

Mechanistic modeling: the pathway to precision medicine

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There is a growing and critical need for integrating molecular systems science with computation to model complex disease processes for accelerating drug discovery, drug repurposing, validation of complementary and alternative medicine (CAM) therapies, and identification of efficacious multi-combination therapeutics, while ensuring a personalized and precise medicine. Such needs cannot be advanced without collaborative integration of knowledge across biological disciplines. This talk will share the recent successes, through multiple case studies, in the use of CytoSolve, a computational systems biology collaboratory, developed at MIT, that provides an integrative approach to address these critical needs. Previous approaches, largely based on statistical techniques, have been unscalable and largely useless to scientists who seek to understand complex biological mechanisms. CytoSolve's successes have been published in peer-reviewed journals and have

received recognition in Nature for its potential to develop multi-combination therapies. These successes including: FDA allowance for a multi-combination pancreatic cancer therapeutic; the Department of Defense (DoD) and the United States Pharmacopeia (USP) understanding of toxicity and adverse reaction multi-combination nutritional supplements; and, modeling of rare diseases in orphan drug domains such as Neuromyelitis Optica (NMO) and Hereditary Angioedema (HAE) have inspired major nutraceutical researchers, cancer centers such as MD Anderson, National Cancer Institute and others to explore the use of CytoSolve for integrating CytoSolve's collaboratory with modern in vitro and in vivo methods to accelerate the development of multicomination therapeutics. This talk that will provide an introduction to a disruptive platform that will likely revolutionize development of therapeutics in the 21st century.

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