



## NETWORK ANALYSIS OF MICROBIAL PATHOGENS

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*Antimicrobial targets, systems biology, pathogenicity*

“Network-driven prediction of antimicrobial targets”

Abstract: The genomics revolution has led to the generation of an enormous amount of data on the composition, regulation, and physiology of cellular networks. There is a need to integrate this information into a computational framework so that testable predictions can be made with an accounting of the complexity inherent in cellular systems. Recent advances on the integration of transcriptional regulatory network data with metabolic network reconstructions will be presented. The resultant genome-scale models have been used to make experimentally testable predictions. Novel methods to identify ideal drug targets and mechanisms of pathogenicity will also be discussed, with results presented from two important human pathogens, *Leishmania major* and *Pseudomonas aeruginosa*. These systems biology approaches hold the promise of revolutionizing drug discovery efforts to tackle challenges in many human diseases as well as address fundamental questions in biology.