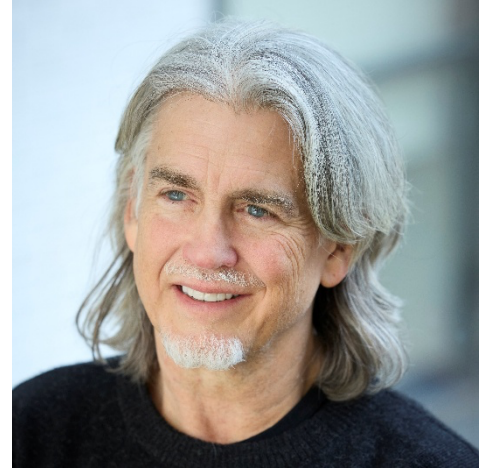


## **Public Talk & Guest Lecture:**

Professor **John Quackenbush**, Chair of the Department of Biostatistics at the Harvard T.H. Chan School of Public Health, Professor in the Channing Division of Network Medicine of Brigham and Women's Hospital, and Professor at Dana-Farber Cancer Institute



### **Why Networks Matter: Embracing Biological Complexity**

#### **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 structures, 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 and for identifying potential therapeutic targets. However, estimating the drivers of disease phenotypes or predicting therapies that might be useful is tremendously challenging—if not computationally intractable. Drawing inspiration from Wolpert and MacReady's "No Free Lunch Theorem for Optimization," we have found that biologically motivated constraints can help guide inference of biologically interpretable in scalable ways that provide meaningful insight into functional changes that can drive cancers and other complex diseases as well as how they are influenced by factors that include biological sex and age.

**When:** Thursday, February 12, 13:00 – 13:40 + Q&A

**Where:** Auditorium, Institute for Cancer Research, ground floor, Research Building (K building), Oslo University Hospital - Radium Hospital site

#### **About John Quackenbush:**

His work has focussed on integrating massive multi-omics datasets to reveal how subtle, combinatorial effects drive human health and disease.

His groundbreaking work in computational biology and systems genomics has advanced precision medicine worldwide. He is interested in AI driven approaches to precision-medicine analytics and pharmacogenomics and treatment predictions in oncology and other areas.

[John Quackenbush | Harvard T.H. Chan School of Public Health](#)