

P-STAR Analysis Workshop – 2012

Tuesday, December 4th & Wednesday, December 5th
Austin, Texas

*** Updated ***

<u>Tuesday Agenda</u>		
7:00-8:00	<i>Registration and Breakfast</i>	
8:00-8:30	<i>Welcome and Introductions</i>	Marylyn Ritchie, P-STAR
8:30-9:10	Integration of cell line and clinical trial genome-wide analyses implicates multiple loci in paclitaxel-induced peripheral neuropathy	Heather Wheeler, PAAR
9:10-9:50	ATHENA: A method for integrating genome-wide gene expression and genotype data to generate meta-dimensional prediction models in CAP	Emily Holzinger, P-STAR
9:50-10:20	<i>Break</i>	
10:20-11:00	The Convergence of Functional Genomics, Heritability Estimation and Polygenic Modeling	Eric Gamazon, PAAR
11:00-11:40	Phenotype-Specific Genomic Network Discovery	Cheng Cheng, PAAR4Kids
11:40-12:20	Polygenic Inheritance of Paclitaxel-Induced Peripheral Neuropathy Driven by Axon Outgrowth Gene Sets	Aparna Chhibber, PMT
12:20-1:20	<i>Lunch</i>	
1:20-2:00	Estimating Heritability Of Drug Induced Liver Injury From Genome-wide Common Variants	Casey Overby, Affiliate
2:00-2:40	Polygenic Prediction of complex phenotypes and drug response	Hae Kyung Im, PAAR
2:40-3:10	<i>Break</i>	
3:10-3:50	Using BioBin to Explore Rare Variant Population Stratification Using 1000 Genomes Project Data	Carrie Moore, Affiliate
3:50-4:50	Statistical methods for association testing with multiple outcomes and (pharmacological) responses	Matthew Stephens, Department of Human Genetics and Department of Statistics, University of Chicago
4:50-5:00	Closing notes for the day	
5:00-6:00	<i>Cocktail Hour</i>	
6:00	<i>Dinner – See Sign-up sheets at the reception table</i>	

<u>Wednesday Agenda</u>		
7:00-8:00	<i>Breakfast</i>	
8:00-9:00	Pharmacogenetic sequencing at the BCM-HGSC	Dr. Steve Scherer, Human Genome Sequencing Center, Baylor College of Medicine
9:00-9:40	A Study of Asthma Pharmacogenomics Using RNA-Seq	Blanca Himes, PHAT
9:40-10:10	<i>Break</i>	
10:10-10:50	Continuing challenges in analysis of RNA-seq data	Courtney French, PMT
10:50-11:30	PGRN RNA-seq Pilot Analysis	Xiang Qin, BCM-HGSC
11:30-12:10	Visually integrating and exploring high throughput results using PheWAS-view, PhenoGram, and Synthesis-View	Sarah Pendergrass, P-STAR
12:10-1:30	<i>Lunch and General Discussion</i>	