

# Building a digital systems microscope

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Abstract: Confronting the complexity behind many biological processes requires the study of systems with multiple proteins or other molecules whose dynamic behavior cannot easily be deduced from studying their individual parts. In this context, proteomics is a key measurement technology for the study of proteins in 'data-driven' mode, which deemphasizes reliance on prior knowledge and concepts. One complication is that, unlike in conventional microscopic images, measurements are not commonly placed in an interpretive 3D context, and dynamic measurements are frequently limited to few time points. Thus, as a first step from data acquisition towards predictive models, even the representation of experimental data is not obvious. Paradigms and tools that can be employed to visually organize the data, and stimulate novel hypotheses and experiments are urgently needed.

My talk aims to show how data visualization, and integration with prior data, knowledge, and concepts can advance the analysis of proteomic data, and our understanding of biological systems. I will present an analytical view of the 'systems' research challenge and Cytoscape, our open-source software platform for the visualization and analysis of interaction networks.