

Data-driven mechanistic modeling of metastasis: cancer at the organism scale

In the majority of solid cancers, secondary tumors (metastases) and associated complications are the main cause of death. Determining the burden of invisible metastases at diagnosis and predicting how they would respond to treatments would allow personalization of adjuvant interventions. I will present research efforts towards the establishment of a predictive computational tool of metastatic development, with a particular emphasis on the assessment of mathematical models to empirical data. The general framework is based on a physiologically-structured partial differential equation for the time dynamics of a population of metastases. Results will be presented about different models – based on different biological hypotheses about dissemination and growth – confronted to clinical imaging data of brain metastasis from non-small cell lung cancer. Integration of the model into a biostatistical approach for individualized predictions of the model's parameters from data only available at diagnosis will also be discussed. Together, these results represent a step towards the integration of mathematical modeling as a predictive tool for personalized medicine in oncology.