



181 Longwood Avenue Boston, Massachusetts 02115-5804 **Department of Medicine** *Channing Division of Network Medicine*

Channing Methods Seminar

March 26 (Tuesday), 2024, 11AM (ET)

MCP 5th-floor conference room & Zoom:

https://us02web.zoom.us/j/579497999?pwd=cHNIWHMzWUIFUUVJTG1EeVJmY05aQT09

Meeting ID: 579 497 999 Passcode: 844168



Georg Hahn

Division of Pharmacoepidemiology and Pharmacoeconomics Department of Medicine Brigham and Women's Hospital and Harvard Medical School

Prediction of disease-free survival for precision medicine using cooperative learning on multi-omic data

In precision medicine, predicting both the disease susceptibility of an individual and forecasting its disease-free survival are key research questions. An established technique is to estimate the risk of an individual with the help of an integrated risk model, that is a polygenic risk score with added epidemiological covariates. However, integrated risk models do not capture any time dependence, and may provide a point estimate of the relative risk with respect to a reference population. In addition, data from multiple (omic) platforms are increasingly available which complement classical epidemiological predictor variables. To integrate this wealth of information, we propose new methodology to combine both cooperative learning, a recent approach to leverage the predictive power of several datasets, and polygenic hazard score models. Polygenic hazard score models provide a practitioner with a more differentiated view of the predicted disease-free survival than the one given by merely a point estimate, for instance computed with a polygenic risk score. Our aim is to leverage the advantages of cooperative learning for the computation of polygenic hazard score models via Cox's proportional hazard model, thereby improving the prediction of the disease-free survival. In an experimental study, we apply our methodology to forecast the disease-free survival for Alzheimer's disease (AD) using three layers of data (epidemiological variables, selected genomic loci, methylation data for selected CpG sites).

Short bio: Georg Hahn is a faculty member in the Division of Pharmacoepidemiology and Pharmacoeconomics of the Department of Medicine at Brigham and Women's Hospital and Harvard Medical School. Additionally, he holds an instructor appointment in the Department of Biostatistics of the Harvard T.H. Chan School of Public Health, where he was a research scientist prior to his current appointment. He earned his Master degree in mathematics and statistics at the University of Cambridge, U.K., as well as his Ph.D. in statistics at Imperial College London, U.K.

Hosted by Julian Hecker

