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Superdiffusion and epidemiological spreading

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ABSTRACT

We describe spreading of diseases in geographical space via superdiffusion. Nowadays people travel a lot over wide distances and therefore the spread of the infection happens not only locally i.e. from one person to the neighbor, but also for large distances. Superdiffusion has been suggested to model this type of epidemiological spreading in space. We consider the analytically tractable case of a diffusion like process on the lattice which is used as a surrogate process of human contacts in epidemiology. A stochastic process for a population is then used where the notion of distance is given by power law decaying connectivities, in good agreement with the analytics. We apply the results to the SIS model on the lattice.

1. Introduction

In order to describe epidemiological spreading, one can use individual based stochastic processes for a given host population of size N, where neighbouring contacts are specified via an adjacency matrix (see e.g. Stollenwerk and Jansen, 2011; Stollenwerk et al., 2010 and many further references there). By default not only regular lattices but also other networks like purely random networks or small world networks can be modelled this way.

However, it is difficult to quantify the connectivity of such epidemiological networks, especially on large scales. From basic knowledge of e.g. physical processes we know that as long as the connectivity is purely local, no matter which neighbourhood is chosen, will on a large scale be always behave as Gaussian diffusion. Besides such purely local or sufficiently fast decaying connectivities, leading to such ordinary diffusion, there are also other possibilities of large scale spreading, the Lévy stable processes of only power law decaying connectivity.

Besides often poor attempts to quantify connectivities of epidemiological spreading directly, there have been also studies conducted of so called surrogate processes for human contacts, as e.g. recently a detailed investigation of the spatio-temporal distribution of money bills, here especially one-US-dollar bills, assuming that these are mainly exchanged from person to person as they meet and travel (Brockmann et al., 2006). It turned out that the connectivity suggested by such surrogate data of human mobility are much more on the side of Lévy processes with power law decay than of ordinary diffusion. These processes are described by superdiffusion rather than ordinary Gaussian diffusion via fractional calculus, see among many others e.g. the following references for the foundation and applications of fractional calculus (Kilbas et al., 2006; Martinez and Sanz, 2001; Rubin, 1996; Samko et al., 1993) with a lot of attention to this date, e.g. Kwaśnicki (2017). For superdiffusion and its connection to fractional calculus see e.g. Brockmann and Hufnagel (2007), Brockmann (2003) with many more references there, and more recently also Skwara et al. (2012a,b) with additional references.

In many cases superdiffusion is modelled by particles moving around, but in epidemiology the most important process is the contact between susceptible and infected persons, no matter who is moving and who is not, but contacted by the moving. In the framework given by e.g. Stollenwerk and Jansen (2011) and Stollenwerk et al. (2010), all is needed is the power law decay in the connectivity given by the adjacency matrix, i.e. who can have contact with whom and hence the probability of spreading a disease from whom to whom. After a revision of various different ways of fractional calculus (Boto and Stollenwerk, 2009), it turns out that the Riesz fractional derivative is most natural and easiest to apply in the case of superdiffusion, since its definition via the Fourier transform is closest to the analytical solution of ordinary diffusion, and as well easily applicable in higher dimensions (as opposed to the most common applications of e.g. Liouville fractional derivatives etc. in one dimensional space), though most of the possible definitions of fractional calculus finally agree with each other when compared well (Brockmann, 2003; Kwaśnicki, 2017; Samko et al., 1993). Analytically, the Riesz fractional derivative is most elegant, but in addition we need for the generalization of the stochastic processes described in Stollenwerk and

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Jansen (2011) and Stollenwerk et al. (2010) a notion of the non-locality of the generalized Laplacian operator as given by an integral representation, which is provided by the convolution theorem of Fourier analysis. With this at hand the connectivity of the epidemiological networks can be expressed via a generalization of the adjacency matrix, now with power law weighted probabilities of the spreading.

The framework provided by the diffusion or superdiffusion process then can be applied easily to any epidemiological process, of susceptible-infected-susceptible (SIS-type), to susceptible-infected-recovered (SIR-type), or any other including reinfection or multi-strain processes. Here we will concentrate on the simplest SIS process which is giving diffusion or superdiffusion processes similar to the well known Fisher-Kolmogorov-Petrovski-Piscounov process (Fisher, 1937; Kolmogorov et al., 1937) with its widely known qualitative behaviour of front propagation from the infected region to the susceptibles.

The present article is structured as follows: We first give in Section 2 a quick outline of the stochastic process formulation for N individuals on a generalizable lattice, here of SIS-type (see Stollenwerk et al., 2010 for generalizations to SIR-type and further processes with reinfection). This formulation can as well formulate processes of exchanging items like money-bills on the same contact networks, leading naturally to diffusion processes, and in the case of regular lattices with nearest neighbour connectivity to ordinary diffusion, in Section 3. Consequently in Section 4 we revisit the solution of the ordinary diffusion equation via Fourier transformation, which immediately leads to the generalization via the Riesz fractional derivative in Fourier space of superdiffusion in Section 5. Since the Lévy stable function, now appearing in superdiffusion instead of the Gaussian function in ordinary diffusion, we need to consider the discrete Fourier transform for numerical investigations in Section 6. In order to compare the stochastic process formulation and its histograms with the numerics of the Fourier analysis we need in addition the integral representation via the convolution theorem of Fourier transforms, this in Section 7. Finally, in Section 8 we give the formulation of diffusion and superdiffusion in higher dimensional space as a straight forward extension of Fourier transforms from one to higher dimensions and in Section 9 the application of the results of superdiffusive spreading to the SIS system, in close connection to Fisher-Kolmogorov-Petrovski-Piscounov processes.

