BRIGHAM AND WOMEN'S HOSPITAL

HARVARD MEDICAL SCHOOL

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Department of Medicine
Channing Division of Network Medicine

Channing Methods Meeting
September 13th (Tuesday), 2022, 11AM (ET)
MCP 5th-floor large conference room
https://us02web.zoom.us/j/579497999?pwd=cHNIWHMzWUIFUUVJTG1EeVJmY05aQT09
Meeting ID: 579 497 999
Passcode: 844168

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De-siloing Genomic Data Science

Abstract: Pursuit of accuracy and efficiency in methods of genomic data science leads to an explosion of parallel efforts in improving the management and analysis of genome-scale data. This "parallel play" phenomenon can be important for evolving superior approaches, but places serious burdens on investigators who must navigate a garden of forking paths populated with tools and data resources that must be compared and evaluated and are oftentimes found to be obsolete. I will discuss approaches to strengthening collaborative work in methods development and data conveyances that aim to reduce redundancy and improve accessibility of effective methodology in genomic data science.

Bio: *Vincent Carey, PhD, is a Professor of Medicine at HMS. He has been a biostatistician at CDNM for over 25 years. As a co-founder of the Bioconductor Project and former Editor-in-Chief of The R Journal, he has developed extensive experience in cross-disciplinary research and analytic methods pertinent to statistical analysis of high-dimensional data arising in general computational biology and in the computational biology of various human diseases. He was an inaugural faculty member in the Cold Spring Harbor Laboratory Summer Course on statistical analysis of genome scale data, contributed to the HarvardX PH525x online curriculum on data analysis for the life sciences, and aught in the Departments of Genetics and Biomedical Informatics at HMS.*