Computational Systems Biology Laboratory

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"Creating computational models of biological systems to tackle dangerous pathogens and human diseases."

UNDERSTANDING BIOCHEMICAL NETWORKS WILL LEAD TO REVOLUTIONARY ADVANCES IN MEDICINE AND BIOTECHNOLOGY.

There is a pressing need for reconstructing and analyzing the biochemical networks that orchestrate cellular processes. Understanding how these biochemical networks function (and malfunction) will lead to revolutionary advances in medicine, biotechnology, and the understanding of fundamental biological processes.

The Computational Systems Biology Laboratory (CSBL) uses computational and experimental approaches to characterize biological systems relevant to human disease. In particular, we reconstruct integrated cellular networks and develop tools to analyze their properties. The analysis of these networks requires sophisticated computing capabilities and advanced experimental and mathematical techniques.

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Systems Analysis of Microbial Pathogens

Infectious disease is the leading cause of death worldwide. While genomics has had a tremendous impact on understanding microbial pathogens, there remains a significant need to use this genomic information to discover novel therapeutic strategies and new understanding of pathogenesis. We are analyzing several clinically important pathogens and using systems biology approaches to identify and validate drug targets and characterize mechanisms of pathogenicity.

Human Metabolic Networks in Disease

Many poorly understood mechanisms of human disease are being elucidated with high-throughput technologies. Systems-level approaches have the potential to integrate this information to make novel predictions regarding disease mechanism, suggest new drug targets, identify molecular markers predictive of prognosis, and catalyze the development of personalized medicine. Deregulated metabolism and regulation are central features of many human diseases. As such, we have ongoing projects on the development and application of network analysis of human metabolism.

Advancing Systems Biology Methods

The integration of high-throughput data into computational frameworks will enable us to interrogate network properties systematically, characterize the underpinnings of disease, design synthetic biology and metabolic engineering strategies, and address other systems-level questions using a quantitative mathematical framework. We actively work on the development of novel approaches to integrate metabolic, regulatory, and signaling networks and to characterize properties of these networks.

RECENT RESEARCH DEVELOPMENTS

- Developed a computational pipeline for drug target identification in microbial pathogens.
- Reconstructed the first reconciled networks of human and rat metabolism to delineate species-specific differences in metabolism.
- Developed algorithms for data integration and model generation to drive developments in metabolic engineering an biomedical systems biology.

RECENT GRANTS

- NIH – Network analysis of pathogenicity in *Pseudomonas aeruginosa*
- NIH – Mapping and predicting metabolic fluxes between the ileal microbiome and host
- DoD – Tissue-specific metabolic networks for toxicology predictions
- Unilever, Inc. – Metabolism of microbial persister cells

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