Editorial: Impacts of heterogeneity on biological complex systems

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Editorial on the Research Topic
Impacts of heterogeneity on biological complex systems

This Research Topic includes six papers centered around heterogeneity, an important characteristic that impacts complex biological systems. There are two papers, Sun et al. and Zhang et al., on the dynamics of human infectious diseases, and one paper Wang et al. on the dynamics of computer worm viruses. These three papers focus on the heterogeneity of epidemic populations and use ordinary differential equations to model the relations between heterogeneity and disease evolution. The work Liang et al. develops an effective connection removal strategy in the epidemic suppression based on the heterogeneous importance of connections, where a complex network is used to model individual connections. Besides infectious diseases, this Research Topic presents two papers, Li et al. and Zhang et al., on ecosystems, where reaction-diffusion equations are used and the heterogeneity lies in the spatial variation of quantities of interests. The following is a brief introduction to each of these papers.

Tracing the contacts of infected individuals is very useful to fight against epidemic because it can allow us to cut the transmission path and identify the infected individuals who can be sent to quarantine and treatment. In the work by Sun et al., one important heterogeneity lies in the infected population, which is divided into three groups. The first is those who are traced, the second is those who recover naturally, and the last is those who are aware of infection and go to hospital for treatment. The model analysis provides the threshold of contact tracing rate. When the contact tracing rate is greater than the threshold, the basic reproduction number will be less than one, then the epidemic will eventually die out. This work has other interesting heterogeneous factors such as age structure and awareness variation.

Zhang et al. studies acute respiratory illness spread by human adenovirus in a closed space. Based on the classic SEIR model, they add two new populations to enrich heterogeneity: one is without symptoms but able to produce invisible infections, and one is with symptoms but isolated or quarantined, thus not infectious. Through analysis including reproduction number and sensitivity, the authors find that the invisible

infection is the main reason to the outbreak of the disease when relevant measures are implemented in schools. In the situation without vaccines, which is the case for outbreaks in many occasion including campus, the work indicates that quarantine can mitigate the infection.

Unlike the human epidemics studied in the above-mentioned papers, the work by Wang et al. investigates the computer worm spreading in cyber community. A computer worm is a programmed code that can reproduce itself and affect the normal use of the computer. The work studies the worm spreading through USB devices, where the heterogeneity is in the four populations of computers (S, E, I, R) and three populations of USBs (S, E, I). The relations between the basic reproduction number and the equilibrium states are given. In addition, the worm propagation model is extended to incorporate three control strategies. The Pontryagin's maximum principle is used to identify the optimal control in minimizing the transmission.

The above three papers are on epidemic dynamics, while the next one focuses on disease suppression. Liang et al. use complex network to model social connectivity, where a node denotes an individual and an edge represents the connection between individuals. The common approaches in epidemic suppression include removal of the important edges and nodes. The existing methods often neglect network connectivity and thus negatively impact the economic status and functionality of the network. The authors propose a novel method based on the heterogeneity features of edge importance. The proposed method can not only protect the connectivity of networks, but also present much better epidemic suppression effects over existing methods.

Another two papers in this Research Topic study ecosystems with partial differential equation models. Li et al. investigate how to protect vegetation via its relationship with water. Vegetation, known as "Ecological Engineer", plays a leading role in the ecosystem. However, desertification has become very severe due to the abnormal global climate change in recent years. Built upon the classic Klausmeier model, the authors incorporate hydrotropism. Hydrotropism is the tendency for vegetation roots to get more water and is modeled by the proportionality of the vegetation spreading to the water diffusion rate. The authors identify the parameter ranges for the various Turing patterns. The computer simulations confirm that when the root hydrotropism increases, the pattern structure goes through the spot, mixed, strip, and gap patterns, which match observations on the Earth. This work also shows complicated relations between root hydrotropism and vegetation growth.

Zhang et al. studies the dynamics of an unstirred chemostat model. A chemostat is a laboratory device used for the culture of microorganisms. Most chemostat models assume the well-stirred culture, which is homogeneous in space. However, the real environment is always heterogeneous due to random motion of microorganisms. The authors study a system of reaction-diffusion equations with nutrient and two competing species of spatial dimension one. Under a competing mechanism, Beddington–DeAngelis response, this work implies the intraspecific competition and diffusion have a great influence on the chemostat dynamics.

The above is the limited view of the Research Topic editors on these papers with an emphasis on their heterogeneity features in modeling, while other important features may be intentionally or unintentionally ignored in this introduction. Readers are encouraged to read the papers to fully comprehend the ideas and implications.

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