

A Next Generation Multi-Scale Modeling Theatre for in silico Oncology

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Abstract : Cancer is a manifestation of multifactorial deregulations in biomolecular pathways. These deregulations arise from the complex multi-scale interplay between cellular and extracellular factors. Such multifactorial aberrations at gene, protein, and extracellular scales need to be investigated systematically towards decoding the underlying mechanisms and orchestrating therapeutic interventions for patient treatment. In this work, we propose 'TISON', a next-generation web-based multiscale modeling platform for clinical systems oncology. TISON's unique modeling abstraction allows a seamless coupling of information from biomolecular networks, cell decision circuits, extra-cellular environments, and tissue geometries. The platform can undertake multiscale sensitivity analysis towards in silico biomarker identification and drug evaluation on cellular phenotypes in user-defined tissue geometries. Furthermore, integration of cancer expression databases such as The Cancer Genome Atlas (TCGA) and Human Proteome Atlas (HPA) facilitates in the development of personalized therapeutics. TISON is the next-evolution of multiscale cancer modeling and simulation platforms and provides a 'zero-code' model development, simulation, and analysis environment for application in clinical settings.

Keywords : systems oncology, cancer systems biology, cancer therapeutics, personalized therapeutics, cancer modelling

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