

Quantitative systems pharmacology model-based drug target discovery for influenza

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Biological processes across organisms are governed by complex, nonlinear network systems that span multiple layers of biological organization, from molecular to cellular to organ and organismal levels. Mathematical and computational modeling has become integral to better understanding the systems' mechanism and dynamics under healthy as well as diseased conditions. In this presentation, discussed will be our efforts in the development and use of a large-scale computational (logical) model of influenza infection of human airway epithelial cells. This host-pathogen model captures the viral replication cycle within the context of the host's comprehensive signal transduction network. Systemic perturbation analyses of the model revealed novel host drug targets that treatments capable of significant reduction of produced viral particles, suggesting potential for new antiviral treatments. Furthermore, discussed will be our technology-driven efforts to address the challenges associated with constructing comprehensive, accurate, and re-usable mathematical models. Specifically, we have developed software, Cell Collective, to enable collaborative construction of large-scale models, while also making modeling accessible to anyone with or without computational background.