Systems Biomedicine and the Multi-Node Drug Target

Joseph Lehár, CombinatoRx Incorporated, Cambridge MA USA.

Systematic testing of chemical combinations in cell-based disease models can yield novel information on *how* proteins interact in a biological system, and thus can make important contributions to biological models of those diseases. Such combination screens can also preferentially discover synergies with beneficial therapeutic selectivity, especially when used in high-order mixtures of more than two agents. We will discuss numerical simulations and experimental results which establish the efficacy and selectivity of synergistic combinations in complex biological systems. These studies demonstrate the value obtainable from combination chemical genetics, and reinforce the growing realization that the most useful paradigm for a drug target is no longer a single molecule in a relevant pathway, but instead the set of targets that can cooperate to produce a therapeutic response with reduced side effects.

Joseph Lehár's biography

Sr. Director, Computational Biology, CombinatoRx.
Adjunct Asst. Prof. Bioinformatics, Boston University

Dr. Lehár has played a central role in developing CombinatoRx's technology and analysis platforms, in addition to many research projects at CombinatoRx over the past five years. Through his faculty position at Boston University, Dr. Lehár is researching the systems biology of drug combinations, with a focus on microbial systems. Prior to CombinatoRx, Dr. Lehár was a postdoctoral scientist at Whitehead Institute's CGR (now the Broad Institute), at the Harvard College Observatory, and at Cambridge University's Institute of Astronomy. Dr. Lehár has a Ph.D. in physics from MIT, and authored over 50 reviewed papers in astrophysics and biology.