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# Big Data Training for Cancer Research

## *Special Lecture Series*

### Why Networks Matter

***Dr. John Quackenbush***

June 8, 2021, 1:00 – 2:30 PM (EDT)

#### Speaker Bio:



John Quackenbush is Professor of Computational Biology and Bioinformatics and Chair of the Department of Biostatistics at the Harvard TH Chan School of Public Health, Professor in the Channing Division of Network Medicine, and Professor in the Department of Data Science at the Dana-Farber Cancer Institute. John's PhD was in Theoretical Physics, but in 1992 he received a fellowship to work on the Human Genome Project. This led him through the Salk Institute, Stanford, The Institute for Genomic Research (TIGR), and to Harvard in 2005. John uses massive data to probe how many small effects combine to influence human health and disease. He has more than 300 scientific papers and over 81,000 citations. Among his honors is recognition in 2013 as a White House Open Science Champion of Change.

#### Abstract:

One of the central tenets of biology is that our genetics—our genotype— influences the physical characteristics we manifest—our phenotype. But with more than 25,000 human genes and more than 6,000,000 common genetic variants mapped in our genome, finding associations between our genotype and phenotype is an ongoing challenge. Indeed, genome-wide association studies have found thousands of small effect size genetic variants that are associated with phenotypic traits and disease. The simplest explanation is that genes and genetic variants work together in complex regulatory networks that help define phenotypes and mediate phenotypic transitions. We have found that the networks, and their structure, provide unique insight into how genetic elements interact with each other and the structure of the network has predictive power for identifying critical processes in health and disease. I will touch on multiple examples illustrating the importance of network models, drawing on my work in cancer, in chronic obstructive pulmonary disease, and in the analysis of data from thirty-eight tissues provided by the Genotype-Tissue Expression (GTEx) project.

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Register at: [https://purdue-edu.zoom.us/webinar/register/WN\\_PiTB4FsWSUyDTbhA1SbF3w](https://purdue-edu.zoom.us/webinar/register/WN_PiTB4FsWSUyDTbhA1SbF3w)