BRIGHAM AND WOMEN'S HOSPITAL

HARVARD MEDICAL SCHOOL

181 Longwood Avenue
Boston, Massachusetts 02115-5804

Department of Medicine
Channing Division of Network Medicine

Channing Methods Meeting
September 27th (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

Peter Castaldi, MD, MSc
Channing Division of Network Medicine
Brigham and Women's Hospital
Harvard Medical School

Learning from Biological Data with Interpretable Machine Learning Models

Chronic obstructive pulmonary disease (COPD) is the third leading cause of mortality worldwide. Despite its large public health impact, progress in treatment for COPD lags behind other leading causes of mortality such as heart disease and cancer, but the genomics revolution has provided massive new datasets and experimental tools that can be used to identify and characterize the genes and biological processes that drive COPD pathophysiology. This talk will review pertinent clinical aspects of COPD, progress in our knowledge of genetic risk factors for COPD identified through genome-wide, the use of high-throughput functional assays and fine mapping strategies to identify the causal variants in GWAS loci and the genes affected by these variants, and finally we will review some applications of machine learning algorithms to genomic data to identify previously unappreciated structure within genomic datasets that may provide new biological insights.

Speaker Bio: Peter Castaldi is a physician-scientist and a principal investigator in the Channing Division of Network Medicine in the Department of Medicine at Brigham and Women's Hospital and Assistant Professor of Medicine, Brigham and Women's Hospital and Harvard Medical School. The goal of his work is to use genomic data to identify the pathobiological processes responsible for the development of COPD, to map variability of these processes to distinct patent subpopulations, and to develop more effective treatments for COPD. My research contributions have been focused in the following areas: 1) genome-wide association studies (GWAS) of novel radiographic measures of COPD-related phenotypes, 2) bioinformatics and functional analyses of gene regulatory data to characterize the gene regulatory mechanisms of GWAS-identified variants, and 3) use of machine learning methods and genomic data to dissect the clinical heterogeneity of COPD. More information on his research is available at castaldilab.org.