Subject: CORRECTION, NEW DATE and TIME: Dissertation Defense - Eric Twum, PhD Bioinformatics & Computational Biology
Date: Thursday, July 10, 2025 at 1:00:07 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: Eric A. Twum

Program: PhD in Bioinformatics & Computational Biology

Date: Tuesday July 22, 2025

Time: 3:00 PM Eastern Time (US and Canada)

Location: Via Zoom

Join Zoom Meeting
https://gmu.zoom.us/j/93857887197?pwd=WWmMb5BUtM8KgwzzXoCavWRgHjaaR0.1

Meeting ID: 938 5788 7197

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Committee Chair: Dr. Aman Ullah

Committee members: Dr. Ancha Baranova, Dr. Saleet Jafri

Title: From Gene Expression to Regulatory Networks: A Multi-omics Framework for Deciphering the Molecular Landscape of Immune Response-Mediated Diseases

Abstract: Advances in high-throughput omics technologies have transformed our ability to interrogate complex diseases at a systems level. This dissertation presents an integrative omics framework to decipher the molecular architecture and regulatory networks underlying diseases with systemic impact, focusing specifically on eosinophilic esophagitis (EoE) and COVID-19. Leveraging bulk RNA sequencing datasets, this work employs a comprehensive pipeline that spans differential gene expression analysis using DESeq2, functional enrichment via Gene Ontology (GO), network-based modeling through Weighted Gene Co-expression Network Analysis (WGCNA), and protein-protein interaction (PPI) mapping using Cytoscape and CytoHubba. These analyses illuminate key pathways involved in immune regulation, epithelial barrier dysfunction, mitochondrial perturbation, and inflammatory signaling.

Transcription factor (TF) activity was inferred using the DoRothEA regulon and the decoupleR framework, enabling the identification of upstream regulators contributing to disease heterogeneity in EoE. Furthermore, unsupervised clustering and Random Forest classification were employed to stratify EoE subtypes and reveal predictive biomarkers with high discriminatory power. In EoE, these methods highlighted transcriptional and immunological diversity among clinical subtypes, whilst in COVID-19, persistent transcriptomic alterations in mitochondrial and inflammatory genes were linked to long-term sequelae across multiple organ systems. In familial EoE, integrative analysis revealed gene networks and transcriptional signatures associated with susceptibility and resilience, offering insights into potential molecular drivers of heritable disease risk.

By integrating omics-based approaches with machine learning, this dissertation provides a systems-level view of disease pathophysiology, offering novel insights into molecular mechanisms, diagnostic markers, and potential therapeutic targets. These findings underscore the utility of integrative transcriptomics in elucidating disease-specific pathways in immune response-mediated conditions.

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