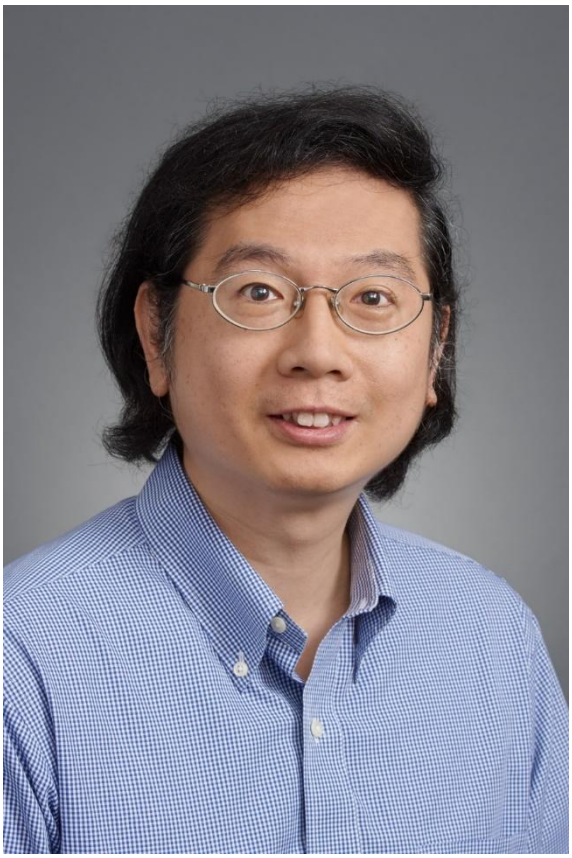

Prof. Yi-Hsiang Hsu is the Co-Director of the Genetic Epi Program and GeriOMICS Center, Marcus Institute for Aging Research, Beth Israel Deaconess Medical Center, Boston, MA. He is an Associate Professor at Harvard Medical School and at Program for Quantitative Genomics, Program of Molecular and Integrative Physiological Sciences, Harvard School of Public Health, Boston, MA. He is also an Associate Faculty at the BROAD Institute of MIT and Harvard, Cambridge, MA.

Prof. Hsu is a Statistical Geneticist/Computational Biologist and has led multiple large-scale NGS and GWAS projects on metabolic relevant disorders, cardiovascular disorders, musculoskeletal disorders and neuropsychiatric disorders. He has published 119 papers in subject of human genetics and is regarded as leading expert in field of using sophisticated statistical genetics and deep-learning machine-learning to conduct advanced statistical analysis.

Research highlights:

Genetic determinants of common aging relevant disorders: Using population-based whole genome sequencing, exome-sequencing and GWAS approaches to identify sequence variants that are associated with complex traits/disorders.

Precision medicine on immuno-oncology: To predict neoantigens from somatic mutations for potential use in cancer vaccine therapies, we apply a CNN deep learning machine learning approach to estimate the binding affinity between patients' HLA type and mutant peptides. The mutated peptides are estimated from somatic mutations. We use the same approaches to also predict the immunogenicity of the MHC-peptide complex to T-cells.

Human primary cell-specific gene regulatory circuits: Using chromatin confirmation capture HI-C seq (3D genomics structure), ATAC-seq, Chip-seq and RNA-seq as well as functional genomics approaches to build human primary cell-specific genomic regulatory circuits and to identify non-coding causal variants from NGS and GWAS loci. We apply AI deep-learning machine learning approaches to model gene regulation.

Statistical methodology development: Develop multi-phenotype analytical approaches (PheWAS approaches) using aggregative results from GWAS or from other large-scale high dimensional association analyses.

AI machine learning approaches: To understand MOA, using AI machine learning deep learning approaches to integrate genomics, transcriptomics, proteomics and metabolomics resources for better understanding relationships between the biological components that work together to drive a complex pathophysiological process of common diseases across signal pathways, organisms and even species on a global scale.