MULTI-SCALE MODELLING OF INHALATIONAL ANTHRAX

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If an individual becomes exposed to a pathogen, it is possible that their immune system will be capable of clearing the pathogen, without resulting in a detectable infection. However, in some cases the infection cannot be contained, and an infection will become established. Hence, an important factor in the spread of an emerging pathogen is the likelihood that infection becomes established, given a certain initial dose of the pathogen. In this talk, I will present a multi-scale stochastic modelling approach, applied to inhalational anthrax, which is caused by the bacterium Bacillus anthracis. This approach involves constructing models for the intracellular, within-host, and population-level infection dynamics, to define key quantities characterising infection at each level, which can be used to link dynamics across scales. At the intracellular scale, we consider a Markov chain model for the intracellular infection dynamics of B. anthracis in a single phagocyte, incorporating spore germination and maturation, bacterial proliferation and death, and the possible release of bacteria due to cell rupture. This model is parameterised with in vitro experimental data and used to predict the distribution of outcomes from this host-pathogen interaction. For example, it is used to estimate the number of bacteria released upon rupture of an infected phagocyte. This key quantity is then incorporated into a within-host model of infection, which aims to provide an overall understanding of the early progression of the infection. This type of mechanistic mathematical model can help to quantify key host-pathogen interactions during infection, improve our understanding of the underlying mechanisms of the infection, and allow us to predict individual infection risk following exposure.