



Hamilton Institute

Dynamics of Some Cholera Models

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Abstract:

The World Health Organization estimates that there are 3m-5m cholera cases per year with 100,000 deaths spread over 40-50 countries. For example, there has been a recent cholera outbreak in Haiti. Cholera is a bacterial disease caused by the bacterium *Vibrio cholerae*, which can be transmitted to humans directly by person-to-person contact or indirectly via the environment (mainly through contaminated water). To better understand the dynamics of cholera, a general ordinary differential equation compartmental model is formulated that incorporates these two transmission pathways as well as multiple infection stages and pathogen states. In the model analysis, some matrix theory is used to derive a basic reproduction number, and Lyapunov functions are used to show that this number gives a sharp threshold determining whether cholera dies out or becomes endemic. In the absence of recruitment and death, a final size equation or inequality is derived, and simulations illustrate how assumptions on cholera transmission affect the final size of the epidemic. Further models that incorporate temporary immunity and hyperinfectivity using distributed delays are formulated, and numerical simulations show that oscillatory solutions may occur for parameter values taken from cholera data in the literature.

Venue: Seminar Room, Hamilton Institute, Rye Hall, NUI Maynooth

Time: 2.00pm - 3.00pm

Travel directions are available at www.hamilton.ie