

Division of Biostatistics, IHE
Medical College of Wisconsin presents

Statistical Methods for Integrative Analyses of High Dimensional Datasets

By: Sean McCabe, PhD

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Thursday, April 14th | 12:00PM – 1:00PM

Data is being generated at an increasing rate, which has given rise to a new field of genomic statistics called integrative analysis. This field involves integrating different types of large genetic and genomic datasets, such as genotype, RNA-Seq, and chromatin accessibility, to identify relationships across data types, as well as to assess relationships in disease severity and susceptibility. I will present several methods for the analysis of this type of data including STAARGEI, which incorporates external functional annotations to improve power in rare-variant gene set by environment interaction studies. STAARGEI also uses functional annotations to define the rare-variant sets to be tested and can efficiently handle population structure and sample relatedness through a generalized linear mixed model (GLMM) framework. STAARGEI was applied to a variety of simulation settings and in an analysis of neutrophil count in the UK Biobank dataset using smoking pack years as the interaction variable.



Sean McCabe, PhD

Sean McCabe is a postdoctoral research fellow working with Dr. Xihong Lin in the Department of Biostatistics at the Harvard TH Chan School of Public Health. Sean received his PhD in May 2020 and his M.S. in 2017 from the University of North Carolina at Chapel Hill and received his B.S. in Mathematics and Statistics from Purdue University in 2014. His research interests are in developing statistical methods for integrative analyses of high dimensional data with applications in genomics and genetics.

Location: Zoom | <https://mcw-edu.zoom.us/j/91808382928?pwd=clpSbFR6UjcwRkEySkFKVIRCREdKZz09>