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Reaction-diffusion processes on heterogeneous metapopulations: Continuous-time formulation and simulations

In some recent models of epidemic spreading, the location of the patches in space is treated explicitly thanks to the increasing of computational power. However, an alternative approach based on the formalism used in the statistical mechanics of complex networks has been recently introduced by Pastor-Satorras, Vespignani and Colizza (2007) and Vespignani and Colizza (2008). Under this approach, the topology of the spatial network of local populations (nodes) is mathematically encoded by means of the degree distribution p(k) defined as the probability that a randomly chosen node has degree k. Moreover, each node contains two types of particles: A particles corresponding to susceptible individuals, and B particles that correspond to infected ones. Within each node, a transmission process (reaction) occurs between particles of different type, and migratory flows take place among nodes (diffusion) at constant rates. Therefore, although the detailed description of the spatial network is lost, the approach offers an elegant description of the epidemic spread in terms of densities of A particles and B particles in patches of degree k at time t.

In this talk I present the derivation of the continuous-time equations governing the limit dynamics of the reaction-diffusion processes on heterogeneous metapopulations introduced by these authors (Saldaña 2008). Moreover, I will show that, when a rigorous time limit is performed, the lack of an epidemic threshold in the spread of infections is not limited to metapopulations with a scale-free architecture, as it has been predicted from dynamical equations in which reaction and diffusion occur sequentially in time.

A similar formulation has been simultaneously introduced by Baronchelli, Catanzaro, and Pastor-Satorras (2008) in the context of the so-called bosonic reaction-diffusion processes, which was already considered by Park in 2005, although with no application to the analysis to the spread of infectious diseases.