

Review Article

Stochastic Reaction-Diffusion Modeling and Epidemiology in a Post-COVID-19 Era

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In the present review, the question is raised whether the classical model of epidemiology as based on the pioneering work of Kendall, and the adaptations of this model such as these made by Thieme and others, are still sufficient to explain the anomalous characteristics of the recent COVID-19 pandemic. A meta-heuristic analysis is proposed in order to compare the results obtained in distinct scientific disciplines such as in geophysical fluid dynamics, and to evaluate their practical usefulness in collective or multi-scale modeling of present or future pandemics. It is concluded that in order to augment the practical usefulness of such a multi-scale approach, more information is needed about the impact of various social-cultural, medical and demographic heterogeneities upon the characteristic time-course of the pandemic.

Keywords: Stochastic reaction-diffusion theory; Epidemiology; Multiscale modeling; COVID-19 pandemic; Stage-structured approach

Introduction: The Fate of S-I-Re Epidemiology

At the moment that a third wave of the COVID-19 pandemic is declining or fading in many countries, but a fourth wave is rapidly rising in others, it is worthwhile to evaluate the past experiences and spend at least some time in reconsidering the current state-of-the-art epidemiology. Whereas in the first year of COVID-19 several studies paid tribute to the classical work of Kendall (1957) [1], founding the epidemiological literature based on the notions of ‘susceptible’ (*S*), ‘infectious/infective’ (*I*) and ‘recovered’ (*Re*) individuals, alternative models for the *S-I-Re*-based model became known in a recent past [2]. In the *S-I-Re*-based model, mathematics determine that an epidemic necessarily develops into a pandemic, once a pandemic threshold is exceeded [1]. The global pandemic COVID-19, however, is marked by a number of anomalies [3]. Observations like the vulnerability to re-infection with the coronavirus while being vaccinated or having recovered from a previous infection with the virus, or the many severely disabled victims next to large parts of the population that relatively easily pass the disease without serious symptoms, have added to the uncertainties regarding the quantification of the effects of the pandemic [4]. Also, the inter-species infectivity, especially the spilling back from humans to farmed minks (*Neovison vison*) [5] and the subsequent transmission from minks to humans [6], as well as animal-to-human infections caused by domestic animals like cats and dogs [7], have raised the stakes for adequately modelling the pandemic [8]. However, since the number of infections in domestic pets was relatively low, not much information on the question whether or not the infected animals could also infect humans, was available to the public [9].

The uncertainties caused by the infectiousness of the disease among youngsters [10], especially with regard to the new Variants of Concern (VOC) and the hitherto unsolved questions like whether animal-to-human infections play a significant role, the differences

between rural and urban environments, et cetera, all have added to the urgent need for a new collective model of socio-epidemic dynamics to quantify the uncertainties caused by COVID-19. But, collective modelling implies also that other effects than those directly related to survival of the inpatients or the proper functioning of Intensive Care Units (ICUs) are envisaged. The various governmental decisions to close schools, universities and education centers, or to impose a general lockdown, have gravely affected child development and well-being. At the same time, these measures evoked an unprecedented cultural deprivation as well as an attack on the fragile texture of social cohesion. On the other hand, the socio-economic effects of teleworking and of impeding local and (inter)continental transportation, resulted - although briefly - in a significant lowering of greenhouse gasses [11]. Therefore, the question rises whether reduction of global transportation and efforts resulting in enhancing economic sustainability in a post-COVID 19 era, can be helpful too for inverting the deleterious effects of climate warming due to greenhouse gasses.

Adaptations of the Classical Model

Previously, we noted that already Thieme (1977) [12] used a quite different approach (deviating from Kendall’s model) to “discriminate the geographical spread of an epidemic due to the contacts between infectious individuals at the one hand, and the spread of an epidemic due to the ‘self-increase’ of the infective agents at the other hand” [2]. Alternatively, adsorption and/or elimination of infective particles could also occur, reflecting a ‘negative’ value for the increase of agents. We consider three levels of adaptations of the classical model:

- Contacts between infectious individuals;
- Self-increase of infective agent;
- Age-structure of the susceptible population.

We’ll first discuss the integration of the former two levels of adaptations in Thieme’s model (*a-b*), and then we will proceed with

the third level (c).

