PURDUE UNIVERSITY | Weldon School of Biomedical Engineering

BME 3rd Year Seminar Series
Friday, September 27th, 2024
1:30 – 2:30 PM EST
MJIS 1001

Evaluation links:
Himabindu Kovvali: https://purdue.ca1.qualtrics.com/jfe/form/SV_2lPynY9U0mbtWXI
Mohammadreza Balouchestani: https://purdue.ca1.qualtrics.com/jfe/form/SV_7OH2BTjlFgBWgRg

Evaluation surveys should only be completed after the seminar has taken place, and only by those who attended the seminar.

Quantifying the Intercellular Mechanisms of Ebolavirus Transmission using Multi-scale Agent-based Modeling

Himabindu Kovvali (Elsje Pienaar, advisor)

Abstract: Ebola Virus Disease (EVD) is caused by an Ebolavirus (EBOV) infection and is associated with fatal hemorrhagic fever. It has caused more than 30 outbreaks, some with 100% mortality. There is a gap in our knowledge of the protein-protein and lipid-protein interactions that drive effective viral production, making it challenging to develop therapies. Matrix protein VP40, when expressed independently, can produce virus-like particles (VLPs) with similar size, shape, entry, and cell attachment properties as EBOV virions. The production of VLPs is enhanced when VP40 is co-expressed with NP, nucleoprotein, which forms NP inclusions encapsulated in the VP40 VLP matrix. The production of VLPs has been quantified in individual cells with a subcellular differential equation model. Here, we employ this existing data to develop a multi-scale Agent-based model to represent the VP40-NP system in a population of cells using a Java-based modeling system called Repast Simphony. The model has five agent types: Transfected Kidney cells, IB-free-VLP (no NP inclusions), IB-containing-VLP (with NP inclusions), Healthy Kidney cells, and VLP-entered cells. Kidney cells are assumed to be adherent. VLP's have movement via Brownian motion. VLP agents are budded from Transfected Kidney cells and enter Healthy Kidney cells through contact. We stochastically quantified the number and type of VLPs that

enter Healthy Kidney cells in a population of cells. Results suggest that irrespective of the kind of VLP produced, their entry into a healthy cell is defined primarily by the number of VLPs in the environment. The findings provide valuable insights to elucidate how single-cell VP40 and NP interactions propagate across a population of cells to sustain robust viral proliferation. This study introduces a novel framework of multi-scale Agent-based modeling in the context of computational virology.

Quantifying Hemodynamic Metrics and Assessing Their Uncertainty in Intracranial Aneurysms with Computational Fluid Dynamics and 4D Flow MRI

Mohammadreza Balouchestani (Vitaliy Rayz, advisor)

Abstract: Proper risk assessment of the stability of unruptured intracranial aneurysms (IA) is crucial for making treatment decisions. In addition to clinical and morphological factors, hemodynamic forces have been linked to both IA growth and rupture, though their exact role remains unclear. Our work is motivated by the relationship between adverse hemodynamic environments and the growth or rupture of IAs. We propose new metrics to assess the spatiotemporal heterogeneity of the wall shear stress (WSS) vector field, to enable comparison between pre- and post-growth stages of IAs. Spatial autocorrelation of WSS is used to evaluate the heterogeneity of the WSS vector field. Additionally, spatial variation of topological shear is introduced to capture sharp directional changes in the vector field. Post-processing analysis is applied to velocity fields derived from computational fluid dynamics (CFD) simulations. The boundary conditions for CFD models are informed by 4D flow MRI measurements and implemented using Windkessel models. An additional focus of this work is to evaluate the reliability of velocity-based metrics derived from 4D flow MRI, by developing an automated, physic-based method for estimating uncertainty. This method uses a standardized mean of patches (SMP) to estimate velocity error correlations by standardizing background patches, regardless of their signal magnitude. Conservation of mass is employed to infer local variance at each voxel, based on observed errors in the velocity divergence and the estimated correlation matrix. The model is capable of capturing various error sources, such as noise, partial volume effects, image resolution and phase wrapping. It also accounts for error correlations between velocity components, as well as spatial and temporal correlations. The statistical distance of the velocity measurement and the modeled velocity error distribution can be used to assess the reliability of both the velocity measurement and the respective velocity-based metrics. The current model has the potential for inferring the uncertainty and improving the accuracy of gradient-based hemodynamic metrics.