Wednesday, September, 10 2025 | 10:30 AM - 11:00 AM

Title: Explainability and interpretability in computational models

Speaker: Paulo Lisboa - Emeritus Professor at School of Computer Science and Mathematics, Liverpool John Moores University

Abstract: Machine learning is synonymous with predictive models of exceptional accuracy. However, do black boxes learn the structure in data? Or do we need structured models to properly understand their predictions? This talk will provide answers to these questions by focusing on the critical role of explainability and interpretability in computational models. It will show how any black box can be fully interpreted, matching the performance of deep learning for tabular data. This will be illustrated with a detailed example using real-world data on heart transplants.

Thursday, September 11, 2025 | 11:30 AM - 12:15 PM

Title: Policy relevant effects in infectious disease studies

Speaker: Mats Julius Stensrud - Associate Professor at Institute of Mathematics, EPFL Lausanne

Abstract: The treatment of one individual often affects the outcomes of others. A canonical example occurs in infectious disease settings, where vaccinating one individual can reduce disease transmission and thereby influence the health outcomes of others. This type of interference implies that individuals cannot plausibly be treated as independent and identically distributed (iid). Extensive methodological research has recently addressed interference problems and the resulting violation of conventional iid assumptions. However, despite growing interest in this topic, there remains controversy over whether and when existing methods capture causal effects of practical interest, particularly in clinical medicine and public health. In this talk, I will present causal methodologies—motivated by infectious disease settings—for addressing interference. The central idea is to define estimands that are insensitive to the interference structure. This approach is not merely a workaround to avoid interference; rather, I will argue that these estimands have a clear interpretation and can guide decisions by doctors and patients. Specifically, these estimands can quantify vaccine waning and sieve effects, as illustrated through examples concerning COVID-19 and HIV.

Thursday, September 11, 2025 | 16:00 PM - 16:30 PM

Title: AI for Mining Multi-Omics Data in Precision Medicine and Pharmacology

Speaker: Natasa Przulj - Full Professor, MBZ University of Artificial Intelligence (MBZUAI)

Abstract: Large amounts of multi-omic data are increasingly becoming available. They provide complementary information about cells, tissues and diseases. We need to utilize them to better stratify patients into risk groups, discover new biomarkers and targets, re-purpose known and discover new drugs to personalize medical treatment. This is nontrivial, because of computational intractability of many underlying problems on large interconnected data (networks, or graphs), necessitating the development of new algorithms for finding approximate solutions (heuristics). We develop versatile artificial intelligence (AI) frameworks for multi-omics data fusion, constrained by the state-of-the-art network science methods, to address key challenges in precision medicine and pharmacology from time-series, multi-omics data, including patient-derived single-cell data, to: better stratify patients, predict new biomarkers and targets, re-purpose existing and discover new drugs; we apply these to different types of cancer, Covid-19, Parkinson's and other diseases. Our new methods stem from graph-regularized non-negative matrix tri-factorization (NMTF), a machine learning (ML) technique for dimensionality reduction, inference, fusion and co-clustering of heterogeneous datasets, coupled with novel graphlet-based network science algorithms. We utilize our new frameworks for improving the understanding of the molecular organization of life and of diseases from the embedding spaces of omics data. Also, we utilize the local network topology to correct for the topological information missed by random walks used in many ML methods, and to enable embedding of multi-omics networks into more linearly separable spaces, allowing for their explainable and sustainable mining. The aim is to develop an overreaching framework encompassing all multi-omics data towards consumer-facing precision medicine products.

Friday, September 12, 2025 | 14:15 PM - 15:00 PM

Title: Decoding tumor heterogeneity: computational methods for scRNA-seq and spatial omics

Speaker: Valentina Boeva - Professor of Computational Genomics of Cancer at Department of Computer Science, ETH Zurich

Abstract: Characterizing and understanding drivers of tumor transcriptional and epigenetic heterogeneity is key to advancing personalized medicine and developing effective therapies. In this presentation, I will discuss our recent work on designing a computational methodology to extract gene signatures for distinct transcriptional states of cancer cells from single-cell RNA sequencing data (scRNA-seq) and show examples of linking intratumor transcriptional heterogeneity to tumor microenvironment and clinical variables. In this context, I will talk about the best-performing existing approaches for the integration of scRNA-seq data from malignant cells across cancer patients and also present our recently developed scRNA-seq-based CancerFoundation model, which, in addition to being capable of data integration across patients, can be used for predicting drug responses. I will conclude with our latest efforts in spatial transcriptomics and demonstrate how supervised machine-learning approaches that use spatial information can further resolve the complexity of cancer and provide explainable clinical biomarkers.