

Complex dynamics of some models of antimicrobial resistance on complex networks

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Abstract

Studying spread of epidemics and diseases are world wide problems especially during the current time where the whole world is suffering from COVID-19 pandemic. Antimicrobial resistance (AMR) and waning vaccination are classified as world wide problems. Both depend on the exposure time to antibiotic and vaccination. Here, a simple model for competition between drug resistant and drug sensitive bacteria is given. Conditions for local stability are investigated which agree with observation. Existence of positive solution in the AMR complex networks is proved. Dynamics of the identical AMR models are explored with different topologies of complex networks such as global, star, line and unidirectional line networks coupled through their susceptible states. Chaotic attractors are shown to be existed as the AMR models are located on all the indicted topologies of complex networks. Thus, it is found that the dynamics of the AMR model become more complicated as it is located on either integer-order or fractional-order complex networks. Furthermore, a discretized version of the fractional AMR model is presented. Complex dynamics such as existence of Neimark–Sacker, flip bifurcations, coexistence of multi attractors, homoclinic connections and multi closed invariant curves are investigated. Basin sets of attraction are also computed. Finally, the discretized system is located on complex networks with different topologies which also show rich variety of complex dynamics. Also, 0-1 test is used to verify the existence of unpredictable dynamics. So, studying the dynamics of AMR models on complex networks is very helpful to understand the mechanism of spread of diseases.

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