Contacts between infectious and self-increase of infective agent

In Thieme's model, the aim is to derive an equation in terms of three main parameters:

- $h(t, x)$: The infectious influence at x exerted from time 0 to time t ;
- $i(t, x)$: The infectious influence at x at time t (by the infective individual);
- $\pi(x, c, \sim c)$: The probability that an infective individual at x with class age c will reach the class age $\sim c$.

As a habitat for the susceptible population, Thieme (1977) choose a Borel measurable subset Ω of \mathbb{R}^n , $n = 1, 2, 3, \dots$ (Mathematically the model works equally well for $n > 3$). Thieme (1977) obtains the following result:

$$i(t, x) = \int_{\Omega \times [0, t] \times [0, \infty)} I(t-s, c-y) \hat{k}(x; d(y, s, c)) + \int_{\Omega \times [0, t]} i(t-s, y) k_0(x; d(y-s))$$

The first integral stands for the infectious influence exerted at x at time t by the infectious individuals, the second integral describes the influence which arises from the self-increase of the infective agent in the whole of Ω . Hereby, $\hat{k}(x; *)$ is a Borel measure on $\Omega \times [0, \infty)^2$ and $k_0(x; *)$ a Borel measure on $\Omega \times [0, \infty)^2$ for every $x \in \Omega$.

From this, $N \int_C C(t, x) dx$ represents the number of individuals that became infectious in a Borel set $B \subseteq \Omega$ in the course of the time interval $[0, t]$. (A Borel set means that an infinite, countable set of open or closed subsets can be found, with cardinal number $\leq N_{\text{card}}$) [12].

After some deduction, Thieme (1977) obtains:

$$\int_c^t I(r, c, x) dr = C(t-c, x) \pi(x, 0, c) \text{ for } x \in \Omega, t > c > 0$$

And $\int_c^t I(r, c, x) dr = C(t-c, x) \pi(x, 0, c) + \int_{c-t}^c \pi(x, r, c) d_r J(x, r)$
for all $x \in \Omega, t > c \geq 0$.

A characteristic feature of the model of Thieme (1977) and similar others (see [2] for review) is that the pandemic affects the whole population in a given domain (Ω), once a certain threshold of infectiousness is reached, the so-called pandemic threshold.

To incorporate a more stochastic approach - or a less 'deterministic' approach - or, in order to incorporate the effects of socio-economic dynamics and human behavioral decision-making (at the individual or group level), reference is made to a Finite State Projection (FSP) algorithm [13,14]. In order to apply such a FSP algorithm to model the epidemiological and socio-economic dynamics, there is a dual challenge: a) is it possible to characterize the complete set of socio-economic interactions of an individual (of a certain age class) or of a group of individuals, e.g. making use of a set of ordinary differential equations (ODE)?; b) is it possible to estimate the socio-economic costs of avoiding the contact opportunities in order to contain the pandemic or prevent further spreading?

According to some, the heuristic of choice has to be derived from so-called structured reaction-diffusion modeling [15-17]. One

particular adaptation of interest forms the age-structured reaction-diffusion [16].

Age-structure of the susceptible population

Al-Omari and Gourley [16], for instance, are very much concerned about the mathematical proof and provability of a specific ingredient of their model. Namely, in order to calculate a realistic (!) delay reaction-diffusion equation for a single species, it is called a necessary step to investigate the travelling wave front solutions of the main prototype equation, which is the KPP-Fisher equation:

$$\frac{\partial u}{\partial t} = u(1-u) + \frac{\partial^2 u}{\partial x^2}$$

In order to describe the number of individuals (u) in time (t) and space (x). What Al-Omari and Gourley actually do, is to present a modification of the Fisher equation in order to account for a delayed 'mobility' of the immature individuals (like larvae of an insect species). The well-known delayed version of the Fisher equation is given by:

$$\frac{\partial u}{\partial t} = u(x, t)(1-u(x, t-\tau)) + \frac{\partial^2 u}{\partial x^2} \text{ for } \tau > 0 [16].$$

Adaptations of this prototype have been forwarded by Aiello and Freedman [18]. The incorporation of age structure and spatial dispersal (the second derivative $\partial^2 u / \partial x^2$) have contributed to a 'considerable interest' and Al-Omari and Gourley [16] refer to another study of the former authors [19], where these investigators "were trying to model Antarctic whale and seal populations". And also where "the maturation time for these species depends on the amount of food (mostly krill) available, which in turn depends on the total population size" (Al-Omari and Gourley, p. 296). According to the latter authors [16], it is realistic to consider the immature members of a species to be 'immobile' ("which is realistic for many populations, especially if the maturation phase is a larval phase") (ibidem, p. 297). So there is some 'ecological' evidence included in their model, but what mostly concerns them, are the stability of the solutions. They are concerned "only with monotone wave fronts" (ibidem, p. 298). It is an intriguing question, whether the youngsters, that seem to have a profound influence on the propagation of the COVID-19 pandemic [10], would embrace the analogy of a less mobile, immature phase as in 'insect larvae'?

