

As show recent reports on the global cancer burden (e.g. [American Cancer Society 2012]) over 14 million new cancer cases were diagnosed and above 8 million people died in 2012 worldwide. More than a half of those occurred in economically developing countries. The expectations are even more alarming by predicting 21.7 million new cancer cases to be diagnosed and 13 million deaths in 2030. Even though a tremendous effort, in terms of intellectual and financial resources, was spent on understanding cancerogenesis and developing an effective anticancer therapies, in general, the neoplasm remains resistant to all currently used drugs, and the anticancer therapies must be planned on a case by case basis. Therefore, personalization of tumor dynamics monitoring becomes so crucial in modern oncology.

Great hopes are pinned on mathematical and computer modeling of cancer, which is one of the greatest challenges in computational biology and the principal goal of computational oncology. There are numerous overview papers and books about modeling of tumor dynamics, which contain the knowledge and experience collected during almost 40 years of history of cancer simulation that planning cancer treatment in oncology of the future will be based on mathematical tumor models. However, though the progress in deeper conceptual understanding of interactions between multiple multiscale processes taking part in the cancerogenesis cannot be underestimated, the habitual application of cancer progression monitoring in clinical medicine by employing computer simulations is still in an infant stage.

Countless of interrelated microscopic and macroscopic factors underlying tumor development from the moment of its birth to its irresistible proliferation throughout the whole organism, highly complicated growth medium, very individual properties of invaded organism and its surrounding environment, and sensibility on current physical conditions, make the whole system computationally irreducible and unpredictable. In this situation, the problem of adaptation of hundreds of parameters of a mathematical model of a tumor to real data, simultaneously taking into account their high spatiotemporal variability, sounds surrealistic. Consequently, making longer and reliable prognosis about tumor dynamics just on the basis of mathematical models and assumed initial conditions (even well defined) is a nonsense like that of weather forecast by using only existing numerical climate models and starting from a given set of measurements of temperature, pressure, humidity and wind fields.

Meanwhile, the importance of mathematical modeling in weather and climate dynamics – the process of similar complexity and non-linear behavior as tumor dynamics – cannot be overestimated. This is despite the fact that many fine-grained phenomena influencing weather and climate are not included in these models. The key factor, which makes mathematical modeling and computer simulation useful for climate science, is a prediction/correction scheme where numerical simulations are continually verified by incoming data and are reinforced by data models. The climate/weather models imperfections, caused by the improper adjustment of parameters and/or the lack of some components of unknown fine-grained phenomena (as well as modeling and numerical errors) are “corrected” by the procedure of matching the model to the real data. Such the “corrections” can be valid on a longer time scale giving acceptable predictions. This suggests that all fine-grained features and other unpredictable events accompanying climate dynamics and not included in the model are hidden in data. Whereas, the formal mathematical framework plays the role of an additional knowledge, which defines more precisely the feature space topology for machine learning tools.

We believe that just a similar scheme, which couples data and mathematical models, will become the principal modeling approach for predicting cancer dynamics. This is the main scientific topic of our research proposal.