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Title:	Agent-Based Modelling of Infectious Diseases
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Abstract:	Understanding the spread of infectious disease in a population of susceptible individuals is an active field of theoretical research involving interdisciplinary fields. The most common approach is epidemiological compartment models (commonly known as the SIR models) represented by differential equations, where the host-pathogen interaction is studied assuming the transfer of individuals between the different infection states, such as the Susceptible, Infected and Recovered classes. This is a mean-field approach and does not consider heterogeneity among individuals in a class/compartment. A microscopic approach to study spread of infection is through the Agent Based Models (ABM), where each agent is an individual at a particular infection state, and the rules of interactions describe the change in infection states. The work presented in this thesis first studies the characteristics of different types of differential equation epidemiological compartment models (SI, SIS, SIR, and SIRS) using mathematical and computational analysis of steady states and their temporal dynamics. As an application of this approach to specific diseases, the basic model of Malaria by Ronald Ross is studied. With an aim to compare and contrast the mean field models with the microscopic approach, a detailed study of the equivalent ABMs is developed and analysed. Analytic solutions and numerical results from differential equation models are compared with individual and averaged dynamics of the Agent-Based Models over 50 runs for many parameter sets and initially infected agent densities. An in-depth comparison between the two approaches of modelling shows that ABMs can lead to low probability states depending on initial conditions, even with the same parameters - a behaviour that is absent in mean field models. The role of spatial structure in the distribution of the same number of initial infected agents is shown to impact the rate of reaching the steady states along with their dynamics. The presence of oscillations, a feature completely absent in differential equation models, is observed in ABMs. Similar studies are done with the ABM realization of the Ross model as well. These results clearly show that in realistic situations, i.e., when a particular infection spreads through the host population, the dynamics and steady state behaviour of the diseased states may exhibit differences due to the inherent randomness in the agents, even in absence of other biological or social factors.
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