In-host Model of Measles infection

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Abstract

Mathematical immunology is the study of disease dynamics within an infected host. The aim is to determine the underlying mechanisms of disease progression by focusing on the interactions between the pathogen and the immune system. Mathematical immunology is a relatively new field but interest in this area is growing rapidly, spurred by successful collaborations between biologists, clinicians and mathematicians. Despite this increase, in-host models of acute diseases such as measles remain few and underdeveloped. We have introduced an in-host model for measles infection. It focuses on the acquisition of immune system memory after natural infection and subsequent booster infections (i.e. when an individual with some immunity to the pathogen is re-infected). The model includes the fact that immunity will wane over time and can be used to determine the number of secondary infections that an infected individual with a certain level of immunity will produce, the basic reproductive ratio (R0). We demonstrate that individuals with a certain threshold of immunity may still contribute significantly to measles transmission, even if they are asymptomatic. To quantify the effect of asymptomatic transmission, we have used the immunologically scaled R0 values calculated above to parameterize a simple epidemiological (SEIR) model. In this presentation we will describe our in-host model and highlight some interesting characteristics of the SEIR model.