RICH BIFURCATION DYNAMICS OF A DIFFERENTIAL MODEL FOR DISEASE SPREAD BETWEEN TWO CITIES

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Modern applied mathematics uses differential equations to model biological phenomena. In this talk, we present an SIVS (susceptible–infected–vaccinated–susceptible) model for the spread of an infectious disease in a human population. To describe how the number of susceptible, infected and vaccinated individuals vary over time, a system of ordinary differential equations will be formulated. We define the basic reproduction number ($\mathcal{R}_0$) for the model, which gives the number of secondary infections generated by an infected individual in a completely susceptible population. This quantity usually serves as an epidemic threshold, since in most disease transmission models the infection is eradicated whenever $\mathcal{R}_0 < 1$ holds. However, in the SIVS model it is possible that the disease persists when $\mathcal{R}_0$ is below unity, because under certain conditions there exist two positive equilibria for some values of $\mathcal{R}_0$ less than one.

Next, we consider the SIVS model for epidemic spread in a population of individuals who travel between two cities. After giving an explicit condition for the existence of multiple positive steady states and disease persistence in the model, we investigate the global dynamics and the stability of equilibria with analytical tools and rigorous numerical computations. In particular, we will show that besides the disease free steady state, eight possible endemic equilibria bifurcate from triple transcritical and double saddle–node bifurcation points.