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Ultrametric diffusion equation on energy landscape to model disease spread in hierarchically 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 numbers. 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.

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1. Introduction

The COVID-19 epidemic has many unusual features. 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 [1,2]):

**As 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 [3–8], 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 [9–13]). In this paper, we shall use ultrametric diffusion equation [14–23] 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 \( \mathbb{Q}_p \). 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 [24–26].

The specialties of COVID-19 epidemic are not reflected in the standard mathematical models [27–29], such as, e.g., the canonical SIR model [30] and its diffusion-type generalizations, e.g., [31]. Consequently, in spite of the tremendous efforts [32–38], 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 AS 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 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 [39–42], 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 [43–49]. 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., [50]). 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 versa. 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., [50] for simple mathematical theory. Such random walk is the discrete version of ultrametric diffusion. Theory of diffusion equations in ultrametric space is well developed [14–22]. 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 [43–50] were at the physical level of rigorously) and opens the door for development of a variety of new mathematical models of disease spread taking into account the hierarchical social cluster structure of population.

We consider a country relatively mild preventing measures\(^1\) 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 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\(^2\) (see, e.g., [51–53] for reports from Public Health Institute of Sweden, [34–36] for attempts of mathematical modeling and [54–58] for reports from mass-media).

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

\[
p_{\text{Im}}(C, t) = 1 - t^{-q}, \quad q > 0.
\]

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

\[
q = T \ln p / \Delta.
\]

Here \(T > 0\) is the social analog of temperature, the degree of activity in a society, \(\Delta\) 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 \(\Delta\) implies slower growth of herd immunity. Quantity \(\ln p\) can be interpreted as entropy of virus spreading inside a social cluster, \(E = \ln p\), (see (32)). 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 asymptotic for approaching herd immunity:

\[
p_{\text{Im}}(C, t) = 1 - t^{-\frac{T E}{\Delta^2}}.
\]

In the present paper, by using results of work [18] 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

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

\(^2\) In particular, by models Tom Britton [34,35] 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.
technique of ultrametric diffusion equations provides the possibility to study this problem for other types of barriers as well as for design of more general mathematical models of disease spread. (We remark that a detailed mathematical study of the \( p \)-adic pseudo-differential equations and the associated Markov processes connected with the energy landscapes is given in [23].)

Just before submission of preprint [1], I found the recent paper of Britton et al. [42] 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 [34,36] 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., [51–53] for reports from Public Health Institute of Sweden, see also [54–58]). In previous modeling [34,36] for COVID-19 epidemic, Swedish population was considered as homogeneous. In [42], 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 and generally paper [42] is supporting for our approach. The main difference is that in [42] 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 [42]. Both models provide the possibility to play with strength of preventive measures and see their effect onto the epidemics’ dynamics.

2. The decision maker viewpoint on epidemic’s dynamics and immunity

One of the distinguishing properties of our model is the appeal to the subjective interpretation of probability. We consider the problem of disease spread as a problem of decision making. And in the latter, decision maker operates with subjective probabilities to make the appropriate decisions [59]. We remark that this approach is widely used not only social and political sciences, economics, and finance, but even in engineering and geology (see [60–66]); for example in petroleum search, e.g., to make the decision whether explore or not some oil field. Thus, the problem of the epidemic dynamics is considered from the viewpoint of say state authorities who monitor the virus spread and who should make corresponding decisions. They have to estimate the probability \( p(t, C) \) that a person in social cluster \( C \) can become infected at the instant of time \( t \).

We remark that the diffusion model is widely applied to decision making [67]. However, up to the author’s knowledge the ultrametric diffusion model has never been considered.

The subjective probability approach and the decision making framework lead to the following definition of immunity,

\[
p_{\text{Im}}(C, t) \equiv 1 - p(t, C),
\]

the herd immunity for the social cluster \( C \). This is the operational definition of immunity, the instrument of monitoring the epidemic situation in population.

