Hopf Bifurcation Analysis for a Delayed Nonlinear-SEIR Epidemic Model on Networks

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Abstract. A delayed SEIR (Susceptible-Exposed-Infected-Removed) epidemic model with a non-linear incidence rate using graph Laplacian diffusion has been considered. The model has a diffusion term that describes population mobility through a network. The local stability analysis for each steady state is demonstrated, and Hopf bifurcation for endemic equilibrium has been examined. Computational experiments are performed to illustrate the theoretical findings on a small-world Watts-Strogatz graph.

Introduction

Population mobility is one of the important key factors for the spatial spread of an epidemic. Many models have been proposed to control an outbreak using a network, but these are based on contact-network between individuals [1]. At the early stage of an outbreak, it is essential to involve a geographical network to understand spatial dynamics. Recently, Tian et al. [2] have investigated delay-driven Hopf bifurcation in a networked Malaria model. Motivated by their work, we investigate Hopf bifurcation in a delayed-SEIR epidemic model on network.

The present model also considers an additional non-linearity called saturated incidence rate [4] of the form $\beta IS/(1 + \alpha I)$, where S and I are the susceptible and infected individuals, respectively. Several studies on dynamical and bifurcation analysis can be found in [3] for which the model have this kind of nonlinear incidence. Since this incidence rate involves the behavioral change and crowding effect of the infective individuals, it appears that this incidence rate is more important than both the bilinear incidence rate and standard bilinear incidence rate [5]. Furthermore, the unboundedness of the contact rate can be prevented by selecting appropriate parameters β and α.

Results and Discussion

The main contributions of this work begin with theoretical results, which include the stability theorems and derivation of the threshold delay time τ_0 for the bifurcations. Then numerical experiments are performed by considering a small-world Watts-Strogatz graph to validate the theoretical findings. One of the important finding is the local behavior of the model, which is governed by basic reproduction number $\mathcal{R}_0$. The disease-free equilibrium is asymptotically stable for $\tau \geq 0$ if $\mathcal{R}_0 < 1$. If $\mathcal{R}_0 > 1$, the endemic equilibrium exists uniquely, and under a certain condition on parameters, the model undergoes a Hopf bifurcation when time delay τ surpasses a critical value τ_0. In Figure.1, the left sub-figure depicts the solutions for all node are stable and converge to the endemic equilibrium simultaneously when $\tau < \tau_0$. The solutions are periodic for the all the nodes when τ greater than the critical value τ_0. For the shake of clarity, the phase plane for the second node has been displayed in the right sub-figure of Figure.1 when $\tau > \tau_0$.
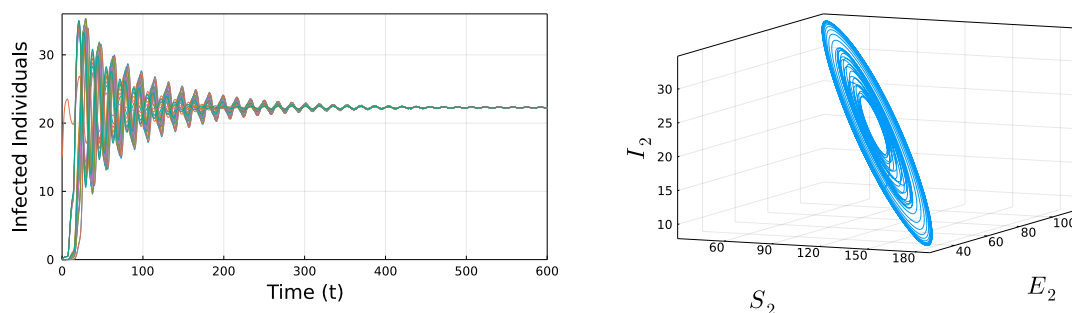

Figure 1: (left) when $\tau < \tau_0$, profile solutions for each infected node, and (right) when $\tau > \tau_0$, phase plane at second node.

References

[1] R. Pastor-Satorras, C. Castellano, P. V. Mieghem, and A. Vespignani, Epidemic processes in complex networks, Rev. Mod. Phys., 87(925)(2015), 925-979.

[2] C. Tian, Y. Liu, Delay-driven Hopf bifurcation in a networked Malaria model, Applied Mathematics Letters, 132(2022), 108092.

[3] Z. Hu, W. Ma, S. Ruan, Analysis of SIR epidemic models with nonlinear incidence rate and treatment, Mathematical Biosciences, 238(1)(2012), 12-20.

[4] V. Capasso, G. Serio, A generalization of the Kermack–Mckendrick deterministic epidemic model, Math. Biosci. 42(1978),41–61.

[5] R. Xu, Z. Ma, Global stability of a delayed SEIRS epidemic model with nonlinear incidence rate, Nonlinear Dyn., 61(2010),229–239.