Surprisingly, the mathematical deduction and proof of the delayed equation for the mature individuals is the most interesting part of the article [16], which (as often) is found in the appendix of the paper (ibidem, p. 309).

Herein, the density of the mature adults $u_m(x, t)$ is given by the following integral:

$$u_m(x, t) = \int_{\tau}^{\infty} u(x, t, a) da$$

With a the age of individuals at point x , time t , with τ the length of the 'juvenile period'. It is assumed that u satisfies the following equation, which is derived from Metz and Diekmann [15]:

$$\frac{\partial u}{\partial t} + \frac{\partial u}{\partial a} = d_i \frac{\partial^2 u}{\partial x^2} - \gamma u$$

$$\text{And } \frac{\partial u_m}{\partial t} = d_m \frac{\partial^2 u_m}{\partial x^2} + u(x, t, \tau) - \beta u_m^2 \text{ with } (x \in -\infty, \infty) \text{ and } t > 0.$$

Elsewhere in their paper d_i and d_m are introduced as the 'constant' diffusion rates of the immature, resp. mature individuals of a species.

Although introducing the adaptation to "allow the individuals to

move around” (ibidem, p. 246) forms the most tedious part of the mathematical deduction, it is not surprising to note that the authors - after some Laplace transform and convolution steps - finally found mathematical proof of the equation:

$$\frac{\partial u_m}{\partial t} = d_m \frac{\partial^2 u_m}{\partial x^2} + \alpha e^{-\gamma \tau} \int_{-\infty}^{\infty} \frac{1}{\sqrt{4\pi d_i \tau}} e^{-\frac{(x-y)^2}{4d_i \tau}} u_m(y, t-\tau) dy - \beta u_m^2$$

(Equation 1.8, ibidem, p. 296). In the case of an immobile ‘immature phase’ (larvae), the d_i becomes zero and a Dirac delta function δ is keenly observed:

$$\frac{1}{\sqrt{4\pi d_i \tau}} e^{-\frac{(x-y)^2}{4d_i \tau}} = \delta(x-y)$$

So that

$$\int_{-\infty}^{\infty} \frac{1}{\sqrt{4\pi d_i \tau}} e^{-\frac{(x-y)^2}{4d_i \tau}} u_m(y, t-\tau) dy = \int_{-\infty}^{\infty} \delta(x-y) u_m(y, t-\tau) dy = u_m(x, t-\tau)$$

quod erat demonstrandum (Q.E.D.), as it was used to conclude in mathematical deductions.

Of course, despite the mathematical robustness, or the mathematical rigor of these proofs, they may not seem of much help in some (or many) of the contemporary catastrophes our world is envisaging, albeit a pandemic or inundation. We previously commented on the complexity of ecological systems and interdependent interactions between species of multiple trophic layers in an ecosystem [20,21]. When little creeks and brooklets are rapidly transforming into enormous rivers, and people are harassed at night by the rising flood destroying their houses and even devastating complete villages, these rigorous proofs are the least of their concern. For the hundreds of victims in the Eifel region, and for the victims of the Belgian Ardennes and in many other regions of the world too, the unforeseen catastrophe (July 2021), even though the most sophisticated scientific analyses and monitoring systems have been in place for many years now, demonstrate the only relevant truth: catastrophes always turn up by surprise! They do not behave like gentle, monotone mathematical solutions do. When forest loggers have left blocks of tree stubs and branches dispersed in the woods on the valley slopes, and all the lumber blocks and debris from these devastated forests roll hillside down and bombard the houses, and mingles with the debris from the houses and furniture inside, and debris and mud is piled up along the river banks, it is not a surprise that people are still searching for the relatives and people lost and, even after one week, many still haven’t been found underneath the debris and ravaged villages...

