Modelling the incidence and transmission dynamics of the Hepatitis A virus

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Background

Hepatitis A is an acute infectious disease caused by the hepatitis A virus (HAV). It is transmitted by the faecal-oral route either by direct contact with infected individuals, contaminated fomites, or through consumption of contaminated food or water [1]. After ingestion, uptake in the gastrointestinal tract, and subsequent replication in the liver, HAV is excreted in bile, and high concentrations are found in stool specimens [2]. The median incubation period (i.e. time from exposure to onset of symptoms) is 28 days (range 15-20 days). Peak infectivity occurs during the 2 week period that precedes the onset of jaundice and declines during the week after onset [2]. About 50% of reported patients with HAV do not have an identified source of infection [2]. Although, asymptomatic and non-jaundiced HAV-infected persons, especially children, are assumed to be important sources [2]. There is only one HAV serotype, and immunity after infection is lifelong [2]. In the US, an incremental approach to vaccination was initiated after the vaccine became available in 1995 [1].

Objective

The goal of this project is to build a simple mechanistic model that can capture the incidence and transmission dynamics of the Hepatitis A virus, as captured in [1]. In particular, we are interested in making estimates of the numbers of asymptomatic Hepatitis A cases through time and identifying their role in sustaining transmission, in the US. Furthermore, given the change in the distribution of Hepatitis A cases across different age groups brought upon by the implementation of vaccination strategies, we would like to identify what further effects control strategies may have on disease burden.

Model

Transmission dynamics were modelled using a SIR model with high risk and low risk classes. The deterministic model was implemented as a system of ordinary differential equations which were numerically integrated using the `lsoda` package in R (version 3.3.1).

Model structure.

Figure 2. SIR model structure. Arrows indicate transitions between classes while the rate at which individuals move in and out of each class appears above or next to the arrows.

Results

Most of the parameter values used here (e.g. infectious periods) were estimated from the literature. Future work should include fitting the model to the data and estimating unknown parameters. It should also incorporate seroprevalence data before and after HAV vaccination was introduced. If possible, different age-structures should be added to the model in an effort to understand the effect on age on HAV transmission.

Parameters of the model, their meaning, and values are given in Table 1. Values are in weeks.

Future Work

References:


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