



Utrametric diffusion equation on
energy landscape to model disease
spread in hierarchic socially clustered
population: taking specialties of
covid-19 into account Andrei Khrennikov

Center Math Modeling in Physics and Cognitive
Sciences, Linnaeus University, Växjö , Sweden

May 28, 2021



Back

Close



Covid-19 epidemic has some specialties. To match these specialties, one has to develop new mathematical models.

AS0 Virus' spread in population is constrained by the hierarchic social cluster structure and it "respects" this structure

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 in air.** The virus is not dangerous at the open air, especially if people follow the recommendation to keep 1, 5 m distance between them.





- **Asymptomatic individuals.** As was recently announced [?], WOH collected a lot of statistical data showing that asymptomatic individuals transmit covid-19 virus to other people with very low probability. US Centers for Disease Control and Prevention estimates that about a third of coronavirus infections (35%) are asymptomatic [?]. 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.
- **Superspreaders.** 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 super-spreaders in appendix 2).



In April-May 2020 for Swedish population we could assume that

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.





Denote the probability, for a person from social cluster C , to become infected at the instance of time t by the symbol $p_I(C, t)$.

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 \mathcal{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 \mathcal{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.)





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.

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.,

$$(1) \quad p_I(C, t) \neq \frac{N_I(C, t)}{N},$$

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 $N_I(C, t)$.

Probability $p_I(C, t)$ is determined by context (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 [?], 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. It is impossible to determine “hidden variables” behind many events.

People and social clusters of people reacts to covid-19 in very different ways: there are bio-medical, social, and may be even psychological hidden variables. Context (C, t) determines their distribution, but it seems to be impossible to find these probability distributions of “hidden variables” and their dependence on contexts.

One of the possibilities **to interpret the probability to become infected in context (C, t) is to use the subjective interpretation of probability.**

This interpretation became popular even in quantum physics, under the name of Quantum Bayesianism (QBism).





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 $C_i, i = 1, \dots, M$, 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_k , to get infection from a person from cluster C_i .

These conditional probabilities represent intensities to become infected.

The master equation has the form:

$$(2) \quad \frac{d}{dt} p_I(C_k, t) = \sum_{i \neq k} [p(C_k|C_i; t) p_I(C_i, t) - p(C_i|C_k; t) p_I(C_k, t)].$$



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

$$(3) \quad p_I(C_k, t+dt) = p_I(C_k) + \sum_{i \neq k} [p(C_k|C_i; t)p_I(C_i, t) - p(C_i|C_k; t)p_I(C_k, t)] dt$$

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 .**

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 (3) is clear.



10/41





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 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_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 $p(C_i|C_k; t)p_I(C_k, t)dt$.



the mechanical model for the above process of infection flow between social clusters.

Clusters are virus reservoirs, $p_I(C, t)$ gives the virus concentration in cluster C at time t .

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.



12/41



Back

Close



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 [?] (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 .



Hierarchical treelike geometry of social clusters

We represent the human society as a system of hierarchically coupled (as a treelike structure) disjoint clusters.

Theory of *ultrametric spaces* is one of the basic mathematical tools for representation of such clusters purpose.

Geometrically ultrametric spaces can be represented as trees with hierarchic levels. Ultrametricity means that this metric satisfies so-called strong triangle inequality:

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

for any triple of points x, y, z .

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.

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 the works of the author and his collaborators, 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 $\mathbf{x} = (x_m)$ characterizing (psycho-)social states of individuals. The treelike representation of *social states* is based on selection of hierarchically ordered social factors enumerated by index $m \in \mathbf{Z} = \{0, \pm 1, \pm 2, \dots\}$.

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, $x_m = 0, 1, \dots, N_m - 1$, 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 [?, ?].

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

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

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





For our purpose, modeling of epidemic, we can consider, for example, the following hierarchic system of social coordinates; for simplicity,

let index $m = 0, 1, 2, \dots$, 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.

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.

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

(6)

$$x = x_{-n}p^{-n} + \dots + x_{-1}p^{-1} + x_0 + x_1p + \dots + x_m p^m, \quad x_j \in \{0, 1, \dots, p-1\}.$$

This is the basis of the number-theoretic representation of the space of social states.