Then, the mathematical beauty and robustness is of little concern, even so that it is becoming an insult to humanity to adhere to these high-tech instruments (mathematics included) and not trying to make them useful to the suffering people of our planet. Maybe, it is time for mathematical biologists too to reshuffle their priorities?

In the next section, inspiration from another major problem area may be found in order to re-think our present heuristics.

Meta-heuristics of Collective Modeling

There has been a lot of discussion and controversy in the media about the causes of several of the immense catastrophes that are sweeping our planet Earth. Both in the spread of viral epidemics or

in the effects of the warming climate, an important anthropogenic contribution is discerned, although some may deny it. However, in order to deal with the damaging consequences, or with setting up an effective prevention or warning system, it is not always instrumental to pinpoint to the primary causes of the distortion of a complex system. For instance, it is not mandatory to predict the exact time-pattern fluctuations in e.g. (heavy) precipitation or in forest-fires in order to predict whether or not the global climate is in a transitional phase [22,23], because the extreme weather fluctuations are already an enormous, real threat to deal with. Also, the question whether or not the SARS CoV-2 is derived from the same or from a genetically linked *Rhinolophus* bat species as the SARS CoV-1 [24], is not very instrumental either in order to contain the pandemic. Neither it may help (or maybe only to some minor degree) to predict whether new variants will still be sensitive to the vaccination programs currently used, until the coronavirus pandemic will eventually become stamped out (or not). The link between global deforestation and the increased risk of zoonotic pandemics [8], indeed offers an interesting framework to understand the anthropogenic involvement, but does not offer a solution to the problem.

Both examples moreover have in common that, although they both have a link with dissipative systems [25], they cannot be simply described by reaction-diffusion theory alone. We proceed with the example of the extreme weather fluctuations, like those resulting in the inundations caused by heavy rainfall [26], and will continue with an example from epidemiology.

Analogy from geophysical fluid dynamics

It is not enough to describe the behavior of a hydrodynamic system in terms of the thermodynamic features of a flow system alone, like following the predictions of a simple effect of gravity on the displacement of water masses. The problem touches on the geological, soil and vegetation characteristics of the landscape as well as on the local atmospheric and weather conditions. Between the (semi-) stable equilibrium systems of the hydrologic cycle, present in cloud forming in moist air layers and in water storage at sea level, several levels of delay of water masses result from a complex system of storage (ground and surface water, barrage reservoir, vegetation, etc.) and transport phases (precipitation, downward and lateral seepage, groundwater discharge, evapotranspiration of a vegetation layer, etc.). It is due to the man-made control of these hydrological delay and transport phases that human culture has found a way to evolve into the present Anthropocene era. However, these man-made control systems now seem to fail, e.g. following the recent, increased precipitation incidents.

Obviously, the contemporary catastrophes point to a globally changing hydrological system. A classical work on global fluid dynamics was first developed by Pedlosky [27], describing the flows in oceans forced by atmospheric wind stress. This work was extended by Grooms and co-workers to incorporate the interactions of mean flow (basin-scale) with local-scale (ca. 100km) eddies [28]. Theoretically, the motion of fluids in global hydrological systems can be described using differential operators dependent on spatial and temporal derivatives, in general, the equations requiring a cubic nonlinearity [29]. The conservation of mass and momentum results in the well-known Navier-Stokes equations, resulting from applying

Newton's second law to fluid motion, and assuming the dependence of the fluid stress on a viscous term (proportional to the gradient of velocity) and a pressure term. Mathematically, a decomposition of the spatial and time derivatives is proposed as well as a decomposition into large- and small-scale as well as fast- and slow-time dynamics, each performed on the characteristic length and timescales [29]. As Grooms and co-workers pointed out, the importance of coupling large and small scales is demonstrated by the impact of a "horizontal gradient of large-scale quantities on the small-scale variables, and the impact on the large scales of a net lateral flux generated by the small scales" [29].

An interesting aspect of some of these multiple-scale analyses is the use of internal boundary layers and matched asymptotic expansions [30], because "the small-scale dynamics do not occur everywhere in the domain, but only in localized parts" [29]. Of course, it remains open to local data collection and measurement to make these general, theoretical predictions practically useful.