The dynamics of the infecting probability \( p(t, C) \) is described by the master equation (see (17)) representing the balance of probability in the concrete social cluster \( C \). As usual, the coefficients of the master equation are given by conditional (transition) probabilities \( p(t, C|C') \) — the probability that a person from cluster \( C \) would be infected by a person from cluster \( C' \).

We note that in probability theory interrelation between subjective and objective (statistical) probabilities is very complex and foundationally unclear. Typically researchers proceed pragmatically by using for subjective probabilities the measure-theoretic calculus (the Kolmogorov axiomatic [68], 1933). We use the same strategy. Roughly speaking, by assigning the subjective probability decision maker takes into account all hidden factors beyond this context. We might say that subjective probability quantifies the distribution of these hidden variables. The dynamics of the COVID-19 spread in populations is characterized by high uncertainty generated by a variety of factors, some of them are still unknown (say the role of genetics). It seems to be impossible to determine and quantify the COVID-19 hidden variables. Therefore the operational subjective probability approach can have some advantages. We can point to similarity with quantum physics, its predictions are structured operationally with referring to hidden variables.3

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3 We do not want to go deeper to quantum foundations and discuss its hottest topic – the Bell inequality and coupling of the existence of hidden variables with nonlocality – spooky action at the distance. One of the possibilities to escape confronting with nonlocality is precisely the subjective interpretation of quantum probability. Quantum Bayesianism (QBism) [69]. We also remark that in geology decision makers widely refer to quantum-like uncertainty of geological data, e.g. [63–65] and especially [66].
3. Comparing with application to covid-19 of the conventional models of disease spread

Of course, it is attractive to use the models determined by just a few parameters such as the basic reproduction number $R_0$. (It quantifies transferability of a disease: the average number of individuals that a single infectious person will infect.) However, as we have seen, in the case of COVID-19 epidemic such simple models led to totally wrong predictions. One of the examples of such prediction is widely known as the Ferguson’s report [32]. This report drastically overestimated the expected number of infected people and led to the decisions for rigid lockdowns in many countries. On the other hands, in Sweden the predictions known as the Briton’s reports [1] overestimated the expected increase of the herd immunity in Sweden. This led to the very mild restrictions (practically no restrictions) and then the Swedish state authorities (when they understood that, in spite of the mathematical predictions, Swedish population is far from approaching the herd immunity) should impose restrictive measures step by step during whole year 2020.

Such inadequate predictions are based (roughly speaking and ignoring the technical details) on the exponential increase–decrease behavior of infection’s spreading:

- $R_0 > 1$ : the infection spreads exponentially,
- $R_0 < 1$ : the infection vanishes exponentially,
- $R_0 = 1$ : the disease is endemic, i.e., it will move throughout the population but not increase or decrease.

The Ferguson’s report was based on the assumption of rapid exponential infection spread for $R_0 > 1$. And the Briton’s reports were based on the assumption of rapid exponential vanishing of infection for $R_0 < 1$.

In our approach, the transition probabilities play the role of model’s parameters. In contrast to the basic reproduction number, it is difficult to determine them experimentally, especially for the population with a complex structure of social clustering. So, the model is merely phenomenological. Its main outcome is the prediction of essentially slower epidemic’s dynamics than given by standard models: the power law, instead of the exponential law. Thus, the model although being phenomenological gives important qualitative predictions.

As was mentioned in introduction, in article [42] Britton et al. started to couple the virus spread with the population clustering (but without using the ultrametric analysis). Their model also predicted essentially slower the epidemic dynamics than in their previous works [32–36].

One of the advantages of the ultrametric model is that it contains as model’s parameters the heights of the barriers between social clusters (in our model barriers increase linearly with the distance between clusters, so we need only one parameter $\Delta$). This parameter reflects the strength of COVID-19 restrictions.

4. Towards models with more adequacy to the real situation: analyzing the mathematical assumptions

Our mathematical model is the simplest ultrametric model reflecting the social clustering of population as the factor slowing approaching the herd immunity. In particular, the simplest $p$-adic trees are in the use. They have the homogeneous branching structure. Of course, in the real population clustering trees are not homogeneous. Such trees can be described as general ultrametric spaces [19,20]. Analysis on such trees is mathematically essentially more complicated. The corresponding diffusion equations have also been studied and applied, e.g., in geophysics [70]. Behavior of their solutions is similar to the $p$-adic case (but a number of mathematical technicalities has to be taken into account).

