ECODAM 2025

Registration: June 16, 15:00; June 17, 09:00 – Senate Hall, building A

June 16, Ferdinand Hall, building A

Session 1

15:30 – 16:30 Daniela Zaharie (West University of Timişoara):
"Evolution and Learning for Dispatching Rules Discovery"
16:30 – 17:30 Panel discussion. *"The Human Factor: Ethics, Opportunities, and Challenges of LLMs in PhD Studies"*

June 17, Senate Hall, building A

9:30 – 10:15 Opening Session: **20 years with ECODAM**

Session 3

10:30 – 11:30 Kenneth DeJong (George Mason University): *"Understanding Co-Evolutionary Algorithms"*
11:30 – 12:30 Darrell Whitley (Colorado State University): *"Genetic Algorithms, Graybox Optimization and the Power of Recombination"*

Session 4

15:00 – 16:00 Gabriela Ochoa (University of Stirling, UK): *"Illuminating Optimisation Trajectories"*
16:00 – 17:00 Bogdan Paşaniuc (University of Pennsylvania): *"Polygenic Risk Scores for Genomic Medicine: Promises and Challenges"*

17:15 – 18:30 PhD students: *3-minute thesis presentations*

June 18 Senate Hall, building A

Session 5. *Dedicated to the Solomon Marcus centenary*

09:30 – 10:30 Liviu Dinu (University of Bucharest): *"On the hidden variables of the natural languages similarity"*
10:30 – 11:30 Dan Simovici (University of Massachusetts, Boston): *"The Curse and Blessings of Dealing with High-Dimensional Data in Machine Learning"*

11:45 – 12:45 Sorin Istrail (Brown University)*: "The Unreasonable Effectiveness of Mathematics in Genome-Wide Association Studies (GWAS) and the Search for Genomic Determinants of Disease"*

Session 6

15:00 - 16:00 Luca Peruzzotti Jametti (University of Cambridge): *"Targeting Microglial Metabolic Dysfunction to Halt Chronic Central Nervous System Inflammation"*

16:30 - 17:30 George Vassiliou (University of Cambridge): "*Clonal haematopoiesis and leukaemia prevention*"

June 19   Ferdinand Hall, building A
Session 7
Satelite Workshop: Applied Machine Learning/Bioinformatics I
- Core Bioinformatics Group -

09:30 – 10:00 Andi Munteanu (PhD student University of Iasi ; RA, Core Bioinformatics group): "*StarLng 2.0: Stability and robustness assessment of single-cell clustering*"

10:00 – 10:30 Rafael Kollyfas (Research Assistent, Core Bioinformatics group): "*Flufftail 2.0: Unveiling Gene Regulatory Network Dynamics through Fuzzy Clustering of Single-Cell RNAseq Data*"

10:30 – 11:00 Miguel Larraz (PhD student, University of Cambridge): "*Computational Analysis of Liver Organoid Self-Organization: Trajectory Modeling, Clustering Stability, and Gene Network Reconstruction*"

11:30 – 12:00 Friedrich-Maximilian Weberling (PhD student, University of Cambridge): "*Crécerelle: Integrating gene expression and transcript usage analysis through multi-modal deep generative models*"

12:00 – 12:30 Eleanor Williams (PhD student, University of Cambridge): "*Integrating multiple modalities in spatial context*"

12:30 – 13:00 Floris Roos (University of Antwerp; former post-doc in the Vallier and Mohorianu labs): "*Human foetal organoid atlas for studying development*"

Session 8
Satelite Workshop: Applied Machine Learning/Bioinformatics II
Core Bioinformatics Group

14:30 – 15:00 Cristian Bulgaru (MSc student, University of Iasi; RA, Core Bioinformatics group): "*Canard2.0: Co-expression ATAC and RNA dynamics (challenges of assessing chromatin openness on single-cell data)*"

15:00 – 15:30 Şerban Doncean (MSc student, University of Iasi; intern, Core Bioinformatics group): "*FALCON: Functional Analysis / Learning of Corrected Omics via (regulatory) Networks*"

(Head of Bioinformatics/ Scientific Computing @ CSCI, **Head of the CORE BioInformatics group**, University of Cambridge): "*RoSignOL: robust signature of Life*".

Session 9

17:00 Closing session

Abstracts

Kenneth DeJong – George Mason University
"Understanding Co-evolutionary Algorithms"

Interest in co-evolutionary algorithms was triggered in part with Hillis' 1990 paper describing his success in using one to evolve sorting networks.

Since then there have been heightened expectations for using this nature-inspired technique to improve on the range and power of evolutionary algorithms for solving difficult computation problems. However, after more than two decades of exploring this promise, the results have been somewhat mixed.

In this talk I summarize the progress made and the lessons learned with a goal of understanding how they are best used and identify a variety of interesting open issues that need to be explored in order to make further progress in this area.

