DESCRIPTION FOR THE GENERAL PUBLIC

Cancer is one of the major causes of death in the world, particularly in the developed countries. Data from the World Health Organisation showed that around 9 million people died from cancer in 2015 and if current trends continue, the prediction is that in 2030 11.5 million people will die. There are few individuals who have not been touched either directly or indirectly by cancer. Undoubtedly, cancer treatment methods are continually improving but a real breakthrough requires a comprehensive approach that can offer even greater insight into the complexity of the disease and its treatment. Therefore, scientists and clinicians are increasingly recognising the need to integrate data across a range of spatial and temporal scales (from genes to tissues) in order to fully understand the disease.

There are many differences between both normal and cancer cells and between healthy and cancerous tissue. Some of these key differences concern properties of individual cells and how quickly they divide, migrate or even evade the normal process of cell death. Other properties are concerned with how a solid tumour spreads to secondary parts of the body through the processes called invasion and metastasis. At some point in the development of a solid tumour, cancer cells from the primary cancerous mass of cells migrate and invade the local tissue surrounding the tumour. This initial invasion of the local tissue is the first stage in the complex process of secondary spread where the cancer cells travel to other locations in the individual and set up new tumours called metastases. These secondary tumours are responsible for around 90% of all (human) deaths from cancer. Knowing precisely how cancer cells invade the local tissue would enable better treatment protocols to be developed and consequently better individualised patient care. Cancer invasion and spread is, by its nature, a complicated phenomenon involving many inter-related processes across a wide range of spatial and temporal scales. Therefore, the theoretical support from mathematical modelling, analysis, computational simulation and systems biology in understanding these processes is extremely necessary. The last decades have witnessed enormous advances in our understanding of the molecular basis of cell structure and function. Scientists have made impressive advances in elucidating the mechanisms mediating cell-signalling and its consequences for the control of gene expression, cell proliferation and cell motility. With the rapid development of experimental methods, huge amounts of genetic, proteomic, biochemical and visual data become available. At the same time, the development of mathematical and computational models of various aspects of cancer growth has significantly contributed to the "theoretical side" - mathematical and computational models constructed in collaboration with biologists and clinicians have repeatedly enabled the verification of existing and formulation of new research hypotheses, and also facilitated the design of new experiments.

This project is devoted to the development of novel mathematical and computational methods for data assimilation in cancer modelling in particular in tumour invasion models. Therefore the goal is to address the main difficulty associated with the use of mathematical models in clinical practice, that is the lack of proper model calibration. Within the project, we would like to develop a methodology for estimating the parameters of the cancer invasion model based on real data, primarily image data. In this way, by combining clinical data with state-of-the-art mathematical modelling, analysis and computational simulation, we will be able to develop a quantitative, predictive simulation platform which will enable oncologists to make improved, more objective clinical decisions, thereby improving individual-patient treatment for cancer sufferers and ultimately improving cancer survival rates.