd immunity during covid-19 epidemic, say in population of Sweden. The basic parameter of the model

$$q = T \ln p/\Delta. \tag{2}$$

Here $T > 0$ is the social analog of temperature, the degree of activity in a society, Δ is the magnitude of the elementary barrier for hopping between nearest social levels. Higher social temperature T implies more rapid approaching of herd immunity; higher social barrier Δ implies slower growth of herd immunity. Quantity $\ln p$ can be interpreted as entropy of virus spreading inside a social cluster, $\mathcal{E} = \ln p$, (see (**??**)). This entropic interpretation leads to conjecture that more general processes of disease spread (with the same linear growth of barriers) would lead to the following asymptotics for approaching herd immunity:

$$p_{\mathrm{Im}}(C,t) = 1 - t^{-\frac{T\mathcal{E}}{\Delta}}. \tag{3}$$

In the present paper, by using results of work [17] on the relaxation dynamics for diffusion pseudo-differential equation on ultrametric spaces we reproduce the power law for dynamics of herd immunity [1], for linearly growing barriers. The technique of ultrametric diffusion equations provides the possibility to study this problem for other

[3] In particular, by models Tom Britton [32, 33] that was used by Swedish State Health Authority predicted that herd immunity will be approached already in May; Anders Tegnell also announced, starting from the end of April 2020, that Sweden would soon approach herd immunity, but it did not happen, neither in May, nor June and July.

types of barriers as well as for design of more general mathematical models of disease spread.

Just before submission of preprint [1], I found the recent paper of Britton et al. [40] in that the role of population heterogeneity in spread of covid-19 was analyzed. We remark that Britton contributed a lot in mathematical modeling of covid-19 spread in Sweden. His models [32, 34] were explored by chief epidemiologist Anders Tegnell to justify the Swedish policy with respect to epidemic - no lock-down as expecting rapid approaching herd immunity. On the basis of Britton's models, Swedish State Health Authority predicted (at the end of April 2020) that the herd immunity will be approached already in May. However, this prognoses did not match the real situation and the herd immunity was not approached neither in May nor in June (see, e.g., [49]-[51] for reports from Public Health Institute of Sweden, see also [52]-[56]). In previous modeling [32, 34] for covid-19 epidemic, Swedish population was considered as homogeneous. In [40], heterogeneity of population was considered as an important factor; the model involves two "social coordinates" (in our terminology): *social activity and age.*

Taking into account population social clustering is the basic similarity of our models (see also appendix 3) and generally paper [40] is supporting for our approach. The main difference is that in [40] the hierarchic structure of social clustering and hence the hierarchy of barriers between clusters is not taken into account. Another crucial difference is in mathematical methods, based on the real metric vs. ultrametric. Surprisingly, these two totally different mathematical models led to graphs of the same shape, see Fig. 2 and see Fig. S2, supplementary material [40]. Both models provide the possibility to play with strength of preventive measures and see their effect onto the epidemics' dynamics.

2 Hierarchic treelike geometry of social clusters

We represent the human society as a system of hierarchically coupled (as a treelike structure) disjoint clusters. There are many ways for mathematical modeling of such representations. Theory of *ultrametric spaces* is one of the basic mathematical tools for this purpose. Geometrically ultrametric spaces can be represented as trees with hierarchic levels. Ultrametricity means that this metric satisfies so-called strong triangle inequality:

$$\rho(x, y) \leq \max\{\rho(x, y), \rho(y, z)\}, \tag{4}$$

for any triple of points x, y, z. Here in each triangle the third side is less or equal not only the sum of two other sides (as usual), but even their maximum. Define balls as usual in metric spaces $B_R(a) = \{x : \rho_p(x, a) \leq R\}$, where a is a center of the ball and $R > 0$, is its radius. The balls have the following basic properties:

- Two balls are either disjoint or one of them is contained in another.
- Any point of a ball can be selected as its center, i.e., $B_R(a) = B_R(b)$ for any $b \in B_R(a)$.

Any ball can be represented as disjoint union of balls of smaller radius, each of the latter can be represented in the same way with even smaller radius and so on. We get hierarchy of balls corresponding to disjoint partitions. Geometrically a ball is a bunch of branches of a tree.

We use the ultrametric balls to represent mathematically social clusters, any cluster is slit into disjoint sub-cluster, each of the latter is split into its own (disjoint) sub-clusters and so on. Inclusion relation generates the hierarchy on the set of social clusters.

In a series of works of the author and his collaborators [2]-[6], ultrametric spaces (geometrically hierarchic trees) were applied for modeling of cognitive, psychological, and social phenomena. This modeling was based on invention of systems of discrete social (or mental in cognitive studies) coordinates $x = (x_m)$ characterizing (psycho-)social states of individuals. The treelike representation of *social states* is based on selection of hierarchically ordered social factors enumerated by index $m \in \mathbf{Z} = \{0, \pm 1, \pm 2, ...\}$. (It is convenient to work with coordinates enumerated by integer numbers.) The social importance of coordinates x_m decreases with increase of m and increases with decrease of m; e.g., social coordinate x_0 is more important than any $x_j, j > 0$, but it less important than any $x_j, j < 0$. The coordinate x_0 can be considered as a reference point. Depending on context (say socio-economic or socio-epidemic) it can be shifted to the right or to the left. Therefore it is convenient to use positive and negative indexes determining two different directions of social importance of coordinates.

