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**Robust Mendelian randomization in the presence of many weak instruments and widespread horizontal pleiotropy**

**Wednesday, November 9, 2022**  
**11:50 AM**

**110 Frelinghuysen Road, Hill Center, Room 552**

**Zoom Meeting: Meeting ID: 99075124232**  
**Password: 952486**

<https://rutgers.zoom.us/j/99075124232?pwd=UDdPVjRncXZFcXpvaFE0OWJyMVdSUT09>

**Light refreshments will be served**

**Abstract:** Mendelian randomization (MR) has become a popular approach to studying the effect of a modifiable exposure on an outcome by using genetic variants as instrumental variables (IVs). Two distinct challenges persist in MR: (i) each genetic variant explains a relatively small proportion of variance in the exposure and there are many such variants, a setting known as many weak IVs; and (ii) many genetic variants may have direct effects on the outcome not through the exposure, or in genetic terms, when there exists widespread horizontal pleiotropy. To address these two challenges simultaneously, we propose a novel estimator, the debiased inverse-variance weighted (dIVW) estimator for summary-data MR and we establish its statistical properties. An extension to the multivariable MR will also be discussed.

**Bio:** Ting Ye is the Genentech Endowed Assistant Professor in Biostatistics at the University of Washington. She received her Ph.D. in Statistics in 2019 from the University of Wisconsin-Madison and spent two years as a postdoctoral fellow in Statistics at the Wharton School, University of Pennsylvania. Her current research focuses on covariate adjustment in randomized controlled trials, Mendelian randomization, and other natural experiment methods for causal inference. Her website is <https://www.ting-ye.com>.

