A framework for modeling immunotherapy and analysis of survival

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This work is concerned with modeling of tumor growth and metastasis, and the response of individual patients to anticancer treatment that involves three modalities: chemo-, radio- and immunotherapy. Treatment effects are taken into account using the models developed in [2, 1] that are expanded by adding a separate compartment representing a sum of all metastatic tumors. Although such incorporation of metastasis in the model may seem an oversimplification, it has been proved to yield reliable computational results in terms of both overall survival, and metastasis free survival in a population of lung cancer patients [3].

Individual patients' responses to treatment are achieved by randomizing model parameters. Distributions of these parameters are chosen in an optimisation procedure that aims at minimizing the sum of squared differences between the predicted and actual time of death (in the first approach) and time of metastasis detection (in the second approach).

To make such modeling feasible, a two-component structure has been devised, consisting of a dynamical model whose input is given by its parameters, and a black-box artificial-intelligence model, with clinical data at the input and model parameters at the output. Model predictions, concerning metastasis-free survival and overall survival will be subsequently checked against a set of clinical data of lung cancer patients treated with combined chemo- and immunotherapy. That comparison will be based on a classification results, in which virtual and actual patients are divived into several classes, depending on survival time, following the line of reasoning applied in [4].

Applicability of the presented approach will be discussed, from the perspective of clinical data available.

References

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