Epidemiology in a post-COVID-19 era

Classically, epidemiological models predict that an epidemic turns into a pandemic, once a pandemic threshold is exceeded [1]. So, the pandemic conditions affecting a population in a given area, leave no space to hide [31]. Since SARS-CoV-2 and its variants of concern (VOC) already seem to have been distributed worldwide, and immunity, either by contact with the virus or by one of the several vaccination programs, doesn't completely prevent the virus to be transmitted from one individual to another, and still making victims among the immune-compromised and vulnerable patient groups, the question rises how to deal with the new situation of a post-COVID-19 era?

Because virus particles do not move freely in absence of human or animal carriers, it is the movement of human (and mammal carriers) that forms the physical basis of the system. The heuristics for modeling the impact of movement-restricting measures - from a general lockdown to more selective impediments - may be derived from the analogy with the physics of dissipative structures, such as in heat transfer modeling (also used in geophysical fluid dynamics, see above). Heat transfer basically occurs through three different mechanisms, conduction, convection and radiation, and so also three levels of socio-economic effects causing dissemination - or economic loss due to restrictive measures - can be discerned:

- Conductivity (diffusion) modeling of social contacting;
- Convection modeling the impact of global transportation (trade and infrastructure);
- Radiation modeling the effects of art, education, culture and (disruptive) innovation.

It has been suggested that the heuristics for calculating the impact of restrictions are also the heuristics for modeling an austerity strategy for preventing a generalized catastrophic climate 'melt-down'. But like in geophysical fluid dynamics, also here it is important to consider the local- versus global-scale dynamics, like in modeling the impact of urban versus rural environments, local versus global economic activities, etcetera. It is tempting to speculate that mixed multi-scale modeling, also here may benefit from "the use of internal boundary

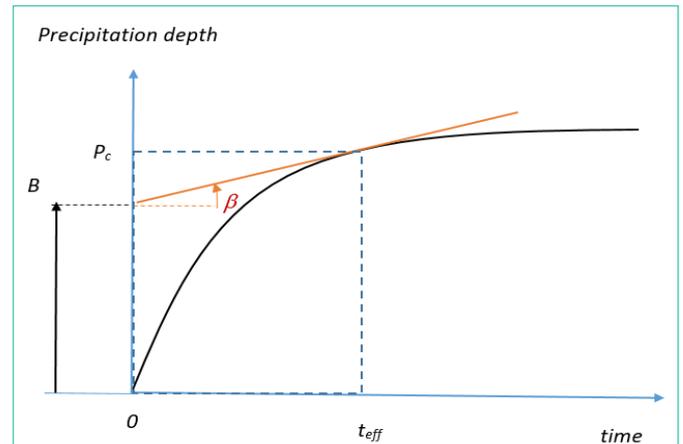


Figure 1: Representation of a local scale approach like in precipitation containment. The critical precipitation depth (P_c) depends on the effective duration of the precipitation (t_{eff}), the precipitation depth (P) and the total storage capacity of an area (B). The maximal discharge capacity is calculated from the local empirical data ($\tan \beta$). (Adapted from Commission Hydrological Research, TNO, The Netherlands).

layers and matched asymptotic expansions" as in fluid dynamics (see above) [30].

Local Solutions and Alternative Approaches

Locality of finding practical solutions

For reasons of practical usefulness, we may again benefit from the analogy with a simple (local) hydrological system. In Figure 1 the critical precipitation depth (P_c) (e.g. for summer period rainfall) is represented in terms of the precipitation depth (P), the (effective) duration of the precipitation (t_{eff}) and the total storage capacity of an area (B). From these empirical data (B , P , P_c , t_{eff}), a (maximal) discharge capacity can be calculated ($\tan \beta$). However, the practical usefulness of this solution, how important it is for a given, local situation, has to be reconsidered for each area again. Some general predictions could be made, e.g. the risk for inundation in old villages built in V-shape valleys without proper man-made or natural storage facilities.

Estimating the long-term precipitation characteristics of a given area, however, is much more complicated and heavily depends on a globalized parametrization approach. Therefore, predictions for the local situation also depend on modeling at a global scale and vice versa.

Similarly, in the example of containment of a pandemic, and especially in containing the health costs, the local approach in many (European) countries has been initiated, starting from the hospitalization and 'storage' capacity of seriously ill inpatients or on the (total) ICU-capacity of an area [4]. Modeling the impact of social and cultural activities on the number of contact-events and consequent hospitalization load, depending on the seasonality of the (social and cultural) events and age-structure of the population involved, however, is still in its infancy.

