



# CoCo Seminar Series Fall 2024

## Challenges and Opportunities for Inferring Networks from Biological Data

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**Wednesday November 20, 2024 12:00-1:00pm EST  
Hybrid (EB-T1 & Zoom; meeting link available on  
<http://coco.binghamton.edu/>)**

Biological networks are not known a priori and cannot be systematically measured at scale. Rather, they are typically “inferred” or “reconstructed” from biomedical data. In the context of molecular networks (where the nodes are biological molecules, and the edges represent relationships between those molecules), methods for modeling networks typically work by synthesizing information from Omics data. Although many methods have been developed to reverse engineer biological networks from data, these approaches typically use multiple experimental samples to estimate a single “aggregate” network, which does not capture population-level heterogeneity. In this talk I will review several approaches my group has developed for inferring networks from Omics data, including a mathematical framework for estimating sample-specific networks. I will show how this approach can be used to associate network connectivity patterns with other sample-specific information, such as patient phenotype. Finally, I will review several other existing and emerging methods for estimating sample-specific networks, examine the caveats and underlying assumptions made by these types of approaches, and discuss some of the broader challenges and opportunities in this area.

Kimberly Glass is an expert in complex networks and genomic data analysis. She obtained her PhD in Physics in 2010 from the University of Maryland. From 2010-2014, Dr. Glass was a postdoctoral fellow at Dana-Farber Cancer Institute and the Harvard T.H. Chan School of Public Health where she received training in computational biology. During her post-doc she developed several computational and data-integration methods for inferring and analyzing gene regulatory networks. In 2014 Kimberly joined the faculty of the Channing Division of Network Medicine (CDNM) at Brigham and Women’s Hospital where she is continuing her research in systems medicine and network methods. Her current research focuses on how to integrate and interpret multiple biological data-types in the regulatory network context and on how to understand the biological mechanisms represented in these networks. She is also investigating potential applications of networks in precision medicine, using network approaches to understand susceptibility to, severity, and treatment of complex diseases.

For more information, contact Hiroki Sayama ([sayama@binghamton.edu](mailto:sayama@binghamton.edu)).

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