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Population-Wide Emergence of Antiviral Resistance during an Influenza Pandemic

The selective pressure induced by anti-viral drugs on their target virus may allow drug-resistant strains to survive and replicate. While these resistant strains may initially emerge with compromised fitness, mutations that compensate for this can arise to produce a resistant strain with only slightly impaired replication and transmission fitness compared to the original wild type strain. I will discuss the modeling of such resistance development in the context of pandemic influenza under several mathematical models.

High treatment levels can encourage a resistant outbreak to occur, by suppressing the spread of the wild type infection, leaving the population susceptible to the resistant strain. Thus, increasing population levels of treatment can, ironically, in some cases lead to increased prevalence of infection. Strategies for controlling the development of resistance, including treatment timing and interruption, and their implications for public health policy, especially given the likelihood of limited drug stockpiles during an influenza pandemic, will be discussed.