Imperial College London

CISBIC

Centre for Integrative Systems Biology at Imperial College

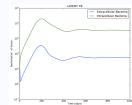
Objectives

- To model the progression of Mtb infection in the host and identify mechanisms that lead to differences in infection outcome.
- To develop a model to predict the outcome of anti-TB chemotherapy and determine factors that may improve the success of treatment.
- To investigate the role of bacterial persistence in determining infection outcome and treatment strategies.
- To predict the outcome of a secondary infection.

Results

- Model is able to simulate different disease trajectories: primary TB, latent TB, reactivation and clearance.
- Uncertainty and sensitivity analyses performed to identify critical model parameters that affect the outcome of infection.





Drug Treatment

- Extended model to include effect of drug treatment.
- Model can be used to investigate different treatment strategies (e.g. different dosing regimens).

Introduction

- Tuberculosis (TB) is a major cause of illness and death worldwide.
- The World Health Organization estimates that one third of the world's population is infected with *Mycobacterium tuberculosis* (Mtb).

Muna El-Khairi, Brian Robertson and Vahid Shahrezaei

- In 2008 there were approximately 9.4 million incident cases of TB and an estimated 1.8 million people died from the disease.
- 5-10% of infected individuals progress to primary disease within 1-5 years, with the remainder experiencing latent infection.

Latent Tuberculosis

- Include population of non-replicating or slowgrowing bacteria in the model.
- Investigate the impact of drug tolerant persister cells on the treatment of latent TB.
- Investigate the use of different dosing regimens (e.g. a pulsedosing regimen) to treat infection.

Future Work

- To extend the model to include immunological memory.
- To extend the model to incorporate drug treatment followed by rechallenge.

Mathematical Modelling

- Developed ODE model of TB infection in the lung and peripheral draining lymph node based on published models.
- Model describes temporal dynamics of major elements of the host immune response and the pathogen M. tuberculosis.