A local scale approach for finding practical solutions like a strategy to contain the virus, however, is obviously too late. What would have been needed, in case of the coronavirus pandemic, was

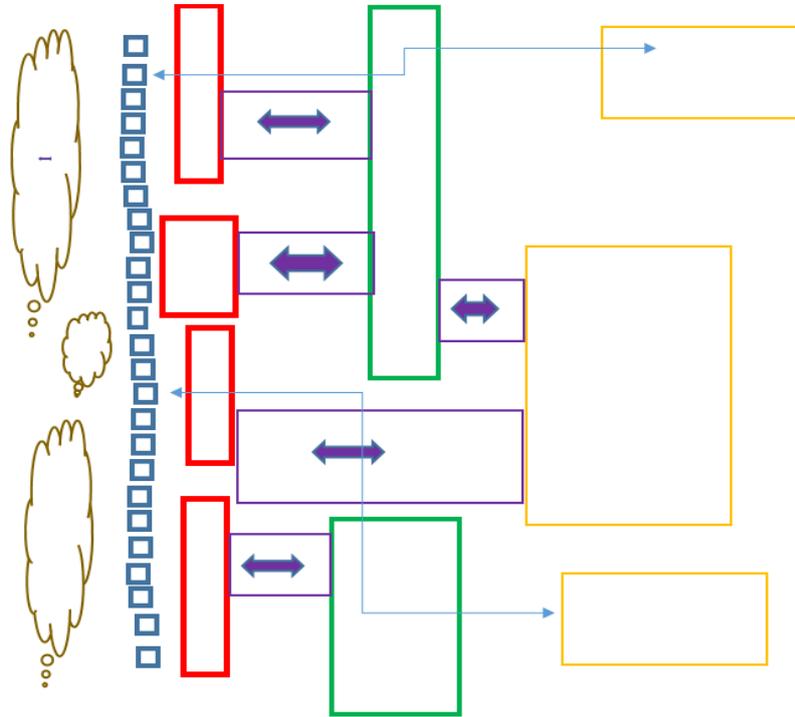


Figure 2: Scheme representing the complexity of multi-stage modeling of the spread of an epidemic. In the two-dimensional plane, blocks with varying width and length (cells) are depicted, symbolizing elderly care centers (brown), family houses (blue), schools (red), youth gatherings, festivals and holiday areas (green), long-distance business travelling and international traveling (yellow), etc. The complexity arises from defining the propagation speed inside and at the borders within each of these cells, being also a function of time (axis not drawn). In general, a statistical analysis of the mean-field characteristics of a population as a whole is considered much more feasible, but the value of a detailed multi-stage analysis lays in the possibility to infer the economic and social drawbacks and costs resulting from imposing specific restrictive measures.

a contingency plan or strategy. In case this contingency plan was not available or deployable, the next best thing would be to have one for the forthcoming pandemics or variants of the virus. Whether or not a vaccination strategy is part of the contingency plan, and how it is deployed worldwide, are still matters of international concern [32]. Especially, the new finding that the SARS-CoV-2 virus may have taken an evolutionary benefit from an analgesic effect (lowered sensitivity to pain without loss of consciousness) and host manipulation mechanism [33], further strengthens the need for a global rather than a local contingency plan.

Alternative approaches

In absence of a global strategy, a great number of countries have followed various local, ad hoc strategies, resulting in the kaleidoscope of (non-) pharmaceutical interventions [4] and a mosaic of multi-colored regional maps reflecting the infection risks in the past two years. The following paragraph is an attempt to model the recent developments following a so-called mean-field approach versus an alternative stage-structured approach.

When differences in socio-economic behavior between infants, adults and elderly people have to be taken into account, it is obvious that some sort of stage-structured approach is recommendable. In contrast to the adaptations of the classical model (see paragraph 3.2), the impact of this stage-structure is not a simple delay or modulation of the susceptibility rate, but a profound disharmony between the movement and migration characteristics (for instance between young

adults and elderly in foster homes). On the other hand, a mean-field approach following general infectivity statistics is always possible, in order to guide state directives. For it is said, statistics in fact reflect the interests of a state [34].