We consider discrete social coordinates, generally, for each m, there N_m possible values, $x_m = 0, 1, ..., N_m - 1$, and N_m can vary essentially with m. In the treelike representation, numbers N_m determine the number of branches leaving vertexes. Such trees are complicated and we restrict modeling to homogeneous trees for that N_m does not depend on m. Moreover, by pure mathematical reasons it is convenient to select $N_m = p$, where $p > 1$ is the fixed prime number. We remark

that the corresponding theory was developed even for arbitrary trees (ultrametric spaces), but it is essentially more complicated [18, 19].

Thus, a social state x is represented by a vector of the form:

$$x = (x_{-n}, ..., x_{-1}, x_0, x_1, ..., x_m),\ x_j \in \{0, 1, ..., p-1\}. \qquad (5)$$

The vector representation of psychical, mental, and social states is very common in psychology and sociology. The essence of our approach [2]-[6] is the hierarchic ordering of coordinates leading to introduction of ultrametric on the state space, see (8).

For our purpose, modeling of epidemic, we can consider, for example, the following hierarchic system of social coordinates; for simplicity, let index $m = 0, 1, 2, ...$, so the coordinate x_0 is the most important. It is natural to use it to denote states (e.g., Sweden, Russia, USA,...); x_1 can be used for age; x_2 for chronic diseases, x_3 gender, x_4 for race, x_5 for the town of location, x_6 for the district, x_7 for profession, x_8 for the level of social activity, x_9 for the number of children, and so on. We understand that such ranking of the basic social factors related to the covid-19 epidemic is incomplete. The contribution of sociologists, psychologists, and epidemiologists can improve the present model essentially, see even the recent article [57] on mathematical model of evolutionary creation of social types and contribution of genetics and natural selection.

Since the majority of states selected the lock-down policy that was not oriented towards approaching herd immunity, we restrict consideration to the Swedish population. So, in the above assigning of social meaning to coordinates they are shifted to the left. We also stress that hierarchy of social factors involved in the covid-19 epidemic can be selected depending on the state, i.e., for each state we create its own system of social clustering coupled to this epidemic. Consider USA, here the population is not so homogeneous with respect to the level of income and the life style connected to income as it is in Sweden. The social factor of belonging to up or low income classes plays the crucial role in covid-19 infecting. It seems that this coordinate should be places as the next (to the right) to the age-coordinate, then the race-coordinate and so on. Thus, the above hierarchy, (age, chronic disease, gender, race, town, district, family,...), that is appropriate for Sweden, should be rearranged for USA, as say (age, income, race, chronic disease, gender, town, district, family,...).[4]

It is convenient to proceed with variable number of coordinates, i.e., not fix n and m. This gives the possibility to add new coordinates. The space of such vectors can be represented by rational numbers of

[4]Income did not play any role in Sweden during the covid-19 epidemic.

the form

$$x = x_{-n}p^{-n} + ... + x_{-1}p^{-1} + x_0 + x_1 p + ... + x_m p^m, \; x_j \in \{0, 1, ..., p-1\}. \tag{6}$$

This is the basis of the number-theoretic representation of the space of social states. We shall consider it later. Now we continue in the vector framework.

To use fruitfully ultrametric models, we have to construct a complete metric space. The standard way to achieve completeness is to consider infinite sequences of the form:

$$x = (...., x_{-n}, ..., x_{-1}, x_0, x_1, ..., x_m, ...), \; x_j \in \{0, 1, ..., p-1\}, \tag{7}$$

where, for each x, there exists n such that $x_{-j} = 0, j > n$. Denote the space of such sequences by the symbol $\mathbf{Q}_p$. On this space, a metric is introduced in the following way. Consider two sequences $x = (x_j)$ and $y = (y_j)$; let $x_j = y_j, j < n$, where n is some integer, but $x_n \neq y_n$. Then the distance between two vectors is defined as

$$\rho_p(x, y) = p^{-n}. \tag{8}$$

So, if n is negative, then distance is larger than 1, if n is nonnegative, then distance is less or equal to 1. The ρ_p is an ultrametric. We remark that each ball can be identified with a ball of radius $R = p^n, n \in \mathbf{Z}$. Ball $B_1(0) =$ plays the important role and it is defined by special symbol $\mathbf{Z}_p$. As in any ultrametric space, each ball is represented as disjoint union of smaller balls,e.g.,

$$\mathbf{Z}_p = \cup_{j=0}^{p-1} B_{1/p}(a^j) = \cup_{j_0 \cdots j_{n-1}=0}^{p-1} B_{1/p^n}(a^{j_0 \cdots j_{n-1}}) \tag{9}$$

where $a^j \in \mathbf{Z}_p$ is constrained by condition $x_0 = j$ and $a^{j_0 \cdots j_{n-1}}$ is constrained by conditions $x_0 = j_0, ..., x_{n-1} = j_{n-1}$, and so on. We recall that in an *ultrametric space, any point of a ball can be selected as its center.*

In our model, p-adic balls represent social clusters corresponding to fixing a few social coordinates. For example $C_j = B_{1/p}(a^j) = \{x \in \mathbf{Z}_p : x_0 = j\}$, in above epidemic coding C_j corresponds to fixing age= j; $C_{ji} = B_{1/p}(a^{ji}) = \{x \in \mathbf{Z}_p : x_0 = j, x_1 = i\}$, age= j, gender $= i$ for Swedish society or age= j, income level= i for American society.

Social states, points of $\mathbf{Q}_p$, can be cosnidered as balls of zero radius, we call them *elementary social clusters.* Partitions of a ball into disjoint balls of smaller radii corresponds to partition of a social cluster into disjoint subclusters of deeper level of social hierarchy.

