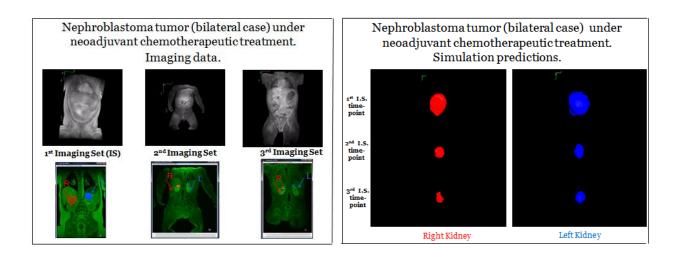


## HIGH PERFORMANCE COMPUTER SYSTEMS IN IN SILICO MEDICINE



In Silico Medicine (<u>https://en.wikipedia.org/wiki/In silico medicine</u>) is a fast evolving scientific and technological domain with already proven great clinical and industrial potential. It aims at the personalized solution of real clinical problems or the personalized optimization of existing solutions through the use of complex mechanistic multiscale models and simulations, artificial intelligence techniques and quite frequently a combination of both.

Due to the particularly high complexity of the problems addressed, the stochasticity of biological systems, the high expectations concerning the calculation reliability in the clinical setting and the very limited computing time acceptable during actual clinical procedures, the exploitation of high performance computer systems (HPC) quite frequently becomes a *sine qua non* requirement. The necessity for the parallel execution of a model with numerous alternative sets of parameter values illustrates this critical need.

In the framework of the present diploma thesis, a mechanistic multiscale computer model of the response of paediatric nephroblastoma tumor (Wilms tumor) to a widely applicable chemotherapeutic scheme will be specially processed so as to automate its parallel execution on several HPC platforms. Each execution thread will represent a different hypothetical instance (avatar) of the patient's tumor and will correspond to a different parameter value set of the model. This has to be done since the cancer patient's data available in clinical practice cannot normally lead to an absolutely precise selection of the model parameter values. Generally speaking, medical data lead rather to estimates of value intervals for each model parameter. Thus, instead of considering a single set of parameter values for a given patient (i.e. one avatar), a rather

large number of possible parameter value sets per patient (i.e. many avatars per patient) are considered and the clinical question addressed is answered in a probabilistic way, following the statistical analysis of execution results for all avatars.

Following completion of the parallel execution of the model code (e.g. for 100 avatars), statistical processing is to take place. Subsequently, the effect of varying the parameter values on the model output (e.g. the volume and the tumor cellular constitution) will be visualized and a probabilistic answer to the problem will be provided.

The effect of varying several model parameters (each one separately and certain of them concurrently) on the outcome will be studied. An algorithm for the optimal construction of avatars, given their total number for a given patient, based on the patient's laboratory, imaging and clinical data will be proposed.

It is worth noting that the In Silico Oncology and In Silico Medicine Group, ICCS, SECE, NTUA (<u>https://www.in-silico-oncology.iccs.ntua.gr/</u>) has a longstanding (more than 15 years) exceptionally fruitful collaboration with the Paediatric Oncology and Haematology Clinic, University of Saarland, Germany, and in particular with its Director Professor Norbert Graf. Prof. Graf is also the global Chairman of the clinical trials branch for renal tumors of the International Society for Paediatric Oncology (SIOP: Societé Internationale d'Oncologie Pédiatrique)

(http://www.uks.eu/de/einrichtungen/kliniken\_institute/kinder-undjugendmedizin/klinik-fuer-paediatrische-onkologie-und-haematologie)

## **PREREQUISITES**

- 1. A very good mathematical and computational background, including probability theory and statistics
- 2. Passion for intensive reading of pertinent biological and medical literature
- 3. Good knowledge of programming languages C++ and Matlab.

Attendance of the postgraduate course No 705 of SECE, NTUA entitled "Cancer Multiscale Modeling and In Silico Medicine"

(<u>https://www.ece.ntua.gr/en/doctoral/courses/705</u>), in parallel with the diploma thesis preparation, is highly recommended.

## ACADEMIC ADVISORS

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