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Technology transfer from climate modeling: Supermodels for simulation of cancer

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Climate models stand at the forefront of computational science, in regard to the number of degrees of freedom and the range of physical scales that must be simulated. It is therefore not surprising that computational methodology needed for very general use would first be developed in climate science. The modeling of the development of cancer tissue – driven by social considerations of importance comparable to those driving climate modeling - faces two important problems in common with climate modeling: 1) a large range of physical scales, the smallest of which are best treated parametrically; and 2) a diversity of imperfect models intended to simulate the same process. As a result, there is a striking parallel between recently proposed methods and those used in meteorology and climate science.

In cancer simulations, countless mutually coupled tumor growth/recession factors underlie the dynamics, particularly during anti-cancer therapy, making the whole system overfitted, ill-conditioned and intractable computationally. Moreover, keeping in mind that the formal models have to be adapted to real data acquired in a fluctuating environment, developing reliable prognoses of tumor evolution is currently unrealistic. Here, we propose to employ a prediction/correction scheme (similar to data assimilation in weather forecast systems) in which the tumor model will be corrected continually taking into account the discrepancies between predicted and measured descriptors of tumor progression. We also advocate using an ensemble of simple formal models (i.e. models representing only the principal factors influencing tumor dynamics) instead of one complex and computationally demanding multi-scale model of cancer.

In this context, we consider two approaches. In the first approach, we define a set of simplified tumor models of various complexity on the base of mixture-theory representations of tissue behavior. In the prediction/correction scheme the best model from this set is selected and calibrated continually to current data. If its prognoses are inconsistent with new data, either the parameters are corrected or a new model is selected. The second approach consists in coupling of a few imperfect models of a tumor to create a “supermodel". We use only a few inter-model coupling strengths, that are continually learned from current data and corrected by incoming data. Consequently, the "latent factors", i.e. microscopic processes and other unpredictable events accompanying tumor dynamics not included in the formal model, are hidden in the couplings between sub-models. We postulate also that there exists a generic coarse-grained computer model of cancer, which can be used as a computational framework for developing high quality "supermodels". The two ideas are illustrated by computer simulations of the evolution of glioma and melanoma. Further synergy with the development of the supermodel approach to climate is discussed.