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Sano Computational Medicine Seminars

Monday, 19 October 2020, 14:00-15:30 (CEST)

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Supermodeling in tumor dynamics prediction

Abstract

We present a novel and faster data-assimilation (DA) scheme that can overcome the curse of dimensionality and overparameterization of biological models such as complex 3D cancer ones. We defined the supermodeling of a tumor as a kind of ensembling scheme that consists of a few sub-models representing various instances of a baseline cancer model (see the figure). The sub-model parameters are fixed and selected with respect to the expert knowledge or pre-trained by using standard DA algorithms. The sub-models are synchronized by a single, the most sensitive, dynamical variable of the baseline tumor model. Assuming that the supermodel consists of only a few coupled sub-models, the number of parameters in the baseline model greatly outnumbers the quantity of the coupling factors in the supermodel. This makes the supermodel the next level of abstraction of the complex cancer model with a small number of latent parameters (the coupling factors of the sub-models) that can be matched to real observations in a relatively short time with a classical DA procedure. We demonstrate that the supermodeling of cancer is an interesting modeling paradigm that can be applied in both predictive oncology and as a generic data-assimilation meta-procedure.

References:

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