Now we turn to the algebraic representation of social states by rational numbers, see (6). The space $\mathbf{Q}_p$ endowed with ultrametric ρ_p

can be considered as completion of this set of rational numbers and algebraically the elements of $\mathbf{Q}_p$ can be represented by power series of the form

$$x = \sum_{k=n} x_k p^k \tag{10}$$

where $x_j \in \{0, 1, ..., p-1\}, x_n \neq 0$, and $n \in \mathbf{Z}$; so only finite number of coordinates with negative index k can differ from zero. Such a series converges with respect to ultrametric ρ_p. Representation by the power series gives the possibility to endow $\mathbf{Q}_p$ with the algebraic operations, addition, subtraction, multiplication, and division (the latter operation is defined only for prime p). Hence, $\mathbf{Q}_p$ is a *number field, the field of p-adic numbers.* This algebraic representation leads to number-theoretic representation of ultrametric, $\rho_p(x, y) = |x - y|_p$, where $x \to |x|_p$ is the p-adic analog of the real absolute value; per definition, for x given by series (10),

$$|x|_p = |\sum_{k=n} x_k p^k|_p = p^{-n}. \tag{11}$$

It satisfies the strong triangle inequality playing the fundamental role in p-adic analysis and implying (4):

$$|x + y|_p \leq \max\{|x|_p, |y|_p\}. \tag{12}$$

3 Probability to become infected as contextual probability

The quantity $p_I(C, t)$, the probability that a person belonging to social cluster C can become infected at the instant of time t, is the basic quantity of our model. Therefore, it is useful to discuss its meaning in more detail.

First of all, we point to the difference from the standard SIR-like models: $p_I(C, t)$ is not the proportion of infected people in cluster C at the instant of time t, i.e.,

$$p_I(C, t) \neq \frac{N_I(C, t)}{N}, \tag{13}$$

where N is the number of people in C and $N_I(C, t)$ is the number of infected people in C at the instant of time t. Thus, $p_I(C, t)$ has no straightforward relation to the number of infected people $N_I(C, t)$. Of course, $p_I(C, t)$ depends on $N_I(C, t)$, but not simply as frequency (13).

Probability $p_I(C, t)$ is determined by context $\mathcal{C}(C, t)$, the complex of social, economic, and epidemiological conditions in cluster C at the

instant of time t, i.e., this is *contextual probability.* Such probabilities are considered, e.g., in quantum theory [58], where it is difficult, if possible at all, to introduce "hidden variables" determining probabilities. We remark that the situation in epidemiology, especially with respect to the covid-19 epidemic, is similar to quantum physics and more general quantum-like modeling in cognition, psychology, and decision making [59, 60]. It is impossible to determine "hidden variables" behind many events (see appendix 3). So, people and social clusters of people definitely reacts to covid-19 in very different ways, there are bio-medical, social, and may be even psychological hidden variables. Context $\mathcal{C}(C,t)$ determines their distribution, but it seems to be impossible to find these probability distributions and their dependence on contexts.

One of the possibilities to interpret the probability to become infected in context $\mathcal{C}(C,t)$ is to use the subjective interpretation of probability.[5] By this interpretation $p_I(C,t)$ is subjective probability that is assigned by an individual to the event that by visiting social cluster C one would become infected (she is an arbitrary individual, she need not belong to social cluster C). We stress that a social cluster is a domain in social space, so it need not be determined simply by geography (although geographic location place the important role in determination of C). Subjective probability is widely used in decision making as a part of subjective utility theory. During some epidemic, people can be considered as decision makers who should estimate the probability to become infected by eating lunch with colleagues or dinner with friends, going to shopping mall, visiting Stockholm - for me, it was everyday decision problem during March-June 2020, and I really estimated the probability to become infected by covid-19; for my American friend from New York, similar decisions were about to go to Bronx or Manhattan, to barber (in June 2020) and so on. So, the subjective probability approach, although not so common in epidemiology, seems to be really natural for individuals' everyday decision making.

The problem under consideration is by knowing probabilities to become infected in social clusters $C_i, i = 1, ..., M$, at time t_0, $p_I(C_i, t_0)$, to estimate the probability for cluster C_k at later instances of time $t > t_0, p_I(C_k, t)$. Dynamics $t \to p_I(C_k, t)$ is described by the *master equation.* To write this equation, we have to consider conditional probabilities (also known as transition probabilities): $p(C_k|C_i;t)$ is the probability, for a person in social cluster C_k, to get infection from a person from cluster C_i. These conditional probabilities represent

[5] We remark that this interpretation became popular even in quantum physics, under the name of Quantum Bayesianism (QBism) [61].

intensities to become infected. The master equation has the form:

$$\frac{d}{dt}p_I(C_k,t) = \sum_{i\neq k}[p(C_k|C_i;t)p_I(C_i,t) - p(C_i|C_k;t)p_I(C_k,t)]. \quad (14)$$

By using infinitesimals, we can write this probability balance equation in the form:

$$p_I(C_k,t+dt) = p_I(C_k)+\sum_{i\neq k}[p(C_k|C_i;t)p_I(C_i,t)-p(C_i|C_k;t)p_I(C_k,t)]dt. \quad (15)$$

The term $p(C_k|C_i;t)p_I(C_i,t)$ gives the intensity of transition of infection from cluster C_i to cluster C_k. Thus the probability to become infected in cluster C_k increases due to transfer of infection from other clusters. Thus meaning of the positive term in the right-hand side of (15) is clear. Negative term describes the "flow of infection" from C_k to other clusters. This flow generates decrease of the probability to become infected in C_k. To describe the latter process, we should consider disease spreaders and their transitions between social clusters, say from Bronx to Manhattan and vice verse. The quantity $p(C_k|C_i;t)p_I(C_i,t)$ gives the probability that somebody from social cluster C_k (Manhattan) would be infected by somebody who comes to C_k from C_j (say from Bronx). But at the same time some infected people from Manhattan, C_k can go to Bronx, C_i, and infect people here. By being busy with infecting people in Bronx, people from Manhattan cannot infect people in their own social cluster, so the probability to become infected in Manhattan decreases by $p(C_i|C_k;t)p_I(C_k,t)dt$.

