Paper Review: Epidemic Processes Over Time-Varying Networks

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Abstract—We will analyze and dissect a paper by Philip E. Paré, Carolyn L. Beck, and Angelia Nedić [1] which focuses on modelling an epidemic spreading process with not the preexisting static graph models but by a dynamic graph model. The paper attempts to formulate a model that captures a more realistic disease transmission network in which the carrier (the people) are characterised as a dynamical as well as time-varying system. Then, using this model, a series of analysis and simulations are conducted to elucidate the convergence condition, or in other words, the condition where the epidemic ceases for both deterministic and stochastic cases.

Index Terms—Epidemic processes; Networked systems; Stochastic systems; Time-varying systems; Markov Chain; Graph theory

I. INTRODUCTION AND MOTIVATION

Beginning from the model by Bernoulli developed based on the smallpox, susceptible-infected-susceptible (SIS) models have been proposed and analyzed to reproduce virus dynamics within the complicated human network. The network model has been refined for both continuous and discrete time systems age time went by. With the introduction of immunization strategy, disease-free equilibrium (DFE), nondisease-free equilibrium (NDFE), convex optimization, vaccination strategy, and Markov chain models allowed a more pragmatic system modelling. However, considering how the models are still restricted to unweighted and undirected graphs which were not suffcient enough to encapsulate virus spread.

To approach this issue, the reviewed paper derives a weighted and directed time-varying graph structure and investigate the sufficient conditions for a global exponential stability of DFE models. For generality, the discussion is extended to a heterogeneous virus with stochastic framework and n-intertwined Markov Chain. Then the theories are simulated and evaluated for empirical verification followed by a conclusion and improvement.

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II. PROBLEM FORMULATION

To formulate the problem the paper first constructs the virus propagating network model with 2^n-state Markov chain. Then defining a state vector that depends on a random variable indicating the probability of infected or healthy, a generalized form of a heterogeneous virus directed graph structure can be modelled. This model consists of infection rate of an agent, a directed, nonnegative, weighted, connection between agents, nonnegative healing rate, and the state vector representing probabilities of infection of the agents. Furthermore, a time-varying extension is employed to the model making it quite costly to deploy, and therefore, a mean-field approximation is utilized to opt the simulations.

Now using this time-varying model the paper conducts a nonlinear analysis to figure out the stability about the DFE and NDFE for a deterministic case and stochastic case. The deterministic case was broken down to several conditions and each of them were evaluate for stability for a certain equilibrium point. Each of these conditions show different stability characteristics for the equilibrium points based on nonlinear analysis using a Lyapunov function. The first condition was a *undirected graph and homogeneous in infection rate case*. In this case the DFE was globally exponentially stable (GES) and the origin was exponentially stable (ES). For a *directed graph and heterogeneous virus case* the stability changes depending on whether the linearized system is Hurwitz or not. If it is Hurwitz the system is GES about the origin and DFE, whereas if not Hurwitz the DFE is ES and the origin is GES. For a stochastic case, randomness is introduced to the model with a generic additive noise model and an Ito's formula type model. For the former model the DFE converges exponentially in expectation and the origin is guaranteed to be asymptotically stable. In the latter the origin is exponetially 2-stable.

III. MAIN RESULTS

In the paper a series of simulations were done to analyze the theories empirically. In an initial analysis the accuracy of the mean-field approximation was done by comparing simulations of static and dynamic

cases of the n-intertwined and 2^n model. With different initial conditions the simulation showed that both n-intertwined and 2^n Markov chain model yield a close result for the static model by taking the norm of the two model's outputs with a convergence to DFE for most values. However, when the n-intertwined model reaches NDFE the 2^n model does not converge to DFE showing that for some certain time-scales the n-intertwined model could be more sufficient. For complete graphs the two perform identically.For dynamic graphs the upper-bounding nature of the n-intertwined model return a decent approximation for some time-step and constant vector in a constant drift condition, however it performs inaccurately for a piecewise constant drift condition leading to insufficient convergence.

Then the paper focuses on implementing the model to a exploratory large scale data for time-varying models which expands a model to the entire map of the United States. Locating nodes at each county and starting the simulation of the virus spread occurring from New York and Los Angeles, a decent model of the virus spread was simulated. Interestingly, the paper discusses an extension of the theory to a condition where a quarantine occurs due to an epidemic. The paper postulates that though an incorporation of a quarantine is complex it is possible to model it as a piecewise constant drift case which limits the movements of a dynamic graph. However, this still needs more investigation.

IV. YOUR IDEAS OF FURTHER IMPROVEMENTS

Personally, I found this paper very interesting in that it extends the theory of consensus and multiagent systems to epidemiology while being a highly imminent and relevant topic for nowadays. This paper was issued before the COVID-19 pandemic and because such calamity happened, it would be wise to recognize the importance of delving into this topic and constructing a more realistic and capturing model for virus dynamics so that future pandemics can be contained with more predictability and accuracy.

REFERENCES

[1] Philip E. Paré, Carolyn L. Beck, and Angelia Nedić. Epidemic processes over time-varying networks. *IEEE Transactions on Control of Networks Systems*, 5(3):1322–1334, 2018.