Invited speakers

Dr. Tizhoosh is a professor in the Faculty of Engineering at University of Waterloo. He is a director of the Knowledge Inference in Medical Image Analysis (KIMIA) Lab in the Engineering Faculty at the University of Waterloo. He is also a member of Waterloo AI Institute, and a faculty affiliate to the Vector Institute. His research activities include artificial intelligence (AI), computer vision, and medical imaging. He has developed algorithms for medical image filtering, segmentation and search. He is the author of many books and over 150 scientific articles. Dr. Tizhoosh has extensive experience in working with industry and holds several patents. He is a member of the advisory board for Huron Digital Pathology, Canada.

Dr. Phedias Diamandis is a Neuropathologist and Clinician Scientist at UHN and Princess Margaret Cancer Centre. His research focuses on using chemical biology, deep learning, and mass spectrometry-based proteomics to resolve phenotype-level heterogeneity in brain glioblastomas. His team is utilizing artificial intelligence and mass spectrometry to define global morphometric and proteomic patterns defining normal development, health maintenance, and disease. His group applies machine learning approaches to interrogate datasets and resolve inter- and intra-patient molecular and phenotypic heterogeneity. These machine learning tools can guide more focused validation studies into mechanisms driving neurological disorders.

Dr. Trevor McKee has a PhD from MIT in Biological Engineering, and has 20 years of experience in preclinical imaging, including the development of new algorithms for image analysis. At the STTARR Imaging Facility, Dr. McKee leads a team of algorithm developers to provide image analysis as a service to academic laboratories and pharmaceutical companies, including ongoing analysis for clinical trial specimens. Dr. McKee has worked on developing relationships with pharmaceutical companies to help bridge the translational divide and bring ideas from basic science, through translation in preclinical models at STTARR, and through clinical trials for drugs and imaging agents.

AGENDA

1:00 – 2:00	**How to go digital in Pathology** Dr. H. Tizhoosh, KIMIA Lab, University of Waterloo Introduction to the Digital pathology, a rapidly evolving and essential technology, with specific support for tissue-based research, drug development, and the practice of human pathology.
2:00 – 2:15	**Artificial Intelligence (AI) algorithms in digital pathology: an overview** Dr. Morteza Babaie and Amir Safarpour, KIMIA Lab, University of Waterloo Foundations and approaches in developing computerized algorithms for high dimensional data and image analysis for predicting disease outcome. How AI uses algorithms to represent data, classify data, and search for similar instances, either in supervised or unsupervised approaches.
2:15 – 2:30	**Image search and diagnosis: a first validation using TCGA data** Shivam Kalra, KIMIA Lab, University of Waterloo An overview, strategies and applications for working on deep networks, metric learning, autoencoders, and searching in large archives of pathology images.
2:30 – 3:30	**Understanding Machine Engineered Reasoning in Pathology** Presenter: Dr. Phedias Diamandis, MD, PhD, FRCPC A pathologist perspective on integration of artificial intelligence and machine learning into diagnostic pathology. Examples of how computer-aided image analysis can be used in various tasks in cancer imaging, e.g. detection, diagnosis, prognosis, and response to therapy. Learn how digital tools can be applied to resolve phenotypic heterogeneity in different glioblastoma niches, empower data mining with patient characteristics to build novel predictive indicators for tumor detection, monitoring and therapy.
3:30 – 4:30	**To use AI or not? Machine Learning in Practice: Clinical trial and translational research applications** Dr. Trevor McKee, PhD, STTARR Imaging Facilities The talk is on principles underlying the development of algorithms for the segmentation analysis of histopathology images. Examples of how semi-automated cell-counting strategies on single and multiplexed stained tissue sections can be uses for obtaining information on cell markers in relation to cell phenotypes and spatial arrangements. Examples from quantitative analysis on clinical trial specimens, and will be used to illustrate the current application of machine learning methods in a high throughput core facility environment.