Latter, in section 5, we shall consider the random walk model of virus spreaders. As was pointed out, the main distinguishing feature of this model is the hierarchic social clustering of population and the presence of barriers between clusters. Barrier's height depends of the (social) distance between clusters.

Finally, we present the mechanical model for the above process of infection flow between social clusters. We can consider clusters as virus reservoirs, $p_I(C,t)$ gives the virus concentration in cluster C at time t. Once again, the presence of barriers increasing with hierarchy levels plays the crucial role in dynamics of virus'spread in population.

This probability is interpreted as in statistical mechanics of gases: as the concentration of virions (virus particles, consisting of nucleic acid surrounded by a protective coat of protein called a capsid) in cluster C that is interpreted as reservoir of virions. Now, we identify probabilities, $P(C,t) = P_I(C,t)$: probability to become infected is determined by concentration of virions in this cluster. Of course, concentration of virions is coupled with concentration of infected people, but not straightforwardly, since

- virions can live on various surfaces;
- covid-19 epidemic demonstrated the crucial role of superspreaders - super-powerful sources covid-19 virions [66] (see appendix 2).

Then $p(C_k|C_i;t)$ describes the intensity of transition of virions from cluster C_i to cluster C_k.

4 Modeling the virus spread with ultrametric diffusion equation

An elementary social cluster (social state) given by a point of $\mathbf{Q}_p$ is a mathematical abstraction. Real clusters are represented by balls of finite radii. Therefore it is interesting to study the evolution of average probability for cluster $C \equiv B_{p^n}(0), n = 0, \pm 1, \pm 2, ...$ Under assumption **AS3**, this quantity is represented as the integral with respect to the Haar measure:

$$p_I(C,t) = \int_C p_I(x,t)\mu(dx). \tag{16}$$

Under the above assumptions on the social structure of population and its interaction with the virus (including restrictions imposed by authorities in connection with epidemic), we can write the following master equation for probability $p_I(x,t)$,

$$\frac{\partial p_I(x,t)}{\partial t} = \int_{Q_p} [p(x|y;t)p_I(y,t) - p(y|x;t)p_I(x,t)]\mu(dy), \tag{17}$$

where $p(x|y;t)$ is the transition probability: the probability that the virus being present in (elementary) cluster y would jump to cluster x. We suppose that this probability does not depend on time t and it is symmetric, i.e., $p(x|y) = p(y|x)$. Under these assumptions, the master equation has the form

$$\frac{\partial p_I(x,t)}{\partial t} = \int_{Q_p} p(x|y)[p_I(y,t) - p_I(x,t)]\mu(dy). \tag{18}$$

It is natural to assume that the transition probability decreases with increasing of the distance between two clusters, for example, that

$$p(x|y) = \frac{C_\alpha}{|x-y|_p^{1+\alpha}}, \ \alpha > 0. \tag{19}$$

Here $C_\alpha > 0$ is a normalization constant, by mathematical reasons it is useful to select distance's power larger than one. This function

rather slowly approaches zero if the distance between points goes to infinity. Thus, *the probability of transmission of infection from cluster y to cluster x for socially distant clusters is practically zero.* This is an important property of the model. In fact, it implies slower (than in the standard models of disease spread) approaching herd immunity: for a virus, it difficult to spread between socially distant clusters. We also remark that if the distance between points goes to zero, then the probability (in fact, its density) approaches infinity. *This implies very rapid spread of infection in small social clusters.* In contrast to the standard SIR-like models, in our model the probability of transmission of infection depends crucially on social distance.

Hence,

$$\frac{\partial p_I(x,t)}{\partial t} = C_\alpha \int_{Q_p} \frac{p_I(y,t) - p_I(x,t)}{|x-y|_p^{1+\alpha}} \mu(dy). \tag{20}$$

The integral operator in the right-hand side is the operator of fractional derivative D^α (the Vladimirov operator), see [13]. Thus, the dynamics of the probability to become infected for those belonging to an elementary social cluster is described by *the p-adic diffusion equation:*

$$\frac{\partial p_I(x,t)}{\partial t} = D^\alpha p_I(x,t). \tag{21}$$

To formulate the Cauchy problem, we have to add some initial probability distribution. We select the uniform probability distribution concentrated on a single ball, initially infected social cluster C,

$$p_I(x,0) = \frac{1}{\mu(C)} \begin{cases} 1, & x \in C \\ 0, & x \notin C \end{cases}$$

This equation and its various generalizations were studied by many authors, for applications to physics and biology and by pure mathematical reasons, see, e.g., [13]. We are interested in the relaxation regime, i.e., asymptotic of average probability $p_I(C,t)$ for large t. We use the mathematical result from [17] (see also [18, 19]) and obtain that the average probability has the power behavior:

$$p_I(C,t) \sim t^{-1/\alpha}, \ t \to \infty. \tag{22}$$

Thus the average probability to become infected in a social cluster decreases rather slowly with time. If parameter α is relatively large i.e., the virus transition probability decreases very quickly with increase of the distance between social clusters, then $p_I(C,t)$ decreases very slowly with time, it is practically constant (see the upper graph at Fig. 1). If parameter α is relatively small, so the virus transition probability decreases slowly with increase of the distance, then

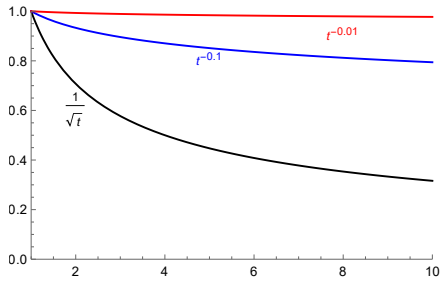

Figure 1: Asymptotic behavior of probability to become infected, transition probability parameter $\alpha = 2, 10, 100$.

