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STATISTICS DEPARTMENT SEMINAR

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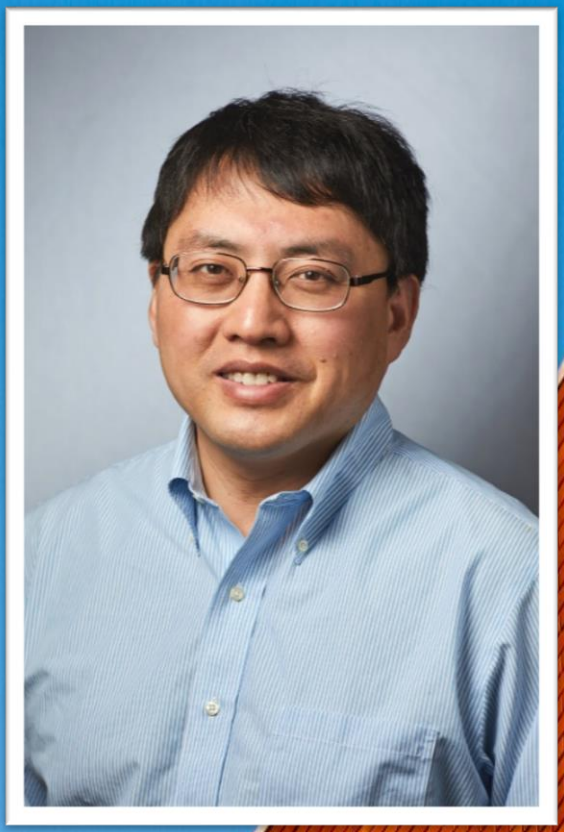

Olmsted Hall 420
May 7th 2019
3:45-4:45pm
Reception in Olmsted 1331 at 3:15 P.M.

"STATISTICAL METHODS FOR GENETIC RISK PREDICTION"

FOR MORE INFORMATION ABOUT THIS SEMINAR, VISIT STATISTICS.UCR.EDU/COLLOQUIA.HTML

Abstract

Accurate prediction of disease risk based on genetic and other factors is an important goal in human genetics research and precision medicine. Well calibrated prediction models will lead to more effective disease prevention and treatment strategies. Despite the identification of thousands of disease-associated genetic variants through genome-wide association studies (GWAS) in the past decade, accuracy of genetic risk prediction remains moderate for most diseases, which is largely due to the challenges in both identifying all the functionally relevant variants and accurately estimating their effect sizes. In this presentation, we will discuss a number of methods that have been developed in recent years to improve prediction accuracy from jointly estimating effect sizes, incorporating functional annotations, and leveraging genetic correlations among complex diseases. We will demonstrate the utilities of these methods through their applications to a number of complex diseases in large population cohorts, e.g. the UK Biobank data. This is joint work with Yiming Hu, Quongshi Lu, Yixuan Ye, and others.


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