

PhD Seminar Talk-I

Analysis and Simulations of Network-Based Nonlinear Epidemic Models

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Abstract: In epidemiology, differential equation systems have emerged as a key tool for controlling the transmission of infectious diseases. It involves mathematical and computational techniques that simulate the dynamics of disease transmission, considering various factors such as population demographics, disease characteristics, social interactions, population mobility, and many more. In the early 20th century, Kermack and McKendrick [1] developed compartmental models like the SIR (Susceptible-Infectious-Recovered) model, where the population was divided into three compartments: S , I , and R . Over time, epidemic modelling has evolved, incorporating complex network structures to represent interactions among individuals and population movements among different regions. Many models have been proposed to control outbreaks using networks, but these models are typically based on contact networks among individuals. In the early stages of an outbreak, when an epidemic is established, involving a geographical network becomes essential for understanding spatial dynamics. Therefore, constructing epidemic models that incorporate population mobility is crucial, as it is a key factor influencing the spatial spread of an epidemic.

In this seminar, we divided the talk into two parts as follows:

Part a: We proposed a network-driven SIR epidemic model as an application to understanding the spatial spreading of COVID-19 using graph Laplacian diffusion. Well-Posedness, epidemic criteria, the emergence of a second wave, and various types of isolation strategies have been demonstrated from scratch by considering a small-world network.

Part b: A time delay networked SIR epidemic model with a nonlinear incidence rate is considered on a graph of Laplacian diffusion. The model introduces population mobility through the graph network. Several stability theorems are proved at all possible different equilibrium points of the model. Further, Hopf bifurcation analysis for the endemic equilibrium is investigated. Applying our generalized weighted graph to Watts-Strogatz network, numerical results are presented to support the theoretical findings.

References

- [1] WO. Kermack, AG. McKendrick, A contribution to the mathematical theory of epidemics, Proc. R. Soc. Lond. A 115 (1927): 700-721.