

Investigating the Co-Dynamics of HIV/AIDS and Influenza in regional Australia

Abstract

The transmission of infectious diseases is rarely independent, with another disease often shaping overall health outcomes in vulnerable populations. Regional and Indigenous populations in Australia experience disproportionately high rates of chronic and infectious diseases due to systematic inequities in healthcare access, lack of awareness and socioeconomic disadvantage. Understanding how multiple pathogens interact in such contexts is critical for designing culturally appropriate and geographically targeted interventions.

This project investigates the epidemiology of both HIV and Influenza in a regional Australian town. Computational epidemiology is used to simulate a disease spread within the Australian town of Bourke with about 2400 individuals. (Australian Bureau of Statistics [ABS], 2021). The project aims to quantify how HIV-induced immunosuppression modifies influenza transmission, prevalence and overall disease burden, with other factors such as demographic and public health responses in rural Australia.

A computational epidemiological model was developed using Python and NetworkX to generate a contact network reflective of Bourke's demographic — namely age structure, gender distribution and Indigenous proportion (30.3%). Each node represents an individual with demographic attributes and infection states, while sexual relationships form subject to age related and monogamy constraints. HIV and influenza transmission probabilities were parameterised using data from existing epidemiological research. Influenza is modelled as a fast-spreading, short-duration infection of greater severity among immunocompromised hosts, while HIV modelled as a more slower spreading, and longer lasting infection

The method of running the simulation consisted of generating the population with nodes, each node having their own distinct parameters. The initial seeding of the two diseases. Once these two initial steps have been done,

Results show distinct patterns between both diseases. HIV prevalence rose gradually across the simulation, reflecting slow person-to-person sexual transmission. In contrast, influenza displayed a sharp epidemic curve, peaking in a short time, before declining, reflective of recovery dynamics. Influenza incidence hit the total population, highlighting that nearly all individuals were exposed.

When HIV was introduced into the population by itself, about 4.5% of the population had acquired HIV during the 730-day period. While influenza was also mixing in the population, by the end of the 730-day period, around 9.8% of the population had acquired HIV, representing about a 118% increase in total HIV infections

The findings suggest that co-dynamics between the two diseases could significantly burden small regional towns. The model demonstrates the value of computational simulations in capturing disease interactions within realistic demographic structures. While preliminary, the results highlight the importance of tailored public health strategies in regional Australian contexts. Future work will refine the network with a more realistic approach, considering interventions such as vaccination and social distancing to reduce epidemic spread.