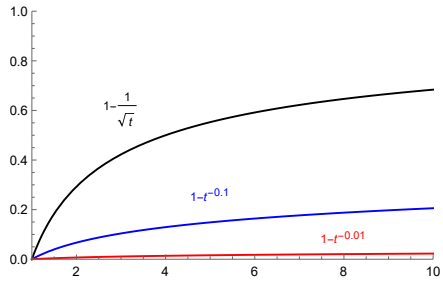

Figure 2: Asymptotic behavior of probability to become immune, transition probability parameter $\alpha = 2, 10, 100$.

$p_I(C,t)$ decreases sufficiently quickly with time (see the lowest graph at Fig. 1). We shall discuss these behaviors in section 5 by assigning bio-social meaning to the parameter α and by coupling it with teh degree of preventing measures established by authorities. We present some graphs corresponding to different values of α at Fig. 1.

Consider now a kind of "integral immunity", combination of innate and adaptive components, defined as the probability of not become infected:

$$p_{\mathrm{Im}}(x,t) = 1 - p_I(x,t) \tag{23}$$

and its average over social cluster represented by ball C,

$$p_{\mathrm{Im}}(C,t) = 1 - p_I(C,t) \tag{24}$$

This function increases relatively slowly with time, see Fig. 2. Its asymptotic behavior depends on the parameter α determining how rapidly the transition probability between social clusters decreases with increase of the distance between them. The lowest graph corresponds to large value of α, i.e., infection transition probability decreases very quickly. Then $p_{\mathrm{Im}}(C,t)$ is practically constant, herd immunity increases very slow.

Parameter α combines two different factors:

- Traditional social constraints in population.
- Preventing measures imposed by state authorities.

It is clear that existing of traditional rigid social barriers in population has similar effect as imposing of rigid preventing measures by

authorities. The parameter α can be represented as sum of two components, $\alpha = \alpha_{\text{soc}} + \alpha_{\text{preventing}}$. For two populations (say countries) with large and small traditional social barriers α_{soc}, respectively, the same dynamics of herd immunity can be approached with small and large preventing barriers $\alpha_{\text{preventing}}$, respectively. Say in Japan α_{soc} is relatively large and in Italy it is relatively small, so mild preventing measures in Japan would correspond to rigid preventing measures in Italy.

However, this decomposition of α into two factors makes the model too complicated. It is better to restrict it to one concrete country; here α_{soc} is fixed and one can play with parameter $\alpha_{\text{preventing}}$ to compare different scenarios.

5 Virus' random walk on the hierarchic social tree

The mathematical result on the relaxation regime for the p-adic diffusion [17] is generalization of studies on random walks on ultrametric spaces describing dynamics on energy landscapes [48]-[47]. There are given energy barriers Δ_m separating valleys, movement from one valley to another valley is constrained by necessity to jump over a barrier between them. This random walk model gives a good heuristic picture of the virus spread, as jumping from one social cluster (valley) to another, where clusters (valleys) are separated by social barriers (mountains) of different heights. Geometrically such random walk is represented as jumps on a tree between the levels of social hierarchy. Our model (selection of the transition probability in the form (19)) corresponds to *barriers growing linearly with the number of elementary jumps.* The relaxation regime of the power form is obtained for the number of hierarchy's levels approaching infinity, i.e., for ideal trees with infinitely long branches, as ultrametric spaces they are represented by $\mathbf{Q}_p$.

The virus plays the role of a system moving through barriers in models of dynamics on energy landscapes (see [48], [41]-[47] and references herein). In our case, these are social barriers between social clusters of population. The virus performs a complex random walk motion inside each social cluster moving in its sub-clusters, goes out of it and spreads through the whole population, sometimes the virus comes back to the original cluster from other social clusters that have been infected from this initial source of infection, and so on. During this motion the virus should cross numerous social barriers.

Instead of virus walking through the social tree, we can consider

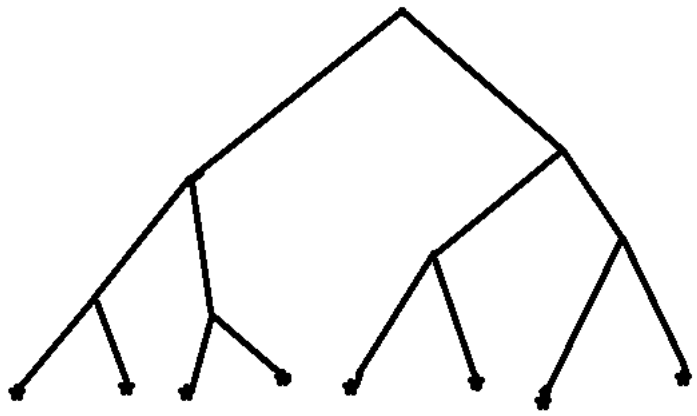

Figure 3: Treelike configuration space

a person. A person of the social type x can interact with persons of other social types. The temporal sequence of social contacts of some persons can have a very complicated trajectory, visiting numerous clusters (but the probability of approaching a cluster depends crucially on social barriers).