Another simplifying assumptions are the time independence and symmetry of transition probabilities for spread of the virus between social clusters,

$$p(t, C|C') \equiv p(C|C'), \quad (5)$$

$$p(C|C') = p(C'|C). \quad (6)$$

These assumptions are neither satisfied in real populations. However, once again behavior of the solutions of the general master equations with non-symmetric transition probabilities does not essentially differ from behavior of the solutions for the symmetric case. Time dependent transition probabilities generate essentially more complicated dynamics and the author does not know any study in this direction.

Generally reduction of model parameters to transition probabilities $p(C|C')$ is based on the infection spread process which takes into account not only sufficiently durable contacts of people, as say seating in a church, restaurant or coffee-house, office, school or university teaching. Infecting impact of short-term contacts, e.g., persons meet in public transport, in shops, etc., is ignored.

We consider very special class of energy landscapes: the barriers between nearby clusters have the same size, i.e., the barrier’s size increase linearly with levels of social hierarchic structuring. In the real social structures, barriers can increase in a variety of ways, depending on country and epidemic restrictions imposed by its authorities. This general situation cannot be handled analytically. Besides the linear increase of barriers, in statistical physics there are well studied the cases logarithmically and exponentially increasing barriers. We plan to consider such models, they have their own specialties.

Finally, we note that averaging is based on the uniform $p$-adic Haar measure: the measure of a ball is equal to its radius. This means that population clusters at the same level of social hierarchy have the same “volume”. Of course, this is the
mathematical simplification. One can consider averaging w.r.t. non-uniform measures and not only on p-adic trees, but on general nonhomogeneous trees (ultrametric spaces) [19,20]. Such modeling is essentially more complicated from the mathematical viewpoint. One cannot use the Fourier analysis on locally compact groups (the p-adic tree can be endowed with the structure of a compact additive group, its elements are branches of the tree). Instead one uses theory of wavelets on ultrametric spaces [19,20].

In the main, diffusion on ultrametric spaces is similar to diffusion on the model p-adic tree, although essentially more complex mathematically. We hope that this section can stimulate other researchers to proceed to more general models by relaxing our simplification assumptions, especially by using the numeric simulation.

I agree with this. But consideration of the general model which matches better to the real situation would make mathematics to complicated, the main result on the asymptotic behavior would be impossible to derive analytically, only numerical simulation would be possible. I am pure theoretician and I prefer analytics. Another argument in the favor of the use of a simple mathematical model is that, in spite of its deviations from the real situation, it, nevertheless, reflects the basic features of disease spread in hierarchically clustered population. I would like to make the analogy with quantum theory. In fact, only for the hydrogen atom Schrödinger equation can be solved analytically; to consider complex atoms, one must appeal to approximations and nonlinear equations. Nevertheless, the basic features of quantum mechanics demonstrated analytically for the hydrogen atom are present even in the approximate models for more complex structures.

5. 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:

\[ \rho(x, y) \leq \max\{\rho(x, y), \rho(y, z)\}, \]

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 \(B_R(a) = \{x : \rho(x, a) \leq R\}\), 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 split 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 [3–7], 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 \(m \in \mathbb{Z} = \{0, \pm 1, \pm 2, \ldots\}\). (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 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, \(x_m = 0, 1, \ldots, N_m - 1\), 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 [19,20].

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

\[ x = (x_{-n}, \ldots, x_{-1}, x_0, x_1, \ldots, x_m), \quad x_j \in \{0, 1, \ldots, p - 1\}. \]

The vector representation of psychical, mental, and social states is very common in psychology and sociology. The essence of our approach [3–7] is the hierarchic ordering of coordinates leading to introduction of ultrametric on the state space, see (11).
For our purpose, modeling of epidemic, we can consider, for example, the following hierarchic system of social coordinates; for simplicity, let index \( m = 0, 1, 2, \ldots \), 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 [71] 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 lifestyle 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, ...).

