BIOSTATISTICS SEMINAR

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Handling Sampling and Selection Bias in Association Studies Embedded in Electronic Health Records

In this talk we will discuss statistical challenges and opportunities with joint analysis of electronic health records and genomic data through " Genome and Phenome-Wide Association Studies (GWAS and PheWAS)". We posit a modeling framework that helps us to understand the effect of both selection bias and outcome misclassification in assessing genetic associations across the medical phenome. We will propose various inferential strategies that handle both sources of bias to yield improved inference. We will use data from the UK Biobank and the Michigan Genomics Initiative, a longitudinal biorepository at Michigan Medicine, launched in 2012 to illustrate the analytic framework. The examples illustrate that understanding sampling design and selection bias matters for big data, and are at the heart of doing good science with data. This is joint work with Lauren Beesley at the University of Michigan.

Thursday September 24, 2020   New time: 3:00 pm - 4:00 pm

Zoom meeting: Please also find a link in the email invite, with the password.
https://uncsph.zoom.us/j/92138801086?pwd=Y011NUNQcS9lZERjalVhbVZSZ3AwQT09

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