18/41



Back

Close



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 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 (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

$$(7) \quad x = \sum_{k=n} x_k p^k$$



where $x_j \in \{0, 1, \dots, p - 1\}$, $x_n \neq 0$, and $n \in \mathbf{Z}$; so only finite number of coordinates with negative index k can differ from zero.



Modeling the virus spread with ultrametric diffusion equation

An elementary social cluster (social state) given by a point of 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 $C \equiv B_{p^n}(0)$, $n = 0, \pm 1, \pm 2, \dots$. Under assumption **AS3**, this quantity is represented as the integral with respect to the Haar measure:

$$(8) \quad p_I(C, t) = \int_C p_I(x, t) \mu(dx).$$

Under the above assumptions on the social structure of population and its interaction with the virus, we can write the following master equation for probability $p_I(x, t)$,

$$(9) \quad \frac{\partial p_I(x, t)}{\partial t} = \int_{Q_p} [p(x|y; t)p_I(y, t) - p(y|x; t)p_I(x, t)] \mu(dy),$$



where $p(\mathbf{x}|\mathbf{y}; t)$ is the transition probability: the probability that the virus being present in (elementary) cluster \mathbf{y} would jump to cluster \mathbf{x} .



Back

Close



We suppose that this probability does not depend on time t and it is symmetric, i.e., $p(\mathbf{x}|\mathbf{y}) = p(\mathbf{y}|\mathbf{x})$. Under these assumptions, the master equation has the form

$$(10) \quad \frac{\partial p_I(\mathbf{x}, t)}{\partial t} = \int_{Q_p} p(\mathbf{x}|\mathbf{y}) [p_I(\mathbf{y}, t) - p_I(\mathbf{x}, t)] \mu(d\mathbf{y}).$$

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

$$(11) \quad p(\mathbf{x}|\mathbf{y}) = \frac{C_\alpha}{|\mathbf{x} - \mathbf{y}|_p^{1+\alpha}}, \quad \alpha > 0.$$

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 \mathbf{y} to cluster \mathbf{x} for socially distant clusters is practically zero.*





This property of the model **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,

$$(12) \quad \frac{\partial p_I(x, t)}{\partial t} = C_\alpha \int_{Q_p} \frac{p_I(y, t) - p_I(x, t)}{|x - y|_p^{1+\alpha}} \mu(dy).$$

The integral operator in the right-hand side is the operator of fractional derivative D^α (the Vladimirov operator), see [?]. 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*:

$$(13) \quad \frac{\partial p_I(x, t)}{\partial t} = D^\alpha p_I(x, t).$$



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 (V. A. Avetisov, A. H. Bikulov, S. V. Kozyrev and V. A. Osipov).

We are interested in the relaxation regime, i.e., asymptotic of average probability $p_I(\mathbf{C}, t)$ for large t . We use the mathematical result of above authors and obtain that the average probability has the power behavior:

$$(14) \quad p_I(\mathbf{C}, t) \sim t^{-1/\alpha}, \quad t \rightarrow \infty.$$

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 $p_I(\mathbf{C}, t)$ 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 $p_I(C, t)$ decreases sufficiently quickly with time (see the lowest graph at Fig. 1).

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

$$(15) \quad p_{\text{Im}}(x, t) = 1 - p_I(x, t)$$

and its average over social cluster represented by ball C ,

$$(16) \quad p_{\text{Im}}(C, t) = 1 - p_I(C, t)$$

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 $p_{\text{Im}}(C, t)$ 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.



