Subject: Dissertation Defense - Aylin Zinde, PhD in Bioinformatics & Computational Biology
Date: Friday, July 10, 2026 at 3:48:08 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: Aylin Zide

Program: PhD in Bioinformatics and Computational Biology

Date: July 24, 2026

Time: 10:30 A.M. Eastern Time (US and Canada)

Location: via Zoom

Join Zoom Meeting

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Committee chair: Dr. Aman Ullah

Committee members: Dr. Saleet Jafri, Dr. Fahad Almsned

Title: Dissecting Molecular Heterogeneity In Neurological Disorders: An

Integrative Genomics And Machine Learning Framework

Abstract: Advances in transcriptomic and genomic technologies have transformed the study of complex neurological disorders by enabling systems-level investigation of disease mechanisms. This dissertation integrates transcriptomics, genomics, network biology, and machine learning to investigate the molecular architecture of Multiple Sclerosis (MS) and Tourette syndrome (TS). Using bulk RNA sequencing, single-nucleus RNA sequencing, and genome-wide genotyping datasets, differential gene expression analysis, Gene Ontology, Gene Set Enrichment Analysis, Weighted Gene Co-expression Network Analysis (WGCNA), high-dimensional WGCNA (hdWGCNA), protein-protein interaction analysis, genome-wide association studies (GWAS), polygenic risk scoring (PRS), and machine learning were applied to identify disease-associated pathways and biological heterogeneity. In MS, transcriptomic analyses revealed disruption of DNA repair, mitochondrial metabolism, oligodendrocyte function, and myelination during disease progression. In TS, GWAS identified three genome-wide significant susceptibility loci, while machine learning revealed genetically distinct patient subgroups. Single-nucleus transcriptomic analysis further identified co-expression networks associated with neurodevelopment, myelination, extracellular matrix organization, protein translation, and TGF-β signaling. Collectively, these findings demonstrate that integrating multi-omics approaches provides new insights into the molecular mechanisms underlying MS and TS, identifies candidate biomarkers and therapeutic targets, and establishes a foundation for future precision medicine research.

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