



Editorial

Transmission dynamics in infectious diseases

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Some emerged or reemerged infectious diseases, such as H1N1 in 2009 [1], H7N9 in 2013 [2], Dengue fever in 2014 [3], and Plague in 2019 [4], are a serious threat to human health and social development. The pathogenesis of infectious diseases, infectious law, prevention and treatment has been becoming a major problem that needs to be solved urgently in the world [5]. Consequently, we need to investigate mechanisms of epidemic, transmission modes and development trends of the infectious diseases, and further provide effective control measures for disease spread. Among the methods in investigations of infectious diseases, mathematical models have been contributing to improve our understanding of infectious disease dynamics and helping us develop preventive measures to control infection spread qualitatively and quantitatively.

Mathematical modelling of infectious diseases mainly focuses on three aspects [6,7]. Firstly, dynamical model is established by combining the dynamics of infectious disease, biostatistics and computer simulation. Through qualitative analysis and numerical simulation of the model, the epidemic law of the disease is revealed and its development trend is predicted. Secondly, we need to obtain the optimal model based on model selection and data analysis. Lastly, in order to find the optimal strategy for its prevention and control, it is necessary to analyze the causes and key factors of the infectious diseases.

This special issue received 17 manuscripts from the scholars in these research fields. The topics of these accepted papers contain descriptions of transmission dynamics of infectious diseases based on complex networks, nonlinear dynamic analysis and control measures for infectious disease models, data-driven approaches in infectious diseases. Some researchers have revealed the dynamic behavior of infectious disease transmission with spatial effects.

It is noteworthy that it is impossible to assemble all the works in the fields of the dynamics of infectious diseases. Although more work is needed, this special issue has provided the theoretical basis

for the transmission mechanism, disease control and prevention of infectious diseases. In our opinion, two research directions need more attentions in the future: (i) how diseases propagate in both space and time, which need a large number of data including spatial locations, human communication network, and so on [8–11]; (ii) the interactions between human infectious diseases and animal diseases, which should be considered as a whole due to collective living environment [12,13].

References

1. D. Cohen, P. Carter, Questioning the timeline of H1N1 flu vaccination contracts, *Nature*, **466** (2010), 315.
2. A. Badulak, Human infections with the emerging avian influenza A H7N9 virus from wet market poultry: Clinical analysis and characterisation of viral genome, *Lancet*, **381** (2013), 1916–1925.
3. J. F. Sun, D. Wu, H. Q. Zhou, H. Zhang, D. Guan, X. He, et al., The epidemiological characteristics and genetic diversity of dengue virus during the third largest historical outbreak of dengue in Guangdong, China, in 2014, *J. Infect.*, **72** (2016), 80–90.
4. <https://news.163.com/19/1128/09/EV2DOAO60001899N.html>.
5. O. Diekmann, J. Heesterbeek, *Mathematical epidemiology of infectious diseases: Model building, analysis and interpretation*, New York: Wiley; 2000.
6. M. J. Keeling, P. Rohani, *Modeling infectious diseases in humans and animals*, Princeton: Princeton University Press; 2007.
7. F. Brauer, C. Castillo-Chavez, *Mathematical models in population biology and epidemiology*, Springer, New York; 2001.
8. G. F. de Arruda, E. Cozzo, T. P. Peixoto, F. A. Rodrigues, Y. Moreno, Disease localization in multilayer networks, *Phys. Rev. X*, **7** (2017), 011014.
9. K. Shioda, C. Schuck-Paim, R. J. Taylor, R. Lustig, L. Simonsen, J. L. Warren, et al., Challenges in estimating the impact of vaccination with sparse data, *Epidemiology*, **30** (2019), 61–68.
10. G. Q. Sun, M. Jusup, Z. Jin, Y. Wang, Z. Wang, Pattern transitions in spatial epidemics: Mechanisms and emergent properties, *Phys. Life Rev.*, **19** (2016), 43–73.
11. M. Tizzoni, P. Bajardi, A. Decuyper, K. K. Guillaume, C. M. Schneider, V. Blondel, et al., On the use of human mobility proxies for modeling epidemics, *PLoS Comput. Biol.*, **10** (2014), e1003716.
12. P. L. Kamath, J. T. Foster, K. P. Drees, G. Luikart, C. Quance, N. J. Anderson, et al., Genomics reveals historic and contemporary transmission dynamics of a bacterial disease among wildlife and livestock, *Nat. Commun.*, **7** (2016), 11448.
13. D. Tilman, M. Clark, Global diets link environmental sustainability and human health, *Nature*, **515** (2014), 518–522.



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