Graphically, the heterogeneity of social contacting (or its opposite: social distancing), movement and migration can be represented by a two-dimensional mosaic pattern of cells with varying width and length, with a third axis representing the time variable (Figure 2). In analogy with the physics of heat transfer, the transfer of infectivity could be represented by a combination of conductivity and convection mechanisms (see section 4.2 above). Because the radiative mechanism, linked to the effects of cultural influencing, is much more difficult to integrate into a status-quo approach, it is left out in the subsequent analysis.

The (local) carrier load of infective agents (density of infectious persons times virus load, in an area at time i) is chosen as the main variable (C_i). In analogy with the topological network model of Albert and Barabási [35], the connectivity in time of this carrier load is given by the differential equation [2]:

$$\frac{\partial C_i}{\partial t} = (p - q)m \frac{1}{N} + m \frac{C_{i+1}}{\sum_j (C_j + 1)} \quad [35]$$

In the latter case, the variables p , q , m are defined by Albert and Barabási [35] as the probabilities to add new links, to rewire new links and the number of links connecting a new node to a network system with fixed number of elements (N). In the epidemiological example,

these probabilities could also be interpreted as the probability of transferring the virus to another person (p), the probability of an infected person going into quarantine (q) or contacting new people (m). Although not a classical description of the epidemiology of infectious diseases, the above model may be regarded as a form of mean-field model, where the (effective) reproduction number of the pandemic (R_{eff}) could be empirically derived from the quantities of p , q and m .

In order to incorporate not only local dissemination, but also long-distance spread of the infective agents, a quadratic term is added (because of the reciprocity of travelers contacting other travelers), reflecting the convection mode (also regarded as 'forced flow') in the above described meta-heuristics (see section 4.2):

$$\frac{\partial C_i}{\partial t} = A_i + m \frac{C_{i+1}}{\sum_j (C_j + 1)} + n \frac{C_{i+1}^2}{\sum_j (C_j + 1)}$$

Herein, n reflects the probability of a person (or group of persons, within a given area) to be engaged or involved in long-distance travelling. The other terms are in agreement with the expression above [35]. The addition of a quadratic term to the differential equation and also second order derivatives - e.g. following changes in behavior or restrictive rules - lead to possible solutions which are a combination of periodic and exponential functions of time [36]. This is in line with the observed periodic behavior of the successive pandemic waves in COVID-19. After some reduction and rewriting, it can be seen that a particular solution of the form is found: $\int \frac{\partial C_i}{1+C_i^2} = \arctan C_i + k_i$ whereas integration of the time-variable results in an exponential term.

Although the above result is purely theoretical, it indicates that inverse goniometric (as well as exponential) solutions follow from this (first order) differential equation with quadratic terms. Boundary conditions at a local scale (individual cell) may be chosen as:

$$\begin{cases} C_0 = (p-q)n \\ C_{t=x} = 0 \end{cases}$$

Meaning that the restrictive measures have been taken to locally stamp out the spreading of the epidemic at some time x . Of course, each cell may yield its own boundary conditions, affecting the dissemination in neighboring cells (where a different propagation speed or different restrictive measurements are taken). In order to increase its practical usefulness, cultural, behavioral, medical and age group-specific data have to be implemented, for instance in order to give a reliable image of the social connectivity patterns in various cultural regions and traditional or adopted community patterns. Obviously, such a complex analysis would reach beyond the scope of the present paper.

Conclusions

In this paper we have shown that adaptations of the classical epidemiological model of Kendall [1] have already been suggested well before the outbreak of the COVID-19 pandemic. These adaptations for instance include the self-increase of an infective agent (like a virus) and so-called age-structured approaches. An important question, however, whether or not these adaptations have been sufficient to make the classical model suitable for explaining the anomalous results of the present pandemic, remains to be answered and translated into practical solutions.

The present study therefore offers a meta-heuristic bypass in order to re-think the classical approaches (including the adaptations

of the classical model) and eventually take some benefit from analogy with distant disciplines or application fields.

The analogy with geophysical fluid dynamics and heat transfer not only points to another form of catastrophic consequences of climate change, it also offers an interesting alternative for combining local and global approaches of a global system, also called a multiple-scale approach. Also in the epidemiological case, this multiple-scale approach may become very valuable, although relevant data about cultural, behavioral and age-group-specific heterogeneities (as well as medical and other demographic data) are indispensable for making this approach practically useful.

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