BIOMEDICAL & COMPUTING FRONTIERS

Ying Lin

Ph.D. – University of Washington
Assistant Professor, Industrial Engineering
Director, Smart Health & Intelligent Engineering Systems (SHINES) Lab

Selected Publications

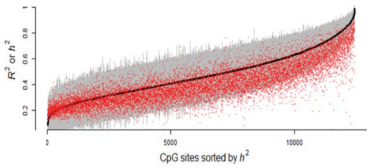
1. Lin, Y., Afsha, S., Rajadhyaksha, A., Potash, J. and Han, S., "A machine learning approach to predicting autism risk genes: Validation of known genes and discovery of new candidates". Frontiers in Genetics, 11, 2020.

2. Han, S., Lin, Y., Wang, M., Goes, F.S., Tan, K., Zandi, P., Hyde, T., Weinberger, D.R., Potash, J.B., Kleinman, J.E. and Jaffe, A.E., "Integrating brain methylome with GWAS for psychiatric risk gene discovery". bioRxiv, p.440206, 2018.

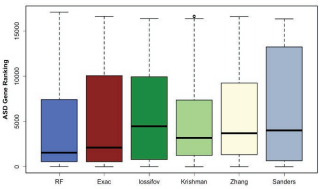
Dr Lin's research involves interaction between machine learning, biomedical informatics and quality engineering. She has developed innovative machine learning models for modeling, monitoring and prognosis of complex and heterogeneous systems. She has also developed computational techniques to integrate massive and network-structured datasets in clinical practice and bioinformatics. Her research is funded by the National Institute of Mental Health and the Advanced Manufacturing Institute at the University of Houston.

CAUSAL GENE IDENTIFICATION FOR PSYCHIATRIC DISORDERS

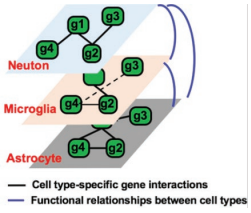
IMPUTE METHYLATION-TRAIT ASSOCIATION FROM GWAS



PREDICT AUTISM RISK GENES



CELL TYPE-SPECIFIC GENE NETWORK



Psychiatric disorders contribute substantially to the disease burden in the United States and worldwide. There is strong evidence that points to genetic contribution in the pathogenesis of many psychiatric illnesses. Recent advancements in high throughput genomic technologies and the availability of large samples have provided unprecedented information infrastructure for risk gene discovery of major psychiatric disorders, e.g. schizophrenia (SCZ) and autism spectrum disorder (ASD). However, few causal genes or variants have been identified due to the high complexity of the human genome, unknown functional relationships between risk genes, and the heterogeneous relationships among different tissues or cell types.

Dr. Lin's research group develops novel machine learning models to integrate the multi-source genomic data for causal gene identification. Specifically, they 1) integrate genome-wide association study (GWAS) with the brain methylome for risk gene discovery; 2) combine spatio-temporal gene expression signatures with the biological network for de novo mutations prediction; and 3) leverage single cell gene expression and biological networks for cell-stype specific network construction and causal gene identification. The identification and characterization of risk genes would help improve our understanding of the biological mechanisms that underlying psychiatric illnesses, moving us closer to designing effective prevention and treatment for these disorders.