

Integration of a Cancer Research KnowledgeBase with a Cross-Hierarchy Modeling Platform

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ABSTRACT

There is a sense of promise that accelerating growth of knowledge about the molecular basis for the behavior of cancer cells, especially about the “cancer genome”, will lead, if not to the “magic bullet”, at least to much better treatments for patients. But there is a tension between pure empiricism pinning hopes on the sheer quantity of data and the use of biological reasoning to draw insights and improve predictions. Our premise is that at least some of the latter approach is essential, and a general cancer modeling system could be key to pulling the information together in a truly useful way. A comprehensive software-based facility to synthesize information, build models, simulate, and validate is in development. We have

built a comprehensive modeling system for the cancer process, integrating the constituent multiple interacting processes at different scales, including the cancer cell, the patient, the oncologist, and the clinical trial. This is called the Oncology Thinking Cap (OncoTCap). This paper describes how the program achieves its generality, how it currently integrates with a knowledge base that serves as a model authoring tool, and how the knowledge base design will extend naturally to include an information-gathering tool. The gathering and structuring of research information lead to its formulation into model-building statements and model-validation goodness-of-fit criteria. With all the pieces in hand, a multitude of ambitious applications could be realizable.