Let virus encounters a barrier of size Δ_m, in hopping a distance m (crossing m levels of hierarchy), where $\Delta_1 < \Delta_2 < ... < \Delta_m < ....$ It is supposed that barriers Δ_m are the same for all social clusters, i.e., they depend only on distance, but not on clusters. This assumption reflects a kind of epidemic égalit'e of all social groups, the barriers preventing spread of the virus that are imposed by state authorities are the same for all social groups.

Consider the tree at Fig. 3. We identify the lengths of branches between vertexes with magnitudes of barriers. Then the barriers on this tree depend on clusters, so from this viewpoint the social tree is not homogeneous.

Consider the energy landscape with a uniform barrier Δ, at every branch point; that is, a jump of distance 1 involves surmounting a barrier Δ, of distance 2, a barrier 2Δ, and so on. Hence, barriers linearly grow with distance m,

$$\Delta_m = m\Delta, m = 1, 2, ... \tag{25}$$

It seems that this type of behavior is the most natural from the viewpoint of social connections during the covid-19 epidemic in Sweden. Barriers are sufficiently high, but they still are not walls as during the rigid quarantine (as say in Italy, France, or Russia). For such linearly increasing barriers one can derive the following asymptotic behavior (23) of the relaxation probability [48],where in physics and biology the parameter

$$q \equiv 1/\alpha = \frac{T \log p}{\Delta}, \tag{26}$$

Here the new parameter T has the meaning of temperature. Thus behavior of distance between valleys of the energy landscape is determined by the size of the barrier for one-step jump Δ and temperature. We rewrite formula (19) for transition probability by using these parameters:

$$p(x|y) = \frac{C_{T,\Delta}}{|x-y|_p^{1+\Delta/(T \ln p)}}. \tag{27}$$

In our model, we introduce the notion of *social temperature* T. As in physics, this parameter calibrates energy, in our case social energy. The latter represents the degree of social activity, the magnitude of social actions. Although the notions of social temperature and energy are not so well established as in physics, they can be useful in sociophysical modeling (see [67] and references herein, starting with the works of Freud and Jung). Probability that the virus jumps from the elementary social cluster y to another cluster x grows with growth of social temperature. For high T, virus (or its spreader) easily move between social clusters. If $T << 1$, the infection is practically confined in clusters. If barrier Δ increases for the fixed parameter T, then the transition probability decreases and vice verse.

Starting with expression (27), we obtain the relaxation asymptotic in the form:

$$p_I(C,t) \sim t^{-\frac{T \log p}{\Delta}}, \ t \to \infty. \tag{28}$$

Thus, for large t, the average probability to become infected in social cluster C decreases quicker with increase of social temperature T. Decrease of the one-step jump barrier Δ implies the same behavior. We stress that such simple asymptotics with dependence only on one

level barrier Δ is a consequence of the linear increase of barriers with increase of difference between levels of social hierarchy. Immunity probability $p_{Im}(C,t)$ behaves in the opposite way. It increases quicker with increase of social temperature and decrease of the social barrier Δ.

The quantity $\ln p$ can be interpreted statistically as entropy of the process of distribution of infection into p subclusters coupled to a vertex. Suppose that a virus can spread with equal probability $q_i = 1/p$ into each of the subclusters $C_{i_0 \ldots i_k - 1, i}$ of the cluster $C_{i_0 \ldots i_k - 1}$. Entropy of this spreading equals to

$$\mathcal{E} = -\sum_{i=1}^{p-1} q_i \ln q_i = \ln p. \tag{29}$$

In terms of spreading entropy asymptotics (**??**) can be rewritten as

$$p_{\mathrm{Im}}(C,t) \sim 1 - t^{-T\mathcal{E}/\Delta}, t \to \infty. \tag{30}$$

Thus, larger spreading entropy of the social cluster tree implies quicker approaching herd immunity. Our conjecture is that this formula is valid for more general process of infection spread, with nonuniform distribution for probabilities q_i.

We turn to representation of $\alpha = \alpha_{\mathrm{soc}} + \alpha_{\mathrm{preventing}}$, its components correspond to traditional social constraints in population and preventing measures introduced by authorities. In the same way, we represent barrier $\Delta = \Delta_{\mathrm{soc}} + \Delta_{\mathrm{preventing}}$ and obtain the formula:

$$p_{\mathrm{Im}}(C,t) \sim 1 - t^{-T\mathcal{E}/(\Delta_{\mathrm{soc}} + \Delta_{\mathrm{preventing}})}, t \to \infty. \tag{31}$$

Since Δ_{soc} is difficult to change, we shall consider it as constant and to simplify the model, we set $\Delta_{\mathrm{soc}} = 0$. Thus we play just with the magnitude of the preventing barrier $\Delta_{\mathrm{preventing}}$. We also assume that the social temperature during the epidemic is constant (and relatively small), again for simplicity we set $T = 1$. Then

$$p_{\mathrm{Im}}(C,t) \sim 1 - t^{-\mathcal{E}/\Delta_{\mathrm{preventing}}}, t \to \infty. \tag{32}$$

If $\Delta_{\mathrm{preventing}}$ is high (rigid anti-epidemic measures of the lock-down type), then approaching herd immunity is very slow, practically impossible. If $\Delta_{\mathrm{preventing}}$ is low, then herd immunity is approached rapidly.

Of course, herd immunity is not the only parameter determining authorities strategy with respect to an epidemic. Much more important is the cumulative death rate. However, our model describes only asymptotic behavior and we cannot calculte cumulative death rates corresponding to preventing barriers of various magnitudes. We shall plan to do this in a forthcoming paper.

