Subject: Dissertation Defense - Andy Huang, PhD in Bioinformatics & Computational Biology
Date: Friday, July 24, 2026 at 5:08:10 PM Eastern Daylight Time
From: SSB Faculty List on behalf of Diane St. Germain
To: SSB-FACULTY-LIST-L@LISTSERV.GMU.EDU

Dissertation Defense Announcement
To: The George Mason University Community

Candidate: Chih-Hao (Andy) Huang

Program: PhD in Bioinformatics and Computational Biology

Date: August 7, 2026

Time: 11:00 A.M. Eastern Time (US and Canada)

Location: via Zoom

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Committee chair: Dr. Aman Ullah

Committee members: Dr. Don Seto, Dr. Feras Batarseh

Title: Explainable and Causal Machine Learning for Multimodal Biomarker-Based Staging of Alzheimer's Disease

Abstract: Alzheimer's disease (AD) is a progressive neurodegenerative disorder for which timely, accurate, and trustworthy characterization of disease stage remains a central clinical and computational challenge. Although machine learning (ML) has demonstrated strong predictive performance on multimodal AD biomarker data, its translational value is limited by opaque decision processes, uncertain causal grounding, and insufficient attention to calibration and assurance. This dissertation develops and evaluates an integrated framework that couples explainable artificial intelligence (XAI) with causal inference to produce interpretable, mechanism-aware, and assurance-oriented models for biomarker-based AD staging, drawing on data from the Alzheimer's Disease Neuroimaging Initiative (ADNI). The work comprises three complementary studies. The first establishes rigorous predictive baselines across multimodal tabular biomarkers and applies SHapley Additive exPlanations (SHAP) to quantify feature contributions and to disentangle the dominant influence of cognitive measures from that of non-cognitive biological markers. The second moves from association to mechanism, introducing a causal-inference-inspired AI workflow that combines constraint-based structure learning (the Peter–Clark and Fast Causal Inference algorithms) with double machine learning to prioritize blood-transcriptomic candidates, surfacing immune- and sex-linked transcripts as hypothesis-generating targets. The third unifies these threads in an explainable multimodal staging model augmented by a causal-contrastive explanation framework (CCEF) and assurance-oriented outputs (including calibration, uncertainty, and domain-level attribution) to support trustworthy interpretation of class-specific predictions. Collectively, the studies trace a deliberate arc from predictive accuracy, to causal mechanism, to explainable and assured decision support, and demonstrate that explainability and causality are complementary rather than competing objectives. The dissertation contributes a reusable computational foundation for building biomarker models that are accurate, interpretable,

mechanistically informed, and suitable for responsible use in Alzheimer's disease research.

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