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Editorial

BioSPICE: A Computational Infrastructure for Integrative Biology

As we enter the postgenomic era in biology, it is widely recognized that an accurate decoding of the genetic sequence is but a first step to characterize, predict, and develop control strategies for the behavior of living cells. To reach the ultimate aim of understanding cellular behavior, we must now tackle an even greater challenge: understanding the execution of this underlying genetic code and characterizing the dynamics of cellular events in a rigorous manner. How is gene expression and protein production regulated and controlled in space and time? How do spatio-temporal extracellular signals modulate these regulatory networks? How do cells adapt to changing environments? To date, answering such questions for many systems has awaited a means to deal with the pathway complexity that is ubiquitous within living cells. The vast majority of biochemical networks that operate within living cells are comprised of nested positive and negative feedback interactions that, even in relatively simplified mathematical representations, vastly surpass the reasoning capabilities of the unaided human.

The Biological Simulation Program for Intra-Cellular Evaluation (BioSPICE) is an open source development movement that is creating computational models, tools, and infrastructure to help deal with this complexity. Begun in 2002, BioSPICE is a major portion of the Defense Advanced Research Projects Agency's (DARPA's) BioComputation Program. The goal of the overall BioComputation Program is to explore, develop, and exploit both the role computation plays in biology and the role biology plays in computation.

The BioSPICE development community is comprised of researchers from various disciplines that include computer science, cellular biology, mathematics, molecular biology, artificial intelligence, neuroscience, and control theory. This interdisciplinary community is working to develop a framework that will allow front-line biologists to readily apply mathematical, engineering, and computer science techniques to characterize, predict, and control cell dynamics. This framework includes software tools for creating new computational models or refinements to existing ones, analyzing experimental data, and accessing public databases. It also includes a growing model library consisting of a set of highly validated computational models that can serve as a starting point for future efforts, as elements from this library are composed in new ways or adapted to investigate other biological systems. Importantly, each computational model in the library is being validated experimentally. This creates a process whereby our understanding of a biological system is refined in an iterative fashion, with model predictions driving experiments and experiments identifying areas in which a given model needs to be enhanced.

This issue begins with articles by Hyduke et al., Vadigepalli et al., Mishra et al., and Ortoleva et al., describing software modules, model construction, and data analysis. Following this, Allen et al., Segrè et al., and Cox et al. present the application of various BioSPICE tools to elucidate the mechanisms underlying cell function in a range of model organisms. We hope this special issue of *OMICS* conveys the sense of excitement that manifests itself throughout the BioSPICE community and entices the readership to join this growing movement. To do so, or to utilize the BioSPICE tools, please visit *www.biospice.org*.

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