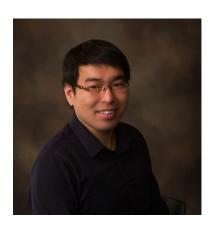# Department of Biostatistics and Medical Informatics Seminar

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Friday, February 16, 2024
12:00-1:00 pm
Biotech Center Auditorium *or* via Zoom Link
https://uwmadison.zoom.us/j/95515534304?pwd=NnR5Tn
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Advancing Precision Medicine: Tailored Genomic Insights and AI-Driven Automation in Complex Disease Research

Abstract: Understanding the genetic basis of complex human disorders is crucial in the realm of medical research, particularly in the context of precision medicine. Complex diseases such as Alzheimer's and various forms of cancer exhibit significant genetic heterogeneity, posing challenges in diagnosis and treatment. This talk will focus on two cutting-edge research projects that integrate genomics and machine learning, driving forward the field of precision medicine. The first part of the presentation introduces the Heteroscedastic Personalized Regression (Het-PR) model, a new approach in genomic analysis for Alzheimer's disease. Het-PR diverges from conventional models by emphasizing personalized treatment trajectories based on individual genetic factors. This model is adept at pinpointing unique genetic mutations and influential genetic factors in patients, which traditional models often miss due to their generalized approach. Demonstrated to be more effective in both simulation and real-world scenarios, Het-PR enhances the capability to devise personalized treatment plans for Alzheimer's patients, taking into account their individual genetic backgrounds. In the second part, the focus shifts to the Team of AI-made Scientists (TAIS), an innovative initiative using Large Language Models (LLMs) to automate the scientific discovery process in disease research. TAIS signifies a paradigm shift in genomic analysis, moving from traditional, labor-intensive methods to a more automated, efficient, and scalable model. This AI-driven team simulates various roles typically found in research teams, working collaboratively to autonomously perform complex tasks like data analysis and gene identification. The application of TAIS in identifying genes predictive of disease status exemplifies its potential to markedly accelerate the pace of discovery in medical genomics.

Bio: Haohan Wang is an assistant professor in the School of Information Sciences at the University of Illinois Urbana-Champaign. His research focuses on the development of trustworthy machine learning methods for computational biology and healthcare applications, such as decoding the genomic language of Alzheimer's disease. In his work, he uses statistical analysis and deep learning methods, with an emphasis on data analysis using methods least influenced by spurious signals. Wang earned his PhD in computer science through the Language Technologies Institute of Carnegie Mellon University. In 2019, Wang was recognized as the Next Generation in Biomedicine by the Broad Institute of MIT and Harvard because of his contributions in dealing with confounding factors with deep learning.

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