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 the form

\[
x = x_0 p^{-n} + \cdots + x_{p-1} p^{-1} + x_0 + x_1 p + \cdots + x_m p^m, \quad x_j \in \{0, 1, \ldots, p-1\}.
\]

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:

\[
x = (\ldots, x_{-n}, \ldots, x_{-1}, x_0, x_1, \ldots, x_m, \ldots), \quad x_j \in \{0, 1, \ldots, p-1\},
\]

where, for each \( x \), there exists \( n \) such that \( x_{-j} = 0, j > n \). Denote the space of such sequences by the symbol \( Q_p \). 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

\[
\rho_p(x, y) = p^{-n}.
\]

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

\[
Z_p = \bigcup_{i=0}^{p-1} B_{1/p}(a^i) = \bigcup_{i=0}^{p-1} B_{1/p}(a^{b_{i-1}-1})
\]

where \( a^i \in Z_p \) is constrained by condition \( x_0 = j \) and \( a^{b_{i-1}-1} \) is constrained by conditions \( x_0 = j_0, \ldots, x_{n-1} = j_{n-1} \), 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 \( C_j = B_{1/p}(a^j) = \{x \in Z_p : x_0 = j\} \), in above epidemic coding \( C_j \) corresponds to fixing age = j; \( C_j = B_{1/p}(a^j) = \{x \in Z_p : x_0 = j, x_1 = l\} \), age = j, gender = l for Swedish society or age = j, income level = l for American society.

Social states, points of \( Q_p \), can be considered 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 (9). The space \( Q_p \) endowed with ultrametric \( \rho_p \) can be considered as completion of this set of rational numbers and algebraically the elements of \( Q_p \) can be represented by power series of the form

\[
x = \sum_{k=-n}^{\infty} x_k p^k
\]

where \( x_j \in \{0, 1, \ldots, p-1\}, x_n \neq 0 \), and \( n \in Z \); so only finite number of coordinates with negative index \( k \) can differ from zero. Such a series converges with respect to ultrametric \( \rho_p \). Representation by the power series gives the possibility to endow \( Q_p \) with the algebraic operations, addition, subtraction, multiplication, and division (the latter operation is defined

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4 Income did not play any role in Sweden during the COVID-19 epidemic.
only for prime \( p \). Hence, \( \mathbb{Q}_p \) is a number field, the field of \( p \)-adic numbers. This algebraic representation leads to number-theoretic representation of ultrametric, \( |p(x, y)|_p = |x - y|_p \), where \( x \rightarrow |x|_p \) is the \( p \)-adic analog of the real absolute value; per definition, for \( x \) given by series (13),

\[
x|_p = |\sum_{k=n}^\infty x_n p^k|_p = p^{-n}.
\]

It satisfies the strong triangle inequality playing the fundamental role in \( p \)-adic analysis and implying (7):

\[
|x + y|_p \le \max\{|x|_p, |y|_p\}.
\]

6. 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.,

\[
p_i(C, t) \neq \frac{N_i(C, t)}{N},
\]

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 (16).

Probability \( p_i(C, t) \) is determined by context \( C(C, t) \), 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 [72], 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 [73,74]. It is impossible to determine “hidden variables” behind many events. So, people and social clusters of people definitely react to COVID-19 in very different ways, there are bio-medical, social, and may be even psychological hidden variables. Context \( C(C, t) \) 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 \( C(C, t) \) 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 \( C_i, i = 1, \ldots, M \), 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 \( t \rightarrow p_i(C_k, t) \) 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 \( C_i \), to get infection from a person from cluster \( C_k \). These conditional probabilities represent intensities to become infected. The master equation has the form:

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

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

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

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 (18) is clear. Negative term describes the “flow of infection” from social cluster \( C_k \) 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 versa. 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 \( C_i \) (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 \( p(C_i | C_k; t)p(C_k, t)dt \). For example, during epidemic I commuted between a rather isolated town’s district (Sandsbro) to university; hence during the day time I was not able to infect people in Sandsbro, but in principle I was able to infect colleagues at university as well as students (I finished class-teaching and completely moved to online-teaching only in November 2020).

