– Master or Diploma Thesis –
Spatiotemporal modelling of viral infection spread in the human respiratory tract

Joint project between AstraZeneca Gothenburg (Sweden) and the Chair of Scientific Computing for Systems Biology, Faculty of Computer Science, Centre for Systems Biology Dresden, TU Dresden.

Motivation

Respiratory viral infections are a major cause of Chronic Obstructive Pulmonary Disease (COPD) and asthma exacerbations. Exacerbations have a significant impact on morbidity in both diseases and, in their most severe form, can lead to death. Therefore, developing drugs with antiviral properties can potentially decrease morbidity and improve patients’ quality of life. The mechanism by which viruses trigger exacerbations is poorly understood. A deeper understanding of the temporal and spatial sequence of events from initial infection to exacerbation is essential for the identification and clinical testing of new therapeutic targets for prevention of viral exacerbations.

Infection of respiratory viruses such as Human Rhinoviruses (HRV) starts from the nose, where viruses find the optimal temperature to replicate. Experimental data suggest that the infection can spread from the upper to the lower part of the respiratory tract (from the nose to the lung). The body responds to the viral infection and employs the host defense mechanism to recruit immune cells to the site of infection. In patients with a dysregulated immune system, immune cells and their secreted signaling molecules (so-called cytokines) may accumulate in the lung and cause deleterious effects such as poor lung function and shortness of breath.

Objectives

Part 1

We would like to develop a theoretical model to simulate the progression of viral infection in time and space based on physiological parameters such as the surface area of the nasal epithelium, the length of trachea and immune system parameters. In this part, the immune system can be modelled as simply as possible to minimize the number of parameters.

Part 2

The next step is to include the kinetics of different immune cells such as cytotoxic T-cells, natural killer cells and their secreted cytokines. The aim is to simulate how quickly immune cells migrate to the site of infection and how the host defense mechanism prevents the infection spread. Such a platform would allow us to demonstrate the impacts of different types of deficiency in the host defense mechanism, as potential models of altered host response in disease.

Qualifications

We are looking for a motivated master or Diploma student with background in mathematics, physics, engineering or computer science, good programming skills, interest in medical applications, especially in immunology, and experience or knowledge of spatiotemporal simulation algorithms. The successful candidate will have a chance to interact with experts in mathematical modelling, pharmacokinetics and immunology from the Centre for Systems Biology Dresden and AstraZeneca. The project will be primarily in Dresden, Germany and it includes travels to Gothenburg, Sweden, for meetings.
Who we are

AstraZeneca is a global, innovation-driven biopharmaceutical business that focuses on the discovery, development and commercialization of prescription medicines for some of the world’s most serious diseases. But we’re more than one of the world’s leading pharmaceutical companies. At AstraZeneca, we’re proud to have a unique workplace culture that inspires innovation and collaboration. Here, employees are empowered to express diverse perspectives - and are made to feel valued, energized and rewarded for their ideas and creativity.

Contact info

For more information about the student research project in cooperation with AstraZeneca, please read on link below:

http://mosaic.mpi-cbg.de/?q=education/sada

If you are interested please send your CV and personal letter to Prof. Ivo Sbalzarini ivos@mpi-cbg.de or Hoda Sharifian hoda.sharifian@astrazeneca.com

References


They applied reaction-diffusion equations with a delay to show different regimes of infection spreading.


An agent based spatial model focusing on T cell migration from lymph nodes through the vascular system to sites of infection.


Clinical data including viral load in nasal lavage and sputum as well as inflammatory cells and cytokines in sputum following an experimental rhinovirus infection.