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**Quantitative modeling of metastasis: cancer at the organism scale**

In the majority of solid cancers, secondary tumors (metastases) are the main cause of death. Determining the burden of invisible metastases at diagnosis is a crucial challenge in the clinic, as it would allow personalization of therapeutic intervention, e.g. in the perioperative setting.

I will present research efforts towards the establishment of such a predictive computational tools of metastatic development, with emphasis on the quantitative calibration of models to empirical data (experimental and clinical). 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 in two clinical settings: brain metastasis from non-small cell lung cancer and early-stage breast cancer. In the first application, comparison of models relying on different biological hypotheses about dissemination and growth indicates periods of dormancy of the order of several months. In the second application, a combination of machine learning techniques and advanced statistical learning methods allows individualized predictions of the model parameters from data available at diagnosis. In turn, this allows patient-specific prediction of the time to metastatic relapse.

Together, these results represent a step towards the integration of mathematical modeling as a predictive tool for personalized oncology.