Latter, in Section 8, 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 on 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 \( C \) is interpreted as reservoir of virions. Now, we identify probabilities, under the above assumption 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 \( p_i(x, t) \),

\[
\frac{\partial p_i(x, t)}{\partial t} = \int_{Q_x} [p(x|y; t)p_i(y, t) - p(y|x; t)p_i(x, t)]\mu(dy),
\]

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

\[
\frac{\partial p_i(x, t)}{\partial t} = \int_{Q_x} p(x|y)[p_i(y, t) - p_i(x, t)]\mu(dy).
\]

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

\[
p(x|y) = \frac{C_\alpha}{|x - y|^{1+\alpha}}, \quad \alpha > 0.
\]

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,

\[
\frac{\partial p_i(x, t)}{\partial t} = C_\alpha \int_{Q_x} p_i(y, t) - p_i(x, t)\frac{|x - y|^{1+\alpha}}{|x - y|^{1+\alpha}}\mu(dy).
\]
The integral operator in the right-hand side is the operator of fractional derivative $D^\alpha$ (the Vladimirov operator), see [14]. 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:
\[
\frac{\partial p(x, t)}{\partial t} = D^\alpha p(x, t).
\] (24)

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

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., [14]. We are interested in the relaxation regime, i.e., asymptotic of average probability $p_l(C, t)$ for large $t$. We use the mathematical result from [18] (see also [19,20]) and obtain that the average probability has the power behavior:
\[
p_l(C, t) \sim t^{-1/\alpha}, \quad t \to \infty.
\] (25)

Thus the average probability to become infected in a social cluster decreases rather slowly with time. If parameter $\alpha$ is relatively large i.e., the virus transition probability decreases very quickly with increase of the distance between social clusters, then $p_l(C, t)$ decreases very slowly with time, it is practically constant (see the upper graph at Fig. 1). If parameter $\alpha$ is relatively small, so the virus transition probability decreases slowly with increase of the distance, then $p_l(C, t)$ decreases sufficiently quickly with time (see the lowest graph at Fig. 1). We shall discuss these behaviors in Section 8 by assigning bio-social meaning to the parameter $\alpha$ and by coupling it with the degree of preventing measures established by authorities. We present some graphs corresponding to different values of $\alpha$ at Fig. 1.

Consider now a kind of “integral immunity”, combination of innate and adaptive components, defined as the probability of not become infected:
\[
p_{in}(x, t) = 1 - p_l(x, t)
\] (26)
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Fig. 3. Treelike configuration space.

and its average over social cluster represented by ball $C$,

$$p_{in}(C, t) = 1 - p(C, t)$$

(27)

This function increases relatively slowly with time, see Fig. 2. Its asymptotic behavior depends on the parameter $\alpha$ 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 $\alpha$, i.e., infection transition probability decreases very quickly. Then $p_{in}(C, t)$ is practically constant, herd immunity increases very slow.

Parameter $\alpha$ 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 $\alpha$ can be represented as sum of two components, $\alpha = \alpha_{soc} + \alpha_{preventing}$. For two populations (say countries) with large and small traditional social barriers $\alpha_{soc}$, respectively, the same dynamics of herd immunity can be approached with small and large preventing barriers $\alpha_{preventing}$, respectively. Say in Japan $\alpha_{soc}$ 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 $\alpha$ into two factors makes the model too complicated. It is better to restrict it to one concrete country; here $\alpha_{soc}$ is fixed and one can play with parameter $\alpha_{preventing}$ to compare different scenarios.

8. Virus’ random walk on the hierarchic social tree

The mathematical result on the relaxation regime for the $p$-adic diffusion [18] is generalization of studies on random walks on ultrametric spaces describing dynamics on energy landscapes [50]-[49]. There are given energy barriers $\Delta_m$ 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 (22)) 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 $Q_p$.

