

DBDS Workshop in Biostatistics

MSOB X303* (in person)

<https://stanford.zoom.us/j/98254419706?pwd=SlpzcDExV0t0b1Nnbi9FazRycXlFQT09> (Zoom option)

DATE:	September 23, 2021
TIME:	1:30-3:00pm
TITLE:	<i>Genetic variants across human populations—how similarities and differences play a role in our understanding of the genetic basis of traits</i>
SPEAKER:	Chiara Sabatti Professor of Biomedical Data Science and of Statistics Stanford School of Medicine

Abstract:

Identifying which genetic variants influence medically relevant phenotypes is an important task both for therapeutic development and for risk prediction. In the last decade, genome wide association studies have been the most widely-used instrument to tackle this question. One challenge that they encounter is in the interplay between genetic variability and the structure of human populations. In this talk, we will focus on some opportunities that arise when one collects data from diverse populations and present statistical methods that allow us to leverage them.

The presentation will be based on joint work with M. Sesia, S. Li, Z. Ren, Y. Romano and E. Candès.

Suggested Reading:

- [“What Happens When Geneticists Talk Sloppily About Race”](#)
- [“FDR control in GWAS with population structure”](#)
- [“Causal inference by using invariant prediction: identification and confidence intervals”](#)

Because the Biostatistics Workshop doubles as a class, the current university response to the pandemic requires us to **restrict in-person attendance to Stanford students, faculty and staff. We hope to be able to revise these restrictions soon and welcome back all our biostatistics workshop community.*