Abstract:

Some human pathogens consist of many types, and each may have a different transmission dynamic. Moreover, transmission dynamics of different types may be linked to one another, if types interact during infection or transmission. Mediated by these type interactions, the effects of vaccination are no more limited to the types for which the vaccine is effective, but extend to the 'non-vaccine types'. In particular, vaccination may lead to an increase of the non-vaccine types in the host population if these types compete with the vaccine types. This phenomenon is called type replacement.

We study the effects of vaccination in a transmission model with interactions between types. We present a predictor for type replacement, one that can be computed from type distribution at the equilibrium before vaccination. To demonstrate its performance, we apply it to predict type replacement in a variety of transmission models and discuss the generalizability of our results if we depart from the initial model assumptions. Overall, we demonstrate that dynamical properties such as type replacement can be predicted by incorporating relevant local interactions.