6 Concluding remarks

In this paper, we continue development of a new mathematical model of disease spread reflecting specialties of covid-19 epidemic (see also []). We especially emphasize the social cluster character of disease spread, **AS0**, for such diseases as covid-19. Clustered spread of say a virus can be modeled with dynamical systems on ultrametric spaces. Social clusters are represented by ultrametric balls. The basic feature of ultrametric balls is that they are either disjoint or one is included in another. This is the root of a the hierarchic structure of an ultrametric space. Geometrically ultrametric spaces are represented by trees with balls given by bunches of branches with the common root.

In this paper, we model the dynamics of coronavirus with ultrametric diffusion equation[6], its simplest version corresponding to p-adic trees and linearly increasing social barriers. Asymptotic of probability $p_{\mathrm{Im}}(t)$ to become immune against the virus is presented at Fig. 2. Generally, it increases slowly, the speed of increasing depends on the basic parameter of the model $q = T \log p/\Delta$.

In a society with low social temperature and high barriers between social clusters, $p_{\mathrm{Im}}(t)$ increase so slowly that there is practically no hope to approach herd immunity.

Acknowledgments

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[6]The use of purely diffusional model is supported by specialties of covid-19 epidemic, presented in appendix 1. Of course, this model is only approximate. But, it seems that it gives the right asymptotic of probabilities, to become infected and immune, in socially clustered society.

Appendix 1: Specialties of covid-19 spread supporting our model

As was emphasized in introduction, covid-19 epidemic has some specialties. To match these specialties, one has to develop new mathematical models. The fundamental specialty is the social cluster character of coronavirus spread, see **AS0**. Further, we shall discuss a few other virus' features. They justify the following assumption distinguishing our purely diffusional model of disease spread from the standard SIR-type models:

AS1 *Intensity of virus spreading is relatively insensible to the total number of those who have already been infected.*

Now we discuss a few biological and social factors behind this feature of the virus.

- **Covid on surface.** As was shown in study [62], the probability to become infected through some surface (say in a buses, metro, shop) is practically zero. It was found that even in houses with many infected (symptomatic) people, the viruses on surfaces (of say tables, chairs, mobile phones) were too weak to infect anybody. (Their were present, but were not able to infect mouths.)[7]
- **Covid in air.** The virus is neither so much dangerous at the open air, especially if people follow the recommendation to keep 1, 5 m distance between them. In in [62] was pointed out: "The fact that COVID 19 is a droplet infection and cannot be transmitted through the air had previously also been confirmed by virologist Christian Drosten of Berlin's Charité. He had pointed out in an interview [63] that coronavirus is extremely sensitive to drying out, so the only way of contracting it is if you were to 'inhale' the droplets."

[7]Mr Streeck, a professor for virology and the director of the Institute of virology and HIV Research at the University Bonn, clarified [62]: "There is no significant risk of catching the disease when you go shopping. Severe outbreaks of the infection were always a result of people being closer together over a longer period of time, for example the apré-ski parties in Ischgl, Austria." During extended and careful study in Heidelberg (the German epicenter of the covid-19 epidemic) his team could also not find any evidence of living viruses on surfaces. "When we took samples from door handles, phones or toilets it has not been possible to cultivate the virus in the laboratory on the basis of these swabs. ... To actually 'get' the virus it would be necessary that someone coughs into their hand, immediately touches a door knob and then straight after that another person grasps the handle and goes on to touches their face." Streeck therefore believes that there is little chance of transmission through contact with so-called contaminated surfaces.

- **Asymptomatic individuals.** As was recently announced [64], WOH collected a lot of statistical data showing that asymptomatic individuals transmit covid-19 virus to other people with very low probability.[8] At the same time, US Centers for Disease Control and Prevention estimates that about a third of coronavirus infections (35%) are asymptomatic [65]. Hence, about 35% of infected people practically do not contribute in disease spread.
- **No mass-events.** Another important restriction supporting **AS1** is that even in Sweden, mass-events were forbidden, so no public concerts, neither football matches.[9]
- **Superspreaders.** As for many infections, spread of coronavirus has the following feature - the presence of superspreaders of infection. One person can infect really many people. Thus, single person's contribution in disease spread can be essentially higher than contribution of a few hundreds of usual asymptomatic individuals or many presymptomatic individuals (see more on superspreaders in appendix 2).

AS2 *The number of susceptible people $S(t)$ is so large comparing with the number $I(t)$ of those who are infected or the number $R(t)$ of recovered that we can consider it as constant, $S(t) = \text{const}$, and exclude it from model's dynamical equations.*

This assumption implies that for an individual in population under consideration the probability to become infected practically does not depend on the number of recovered. The population is rather far from approaching herd immunity and a disease spreader is surrounded (with the high degree of approximation) by susceptible people. Thus the number of recovered people R also can be excluded from dynamics. Of

[8] "We have a number of reports from countries who are doing very detailed contact tracing. They're following asymptomatic cases, they're following contacts and they're not finding secondary transmission onward. It is very rare – and much of that is not published in the literature," Van Kerkhove, WOH official said on June 6, 2020. "We are constantly looking at this data and we're trying to get more information from countries to truly answer this question. It still appears to be rare that an asymptomatic individual actually transmits onward." [64].

[9] In Sweden, restaurants and night clubs were open, but such events were not of mass-character. The presence in a night club or in a restaurant of one infection spreader has practically the same impact as say 5 spreaders, the effect of closed space. Moreover, the distance between the tables in restaurants also diminished the effect of high number of infected in the population. During the intensive phase of the covid-19 epidemic (the end of March and April 2020) restaurants terminated self-serving during lunches (so typical in Sweden).

course, this model provdies only the rough picture of the real disease spread, but it reflects the basic features of the covid-19 spread in the states that imposed relatively soft restrictions in relation with epidemic (as, e.g., Sweden, Japan, Belarus).