Back

Close

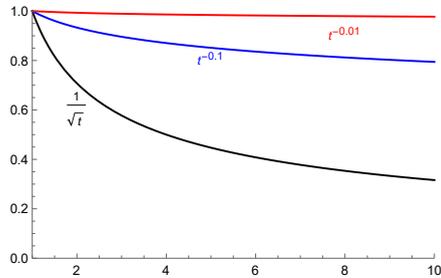


FIGURE
1. Asymptotic
behavior
of proba-
bility to
become
infected,
transition
prob-
ability
parameter
 $\alpha = 2,$
 $10, 100.$

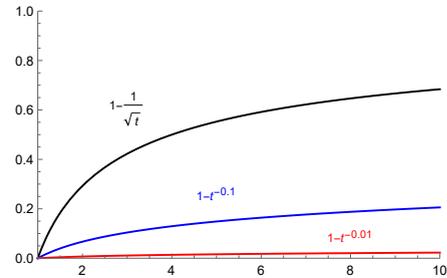


FIGURE
2. Asymptotic
behavior
of proba-
bility to
become
immune,
transition
prob-
ability
parameter
 $\alpha = 2,$
 $10, 100.$





Virus' random walk on the hierarchic social tree

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 (11)) 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.

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



Back

Close

(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 $\Delta_1 < \Delta_2 < \dots < \Delta_m < \dots$

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 ,

$$(17) \quad \Delta_m = m\Delta, m = 1, 2, \dots$$

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 (15) of the relaxation probability [?], where in physics and biology the parameter

$$(18) \quad q \equiv 1/\alpha = \frac{T \log p}{\Delta},$$

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 (11) for transition probability by using these parameters:

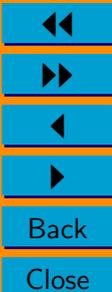
$$(19) \quad p(\mathbf{x}|\mathbf{y}) = \frac{C_{T,\Delta}}{|\mathbf{x} - \mathbf{y}|_p^{1+\Delta/(T \ln p)}}.$$

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.

Probability that the virus jumps from the elementary social cluster \mathbf{y} to another cluster \mathbf{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 Δ increases for the fixed parameter T , then the transition probability decreases and vice versa.



Starting with expression (19), we obtain the relaxation asymptotic in the form:

$$(20) \quad p_I(\mathbf{C}, t) \sim t^{-\frac{T \log p}{\Delta}}, \quad t \rightarrow \infty.$$

Thus, for large t , the average probability to become infected in social cluster \mathbf{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 $p_{Im}(\mathbf{C}, t)$ 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 $C_{i_0 \dots i_{k-1}, i}$ of the cluster $C_{i_0 \dots i_{k-1}}$. Entropy of



this spreading equals to

$$(21) \quad = - \sum_{i=1}^{p-1} q_i \ln q_i = \ln p.$$

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

$$(22) \quad p_{\text{Im}}(\mathbf{C}, t) \sim 1 - t^{-T/\Delta}, t \rightarrow \infty.$$

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:

$$(23) \quad p_{\text{Im}}(\mathbf{C}, t) \sim 1 - t^{-T/(\Delta_{\text{soc}} + \Delta_{\text{preventing}})}, t \rightarrow \infty.$$





Since Δ_{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

$$(24) \quad p_{\text{Im}}(C, t) \sim 1 - t^{-/\Delta_{\text{preventing}}}, t \rightarrow \infty.$$

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.



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.



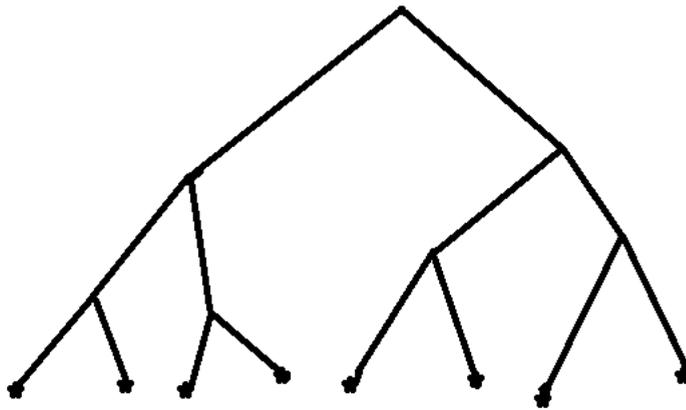


FIGURE 3. Treelike configuration space

Navigation controls:

- Left arrow button
- Right arrow button
- Back button
- Close button