2. Spatially extended stochastic epidemiological models

We consider a host population of size N, where each individual is labeled by the index $i = 1, 2, ...,N$ and can in the simplest case of an SIS epidemiological model be infected, $I_i = 1$, or susceptible, in which case $S_i = 1$ and $I_i = 0$. The concepts presented here can be easily generalized to more complex models like the SIR-model etc. (Stollenwerk et al., 2010). In the case of the SIS epidemiological model we only need to consider the N variables I_1 to I_N and $I_i \in \{0, 1\}$. Via $S_i = 1 - I_i$ we always know then also the number of susceptibles. The state of the individual based system is at any time t defined by the set of variables $(I_1, I_2, ..., I_N)$.

Any spatial or contact network structure can be given by an $N \times N$ matrix J which codes which individual i is neighbour to which other j via the matrix elements $J_{ij} \in \{0, 1\}$ of the adjacency matrix J, hence $J_{ij} = 1$ for neighbouring sites i and j, else $J_{ij} = 0$. Since contacts are mutual, we have no directional network, and the adjacency matrix is symmetric, hence $J_{ij} = J_{ji} \in \{0, 1\}$ for $i \neq j$. Further we assume no self-contact, hence $J_{ii} = 0$.

A susceptible individual S_i can become infected when one or more of its neigbours I_j are infected, $I_j = 1$, by the infection rate β, and infected can recover with recovery rate α, hence we have the reaction scheme for the spatial SIS model

$$\begin{aligned} S_i + I_j &\xrightarrow{\beta} I_i + I_j \\ I_i &\xrightarrow{\alpha} S_i \end{aligned} \tag{1}$$

as analyzed in Stollenwerk and Jansen (2011). The transition rates are probabilities per time, hence for the states $(I_1, ..., I_N)$ at any time we have to consider probabilities $p(I_1, ..., I_N, t)$ and with the transition rates we can give the dynamics of the probabilities via a master equation to describe the time continuous Markov process, which we have just defined.

For the SIS model the master equation is given by

$$\begin{aligned} \frac{d}{dt}\, p(I_1, I_2, ...,I_N, t) \;=\; & \sum_{i=1}^{N} \beta \left(\sum_{j=1}^{N} J_{ij} I_j \right) I_i \; p(I_1, ...,1 - I_i, ...,t) \\ & + \sum_{i=1}^{N} \alpha (1 - I_i) \; p(I_1, ...,1 - I_i, ...,I_N, t) \\ & - \sum_{i=1}^{N} \left[\beta \left(\sum_{j=1}^{N} J_{ij} I_j \right) (1 - I_i) + \alpha I_i \right] p(...,I_i, ...,t) \end{aligned} \tag{2}$$

and defines the dynamics of the stochastic system, ones the initial distribution of probabilities $p(I_1, ..., I_N, t_0)$ is given (Stollenwerk and Jansen, 2011).

Via simulation techniques, like e.g. the Gillespie algorithm, we can obtain single realizations of the stochastic process. Superimposing many such realizations we can estimate the expectation values to have an infected on any lattice site i, i.e. $\langle I_i \rangle$. Such local expectation values are defined by the usual expression for expectation values, hence any function of state variables multiplied by the probability of the states and summed up over all possible states, we have here

$$\langle I_i \rangle (t) := \sum_{I_1=0}^{1} \cdots \sum_{I_N=0}^{1} I_i \; p(I_1, ...,I_N, t) \quad . \tag{3}$$

Then, the time evolution of the local expectation values are determined by

$$\frac{d}{dt} \langle I_i \rangle (t) := \sum_{I_1=0}^{1} \cdots \sum_{I_N=0}^{1} I_i \, \frac{d}{dt} p(I_1, ...,I_N, t) \tag{4}$$

where the master equation has to be inserted for $\frac{d}{dt} p(I_1, ...,I_N, t)$. After some calculations, which are described in more detail in Stollenwerk and Jansen (2011), pp. 23–32, we obtain the following form for the dynamics of the local expectation values

$$\begin{aligned} \frac{d}{dt} \langle I_i \rangle \;&=\; \beta \sum_{j=1}^{N} J_{ij} \langle I_j (1 - I_i) \rangle - \alpha \langle I_i \rangle \\ &=\; \beta \sum_{j=1}^{N} J_{ij} \langle S_i I_j \rangle - \alpha \langle I_i \rangle \end{aligned} \tag{5}$$

which provides an easy and intuitive way to calculate generally dynamics of these local expectation values. In the last line we used $S_i := 1 - I_i$. The dynamics of $\langle I_i \rangle$ now contains higher moments, here $\langle I_i I_j \rangle$, respectively $\langle S_i I_j \rangle$, which leads to differential equations for these higher moments etc. To obtain a closed ODE system for the set of variables $\langle I_1 \rangle$ to $\langle I_N \rangle$, we can use a mean field approximation where here the local cross variances are neglected. We will discuss this approach further in Section 9.

First, we will describe another individual based stochastic process, which was suggested to investigate as a surrogate process the human contact network, on which also epidemics spread. This surrogate process is the dynamic spreading of money bills between individuals which meet each other, hence are neighbours in the sense of the same adjacency matrix J on which also diseases can spread (Brockmann et al., 2006).

3. An individual based random walk model

In order to investigate the human contact structure, here specified by the adjacency matrix J, we consider individuals I_i which have an