The virus plays the role of a system moving through barriers in models of dynamics on energy landscapes (see [43–50] 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 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 $\Delta_m$, in hopping a distance $m$ (crossing $m$ levels of hierarchy), where $\Delta_1 < \Delta_2 < \cdots < \Delta_m < \cdots$. It is supposed that barriers $\Delta_m$ 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 égalité 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 $\Delta$, at every branch point; that is, a jump of distance 1 involves surmounting a barrier $\Delta$, of distance 2, a barrier $2\Delta$, and so on. Hence, barriers linearly grow with distance $m$,

$$\Delta_m = m\Delta, \; m = 1, 2, \ldots \tag{28}$$

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 (26) of the relaxation probability $[50]$, where in physics and biology the parameter

$$q \equiv 1/\alpha = \frac{T \log p}{\Delta} \tag{29}$$

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 $\Delta$ and temperature. We rewrite formula (22) for transition probability by using these parameters:

$$p(x|y) = \frac{C_{r,\Delta}}{|x-y|^\Delta/(T \log p)} \tag{30}$$

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 socio-physical modeling (see $[72,73]$ 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 $T \ll 1$, the infection is practically confined in clusters. If barrier $\Delta$ increases for the fixed parameter $T$, then the transition probability decreases and vice versa.

Starting with expression (30), we obtain the relaxation asymptotic in the form:

$$p_l(C, t) \sim t^{-\frac{T \log p}{\Delta}}, \; t \rightarrow \infty. \tag{31}$$

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 $\Delta$ implies the same behavior. We stress that such simple asymptotics with dependence only on one level barrier $\Delta$ is a consequence of the linear increase of barriers with increase of difference between levels of social hierarchy. Immunity probability $p_{\text{imm}}(C, t)$ behaves in the opposite way. It increases quicker with increase of social temperature and decrease of the social barrier $\Delta$.

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 $C_{0,\ldots,k-1,i}$ of the cluster $C_{0,\ldots,k-1}$. Entropy of this spreading equals to

$$\mathcal{E} = - \sum_{i=1}^{p-1} q_i \ln q_i = \ln p. \tag{32}$$

In terms of spreading entropy asymptotics (29) can be rewritten as

$$p_{\text{imm}}(C, t) \sim 1 - t^{-\frac{T \mathcal{E}}{\Delta}}, \; t \rightarrow \infty. \tag{33}$$

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

$$p_{\text{imm}}(C, t) \sim 1 - t^{-\frac{T \mathcal{E}}{(\Delta_{\text{soc}} + \Delta_{\text{preventing}})}}, \; t \rightarrow \infty. \tag{34}$$

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

$$p_{\text{imm}}(C, t) \sim 1 - t^{-\frac{\mathcal{E}}{\Delta_{\text{preventing}}}}, \; t \rightarrow \infty. \tag{35}$$

If $\Delta_{\text{preventing}}$ is high (rigid anti-epidemic measures of the lock-down type), then approaching herd immunity is very slow, practically impossible. If $\Delta_{\text{preventing}}$ 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 calculate cumulative death rates corresponding to preventing barriers of various magnitudes. We shall plan to do this in a forthcoming paper.
9. Concluding remarks

In this paper, we continue development of a new mathematical model of disease spread reflecting specialties of COVID-19 epidemic. We especially emphasize the social cluster character of disease spread, as, 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 the hierarchical 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, its simplest version corresponding to \( p \)-adic trees and linearly increasing social barriers. Asymptotic of probability \( p_{\text{Im}}(t) \) 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, \( p_{\text{Im}}(t) \) increase so slowly that there is practically no hope to approach herd immunity.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

The author would like to thank Philippe Grangier who stimulated this research by his own attempt to model COVID-19 spread (unpublished) and provided interesting information about disease clustering in France as well as for discussion on COVID-19 “hidden variables”, Sergey Kozyrev for discussions on ultrametric dynamics, Anja Nertykin information about spread (unpublished) and provided interesting information about disease clustering in France as well as for discussion appeared to influence the work reported in this paper.


elected as part of the program of the Mathematical Center for Fundamental and Applied Mathematics under the agreement N 075–15-2019-1621.

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