Subject: Dissertation Defense - Soukaina Amniouel, PhD Bioinformatics & Computational Biology
Date: Wednesday, April 17, 2024 at 3:45:06 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: Soukaina Amniouel

Program: PhD Bioinformatics & Computational Biology

Date: Thursday, May 2, 2024

Time: 1:00 PM Eastern Time (US and Canada)

Location: Via Zoom

Join Zoom Meeting
https://gmu.zoom.us/j/91767841843?pwd=ZjQyZ3YzOGNGc2FlQTIrN01tUmhGZz09

Meeting ID: 917 6784 1843
Passcode: 575185575185

One tap mobile

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Dial by your location

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    +1 267 831 0333 US (Philadelphia) Meeting ID: 995 7513 1598 Passcode: 283049

Find your local number: https://gmu.zoom.us/u/abKu8mzV9Y

Committee Chair: Dr. Saleet Jafri
Committee members: Dr. Iosif Vaisman, Dr. Ancha Baranova
Title: "Prediction Of Solid Tumors Chemotherapy Efficacy Using Machine Learning Applied to

Gene Expression Data"

Abstract:
Solid tumors present a significant challenge in oncology, often developing resistance to standard treatments. Recent advancements in cancer therapies have significantly improved patient survival rates and quality of life. Despite these advancements, treatment resistance frequently leads to tumor relapse and recurrence, contributing to a high number of cancer-related deaths. This resistance, caused by various mechanisms including changes in drug targets and activation of DNA repair mechanisms, remains a major obstacle in successful chemotherapy for solid tumors. The ability to predict how tumors will respond to specific treatments is crucial for developing personalized oncology strategies. Advances in molecular profiling and machine learning offer new opportunities to tackle this challenge by identifying gene signatures that predict treatment response with high accuracy. Our project aims to use machine learning to uncover these signatures in solid tumors, proposing a novel machine-learning strategy to improve prediction accuracy and address overfitting. Our approach has shown promising results, with drug response prediction accuracy ranging between 85% and 96% across different types of solid tumors, including colorectal, serous ovarian, and triple-negative breast cancer. This success suggests that our method could, upon further validation, significantly impact clinical practice and precision oncology, paving the way for personalized treatment plans that could transform patient care.

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