Subject: Dissertation Defense - Aliye Hashemi, PHD Bioinformatics & Computational Biology

Date: Tuesday, June 25, 2024 at 12:27:05 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: Aliye Sadat Hashemi Program: PhD Bioinformatics & Computational Biology

Date: Tuesday, July 9, 2024

Time: 10:00 AM Eastern Time (US and Canada)

Location: Via Zoom All are invited to attend the defense.

Join Zoom Meeting https://gmu.zoom.us/j/99758881338

Meeting ID: 997 5888 1338

One tap mobile +13017158592,,99758881338# US (Washington DC) +12678310333,,99758881338# US (Philadelphia)

Dial by your location +1 301 715 8592 US (Washington DC) +1 267 831 0333 US (Philadelphia) Meeting ID: 997 5888 1338 Find your local number: <u>https://gmu.zoom.us/u/ablsrkVHUC</u>

Join by SIP 99758881338@zoomcrc.com

Committee Chair: Dr. Iosif Vaisman **Committee Members:** Dr. Ancha Baranova and Dr. Dmitri Klimov

Title: "Topology-Based Protein Classification Using Deep Learning"

Abstract:

Utilizing Artificial Intelligence (AI) in computational biology techniques could offer significant advantages in alleviating the growing workloads faced by structural biologists, especially with the emergence of big data. This study serves as a proof of concept, demonstrating how Delaunay tessellation and deep learning models can be

used to classify proteins with high accuracy into superfamilies and potentially families, based on the local arrangement of neighboring residues. We employed Delaunay tessellation as a promising method to obtain the overall structural topology of proteins. Subsequently, we developed multi-class deep neural network models to classify protein superfamilies based on their topology. Our models achieved a est accuracy of approximately 0.92 in classifying proteins into 18 well-populated superfamilies. This result suggests that the deep learning models developed in this research have successfully captured complex patterns within protein topology.

###