Matrix and Bifurcation Analysis of Networked Connectivity Models of Waterborne Disease Epidemics (J. Rebaza)

A typical susceptible-infected-recovered (SIR) mathematical model considers only isolated communities, where the corresponding onset condition for outbreak of the disease is directly related to what is called a *basic reproduction number*, a quantity related to recovery rates and disease-induced mortality rates, among other factors. In practice however, infection patterns are influenced by spatial distributions of human settlements, and by pathogen transmission via hydrological and human mobility networks. Thus, integrating hydrology and human mobility into epidemiological models is mandatory [1, 2, 6].

The hydrological networks can be those of river basins, and/or those of human-made water distribution and sewage systems. Network nodes can be cities, towns or villages, depending on spatial resolution [5]. The connections between communities can be described by two stochastic matrices, one for the hydrological network and one for human mobility. Pathogens can move in water from node one node to another with a given probability, but they can also be spread by human mobility [5, 6]. The model under consideration will consider a graph which is the union of the two graphs associated with the stochastic matrices described above, and we will assume that the resulting graph is strongly connected, and therefore its associated matrix A is irreducible.

The dynamics of the model can be described by a three-dimensional system of differential equations on the susceptible, the infected/infectives, and the transport of pathogens over the network [5, 6]. Unlike typical SIR models, in this networked model, the requirement that the basic reproduction number be larger than one is neither necessary nor sufficient for outbreaks to occur. Instead, we must study the behavior of the dominant eigenvalue and corresponding dominant eigenvector of A [3, 4,5,7] as this will allow us getting conclusions about conditions for outbreak as well as about a short-term geographical distribution of disease insurgence. The analysis of the model also includes the study of bifurcations in the model that can be related to the onset conditions for outbreak. We plan to extend current results by studying and rigorously proving existence of bifurcations beyond transcritical ones, including codimension-two bifurcations. Our study should also include a full analysis of local and global stability of the system.

Prerequisites: A basic background on differential equations and linear algebra, in addition to the calculus sequence. Some programming experience is desirable but not required.

References Cited

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