Subject: Dissertation Defense - Yiyang Lian, PhD in Bioinformatics & Computational Biology
Date: Thursday, April 2, 2026 at 9:15:11 AM 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: Yiyang Lian

Program: PhD in Bioinformatics and Computational Biology

Date: April 17, 2026

Time: 2:00 P.M. Eastern Time (US and Canada)

Location: via Zoom

Join Zoom Meeting

https://gmu.zoom.us/j/94978848663?pwd=mtfOSxaTjDrb1Jkdr6d5LtwjqMjn0X.1

Meeting ID: 949 7884 8663

Passcode: 800953

One tap mobile +13017158592,,94978848663# US (Washington DC)
+12678310333,,94978848663# US (Philadelphia)

Dial by your location +1 301 715 8592 US (Washington DC) +1 267 831 0333 US (Philadelphia)

Meeting ID: 949 7884 8663

Find your local number: https://gmu.zoom.us/u/acikTqmCuH

Committee Chair: Dr. Donald Seto

Committee Co-Chair: Dr. Amarda Shehu

Committee member: Dr. Jeffrey Solka

Title: Linking Genetic Mutations to Disease Outcomes: A Case Study of Fgfr2 in Developmental Disorders and Cancer

Abstract:

The fibroblast growth factor receptor 2 (FGFR2) is a vital component of cellular signaling pathways, playing a critical role in processes such as proliferation, differentiation, and survival. Mutations in the FGFR2 kinase domain have been implicated in diverse pathologies, ranging from craniosynostosis syndromes to various cancers. Despite the cataloging of thousands of variants by next-generation sequencing, a significant portion remains classified as Variants of Uncertain Significance (VUS). Accurate interpretation of these variants is a critical challenge in precision medicine, as traditional sequence-based predictors often lack mechanistic insight, and static structural methods fail to capture the dynamic conformational landscapes that govern kinase activation and dysregulation. To address this gap, this dissertation makes a series of methodological contributions culminating in an interpretable structural-learning framework that integrates conformational dynamics with machine learning to classify pathogenic missense variants. Applied to cancer-associated FGFR2 mutations, the framework effectively distinguishes pathogenic variants from benign ones by capturing subtle shifts in conformational equilibria. Integration of SHapley Additive exPlanations furthermore provides mechanistic attributions for individual predictions. This research bridges the gap between static structure prediction and dynamics-aware functional assessment. By offering a robust framework for predicting disease-specific functional impacts, this work generates testable hypotheses for experimental validation and demonstrates the value of incorporating conformational dynamics into variant effect prediction for precision oncology.

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