BRIGHAM AND WOMEN'S HOSPITAL
HARVARD MEDICAL SCHOOL

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Department of Medicine
Channing Division of Network Medicine

Channing Methods Seminar

November 7 (Tuesday), 2023, 11AM (ET)

MCP 5th-floor large conference room
https://us02web.zoom.us/j/579497999?pwd=cHNlWHMzWUlFUUVJTG1EeVJmY05aQT09
Meeting ID: 579 497 999
Passcode: 844168

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Deriving sparse polygenic risk models via statistical boosting on large genotype datasets: a phenome-wide analysis of the UK Biobank

Polygenic risk scores (PRS) are designed to model the genetic predisposition to various traits. Most PRS methods are based on linear additive models, derived from genome-wide association studies (GWAS), and applied to independent target genotype datasets. In recent years, numerous methods based on summary statistics and LD-reference panels have been developed to enhance polygenic risk score prediction and generalizability. Given the availability of large biobank datasets, classical statistical learning approaches can be employed to train polygenic risk models directly from genotyping data. For example, boosting algorithms can be applied on genotype/phenotype input data to derive sparse polygenic models that can be used to unravel the genetic architecture of the underlying traits.

Bio: Carlo Maj is a Principal Investigator at the Center of Human Genetics, University of Marburg (Germany). He studied Bioinformatics (MSc) and Computer Science (PhD) at the University of Milano Bicocca (Italy). His research group is specialized in the use of statistical genetics methods to analyze complex multifactorial traits and his primary methodological research interests are focused on polygenic risk score modelling.