Denote the probability, for a person from social cluster C, to become infected at the instance of time t by the symbol $p_I(C,t)$. (We recall that in our ultrametric model social clusters are represented by balls.) Later we shall discuss the interpretation of the notion "probability to become infected" in more detail (section 3). To write the evolution equation for probability $p_I(C,t)$, we impose the additional assumption:

AS3 *The distribution of social clusters in the society is uniform: all clusters represented by balls of the same radius have the same measure that is equal to balls' radius.*

Mathematically **AS3** is formalized through the use of the Haar measure μ on $\mathbf{Q}_p$. We understand that this is a strong restriction on the social structure of society. But, the main reason for its imposing is just simplification of mathematics. We can consider other distributions on $\mathbf{Q}_p$ assigning different weights to social clusters represented by balls of the same radius. (We recall that any point of a ball can serve as its center.)

Appendix 2: Superspreaders

Superspreader is an unusually contagious individual who has been infected with disease; someone who infected the number of people far exceeding the two to three. As was pointed out in MIT Technology Review [66]: "For covid-19, this means 80% of new transmissions are caused by fewer than 20% of the carriers – the vast majority of people infect very few others or none at all, and it is a select minority of individuals who are aggressively spreading the virus. A recent preprint looking at transmission in Hong Kong supports those figures, while another looking at transmission in Shenzhen, China, pegs the numbers closer to 80/10. Lots of outbreaks around the world have been linked to single events where a superspreader likely infected dozens of people. For example, a choir practice in Washington State infected about 52 people; a megachurch in Seoul was linked to the majority of initial infections in South Korea; and a wedding in Jordan with about 350 guests led to 76 confirmed infections." The bad news is that, for the moment, we cannot identify diagnostically superspreaders.

Appendix 3: Hidden variables of covid-19 spread

As was discussed in section 3, probability $p_I(C,t)$ is determined by the epidemic context in cluster C at time t, $\mathcal{C}(C,t)$. In principle, this context can be described by hidden variables of epidemiological, social, geographic, economic nature. However, as was already stressed, it is difficult if possible at all to determine these variables for concrete social cluster C and the instant of time t. We illustrate this problem by a number of examples.

For example, covid-19 epidemic in Sweden was characterized by mass spread of infection in nursing homes in Stockholm, but nothing similar happened in other Swedish towns, say in Gothenburg, the second largest city in Sweden. This town is very densely connected with Stockholm with intensive train connection. Trains connection was not restricted during epidemic and (what is more important) during the initial stage of epidemic, in March, people traveled very actively between two towns. Then, theoretically the virus approached Sweden with tourists coming back from skiing in Alps and Stockholm is pointed as the place of arrival, this justifies the mass spread of covdid-19 in Stockholm. But, essential part of tourists living in South Sweden (the most densely populated) returned from Alps via the Copenhagen airport (with intensive train communication over the bridge between Denmark and Sweden). However, the virus did not spread in South Sweden, including the third largest city Malmö, neither in Copenhagen. What is the difference between Swedish tourists (coming from the same place in Italian and Austrian Alps) arriving to Stockholm or to Copenhagen? There are hidden variables, but it is difficult if possible at all to determine them. The same can be said about disease spread in nursery homes in Stockholm vs. Gothenburg. Of course, there were attempts to determine "covid-19 hidden variables"; say, for Stockholm's nursery homes, responsibility for infecting of elderly people was appointed to the personal of these homes. However, there were reported numerous cases in that the personal of nursery homes was widely infected, but the disease did not spread to elderly patients of these homes.

Another interesting fact is about French hospitals: at the beginning, many nurses and doctors got sick, so they were taking extreme precautions. But some (actually most) of them did not get sick, and as time went they all relaxed the precautions, and they still did not get sick, at least not at a noticeable level. Another fact is the gigantic air carrier Charles de Gaulle, with 1700 staff on board, extremely confined. Within a few days more that 60% were tested positive, but

actually very few got really sick, only one was seriously ill, and none died. This kind of reaction of the personal of Charles de Gaulle airport is amazing contrast with reaction of the personal of Stockholm's airport Arlanda, many workers and members of their families were heavily sick.

Of course, the most amazing is difference between social clusters determined by nationalities, especially clusters of immigrants. For example, in New York the situation is described as following [68]:

"At a clinic in Corona, a working-class neighborhood in Queens, more than 68 percent of people tested positive for antibodies to the new coronavirus. At another clinic in Jackson Heights, Queens, that number was 56 percent. But at a clinic in Cobble Hill, a mostly white and wealthy neighborhood in Brooklyn, only 13 percent of people tested positive for antibodies. As it has swept through New York, the coronavirus has exposed stark inequalities in nearly every aspect of city life, from who has been most affected to how the health care system cared for those patients. Many lower-income neighborhoods, where Black and Latino residents make up a large part of the population, were hard hit, while many wealthy neighborhoods suffered much less."

Similar picture we can see in Sweden:

"New figures in Stockholm confirm the picture that so-called vulnerable areas are hardest hit by the coronavirus. In the immigrant-rich districts of Rinkeby and Tensta, around 40 people per 10,000 have been infected, which is three times more than the average for the entire region. The figures show that the difference with more disease cases in Rinkeby-Kista and Spanga-Tensta has persisted", says Per Follin, infection control doctor in the Stockholm region [69].

Generally evolution of such epidemics as covid-19 have to be studied by using information methods similar to paper [70, 71].

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