Threshold-based epidemic dynamics in distributed systems

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In this work we analyze an epidemic dynamics model (SI) where we assume that there are k susceptible states, that is a node would require multiple (k) contacts before it gets infected motivated from the fact that not all agents in the network are equally susceptible o a disease. In specific, we provide a theoretical framework for studying diffusion rate in complete graphs and d-regular trees with extensions to dense random graphs. Interestingly we observe that irrespective of the topology, the diffusion process could be divided into two distinct phases: (i) the initial phase, where the diffusion process is slow, followed by an almost exponential increase in diffusion rate which we term as (ii) the residual phase. In fact, the initial phase acts as an indicator for the total diffusion time in dense graphs. The most remarkable from this investigation is that such a diffusion process could be controlled and even contained if acted upon within its initial phase.