

Mathematical modeling and prediction of metastasis

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In the majority of cancers, secondary tumors (metastases) and associated complications are the main cause of death. In order to design the therapy for a given patient, one of the main challenge is to estimate, at diagnosis, the burden of invisible metastases and the future time of emergence of these, as well as their growth speed. In this talk, I will present the current state of research efforts towards the establishment of a predictive computational tool for this aim. I will first shortly present the model used, which is based on a physiologically-structured partial differential equation for the time dynamics of the population of metastases, combined to a nonlinear mixed-effects model for statistical representation of the parameters' distribution in the population. Then, I will show results about the descriptive power of the model on data from clinically relevant ortho-surgical animal models of metastasis (breast and kidney tumors). The main part of my talk will further be devoted to the translation of this modeling approach toward the clinical reality. Using clinical imaging data of brain metastasis from non-small cell lung cancer, several biological processes will be investigated to establish a minimal and biologically realistic model able to describe the data. Integration of this model into a biostatistical approach for individualized prediction of the model's parameters from data only available at diagnosis will also be discussed. Together, these results represent a step forward towards the integration of mathematical modeling as a predictive tool for personalized medicine in oncology.