

## **MS/BS Thesis Project in Bioinformatics, Mathematics, Computational Biology, Computer Science, Physics**

### **Mathematical and computational modeling of host-pathogen interaction in the lung lesion development due to *Mycobacterium tuberculosis* in humans**

Tuberculosis (TB) has a long history as a major disease in humans and animals. In 2016 1.7 million people died from the disease mostly in the developing countries. New resistant strains are jeopardizing the advanced in the battle against TB. 40% of HIV deaths occurs due to concurrent TB illness. A causative agent of TB – *Mycobacterium tuberculosis* causes severe implications for a patient. The tuberculosis development is usually accompanied by the lung tissue destruction associated with manipulation of host immune response by pathogen. This leads to the overexpression of specific metabolites – proteinases. It is assumed that different proteinases are associated with the processes of cavitation and fibrosis in the tuberculosis. Thus, it was shown that an increase in the concentration of metalloproteinase-1 (MMP-1) is observed in the presence of a cavity of destruction while an increase in the concentrations of MMP-9 and MMP-8 are proportional to the extension of volume destruction and associated with the activity and severity of the process. At the same time, pathogen (*Mycobacterium tuberculosis*) can stimulate an inflammatory process leading to an even greater imbalance MMP/TIMP, that results in the strengthening of tissue destruction. Such positive feedback also could be conditioned by the initially damaged immune status of the host.

The goal of the project is to create a model based on the study of immune signaling and biochemical metabolic pathways by *Mycobacterium tuberculosis* that reveal key factors contributing to the beginning of reparative changes or the transition of the disease to a chronic form. Such modelling, including clinical observations will allow to identify key factors which stimulate the restoration of the structure and functions of tissues. It also facilitates the analysis of the dynamics of cellular populations for the diagnosis of functional and pathological conditions of the host.

The topic could serve as a **BS/MS thesis project in Bioinformatics, Mathematics, Computer Science, Physics or similar and can be written in English or German.** Profound knowledge of stochastic modeling of nonlinear dynamical systems and programming experience (Python, or C/C++, Matlab, R, Mathematica, etc.) is required or, alternatively, a strong motivation to quickly acquire the expertise should be present.

The project will be jointly supervised by Prof. V. Belik (Institut für Veterinär-Epidemiologie und Biometrie, Arbeitsgruppe Systemmodellierung, FU Berlin) und Dr. A. Lavrova (Saint-Petersburg) in collaboration with Prof. T. Ulrichs (Akkon University for Human Sciences, Berlin).

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