DREXEL UNIVERSITY
A.J. Drexel Autism Institute

"Elucidating the Genetic Architecture of Complex Disorders: Challenges and New Approaches"

Wednesday May 22
1:00 PM — 3:00 PM

Rush Building - iSchool
Room 014
30 North 33rd Street
Philadelphia, PA 19104

A clear understanding of the genetic etiology of complex traits and disorders, including Autism Spectrum Disorders, is still limited. Genome-wide association studies (GWAS) have provided some information about the contribution of genetic variation to various traits, however, other approaches are necessary for further discovery. This talk will describe the application of novel tools and analyses for exploring the relationship between genetic variation and complex outcomes.

Her projects have included phenome-wide association studies (PheWAS), where the relationship between genetic variation and thousands of traits are explored. She has also been expanding the software tool Biofilter for the annotation, filtering, and development of interaction models for genetic data (https://ritchielab.psu.edu/ritchielab/software/). She is a member of the Population Architecture Using Genomics and Epidemiology (PAGE) consortium, the Electronic Medical Records and Genomics (eMERGE) network, and the Pharmacogenomics Research Network (PGRN). She is a co-organizer of a workshop at the Pacific Symposium on Biocomputing in 2014 titled: "Uncovering the Etiology of Autism Spectrum Disorders: Genomics, Bioinformatics, Environment, Data Collection and Exploration, and Future Possibilities", and encourages anyone with an interest in future collaborative work on Autism Spectrum Disorders to attend (http://psb.stanford.edu/wkshop-autism.html).

Sarah Pendergrass, Ph.D.

Dr. Sarah Pendergrass is currently a staff scientist at The Pennsylvania State University, in the Center for Systems Genomics and the lab of Dr. Marylyn Ritchie. She has a MS in Biomedical Engineering from Thayer School of Engineering at Dartmouth College, and a PhD in Genetics from Dartmouth College. Her current research interests include the characterization of the relationship between genetic variation, phenotypic outcome, and common complex disease, within the framework of ancestry. She has developed novel computational and data visualization approaches for the analysis and display of large high-throughput datasets (http://visualization.ritchielab.psu.ed u/)

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