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*Disease transmission at home and abroad*

Most models of disease transmission make very simple assumptions about the incidence of infection. In differential equation models these are usually bilinear and assume a well-mixed population. Many models have been proposed to study heterogeneities arising from age structure, behavioural groups, stages of infection and spatial variation. More recently, network models, in various forms, have been used to model heterogeneities in the transmission setting. For example, transmission may occur in a household, a hospital, a workplace, or on a transit system. In this talk I present a simple ordinary differential equation model for disease transmission with multiple groups and multiple settings and formulate conditions for the spread of the disease through a population. The assumptions lead to a model that has no explicit spatial variable, yet still account for spatial variation through the various transmission settings.