Darrell Whitley – Colorado State University
"Genetic Algorithms, Graybox Optimization and the Power of Recombination"

Abstract. Graybox Optimization exploits the idea that information can be extracted from the evaluation function, and that this information can be used to create more intelligent and informed Hybrid Genetic Algorithms. For k-bounded Boolean functions, improving moves can be located in O(1) time and intelligent recombination operators can be implemented in O(n) time that provide guarantees of monotonic improvement in the sense that an offspring is produced that is equal or better than the best parent. Two forms of intelligent recombination are now part of the LKH code for the Traveling Salesman Problem. And the DRILS algorithms, which also exploits intelligent recombination, has been able to optimize NK Landscape problems with 1 million variables, smashing previous records.

This talk will also explore the hypothesis that biological evolution is not fully a "Black Box" optimizer. What would be necessary for biological evolution to also exploit some form of intelligent recombination?

Gabriela Ochoa – University of Stirling
"Illuminating Optimisation Trajectories"

Abstract. Many nature-inspired optimisation algorithms have been proposed over the years. It is unclear, however, to what extent recent algorithms are really "new", or how and why to select one of them to solve a given task. Search trajectory networks (STNs) are a data-driven, graph-based modelling tool to analyse, visualise and contrast the behaviour of different types of optimisation algorithms. STNs offer a visual and intuitive fresh perspective to explain and interpret search and optimisation. This talk overviews our methodology including recent developments: applications to neuroevolution, multi-objective optimisation, STNWeb, and the use of generative AI to automate the analysis.

Daniela Zaharie – West University of Timişoara
"Evolution and Learning for Dispatching Rules Discovery"

Evolution and learning can be viewed as optimization processes that use exploration and exploitation strategies to search for effective solutions or strategies. Evolutionary algorithms and

machine learning methods embody these principles. While sharing some similarities, they differ significantly in their underlying mechanisms and levels of interpretability.

This talk explores the similarities and differences between evolution and learning in the context of designing dispatching rules (decision guidelines for assigning tasks to available resources). The comparison focuses on Genetic Programming – evolving symbolic expressions to prioritize tasks –, and Reinforcement Learning – learning scheduling policies by interacting with the problem environment.

Liviu Dinu – University of Bucharest

"On the hidden variables of the natural languages similarity"

One of the last challenges of Darwin (1859) claims that the genealogy of languages is consistent with the genealogy of the nations (analyzed based on DNA similarity). If grouping of languages in linguistic families is today generally accepted, the degrees of similarity between languages are far from being certain. 150 years after Darwin's claim, the languages intelligibility problem is officially mentioned in a report published in 2007 by the European Commission (inside of the High Level Group on Multilingualism conducted by the Romanian commissar Leonard Orban), which emphasizes "a lack of knowledge about mutual intelligibility between (even closely) related languages in Europe". We will adress in this talk a map of linguistics distances between European languages (with a focus on Romanian) at different levels: phonetic, lexical and syntactic.

Dan Simovici – University of Massachusetts at Boston

"The Curse and Blessings of Dimensionality in Machine Learning"

Abstract. The term "curse of dimensionality" refers to the apparent intractability of searching through a high-dimensional space and to the intractability of accurately approximating or integrating a general high-dimensional function. The "blessing of dimensionality", refers to the concentration of measure phenomenon, which suggest that statements about very high-dimensional settings may be made where for relative moderate dimensions this would be too complicated.

We discuss a number of geometrical aspects of spaces of higher dimension and the challenges the pose to machine learning activities such as clustering and classification.
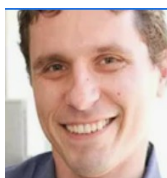
Sorin Istrail – Brown University

"The Unreasonable Effectiveness of Mathematics in Genome-Wide Association Studies and the Search for Genomic Determinants of Disease"

Bogdan Paşaniuc – University of Pennsylvania

"Polygenic Risk Scores for Genomic Medicine: Promises and Challenges"

Abstract. Polygenic scores (PGS) have emerged as the tool of choice for predicting complex traits and diseases in a wide range of fields from agriculture to personalized medicine. This talk will cover the promise of PGS as a predictive biomarker for genomic medicine. Contextual information (e.g., age, sex, genetic ancestries, income) needs to be accounted for in the interpretation of genomic predictions towards equitable genomic medicine. Analyzing data from large biobanks within medical systems showcases the promise and challenges of PGS as clinical tool. Results provide a path forward towards utilization of PGS as a prediction tool across all individuals.

ALEXANDRU IOAN CUZA
UNIVERSITY of IAȘI

FACULTY OF
COMPUTER SCIENCE

Luca Peruzzotti-Jametti – Senior Clinical Research Associate and Group Leader in the University of Cambridge's Department of Clinical Neurosciences, and an Honorary Neurology Consultant at Addenbrooke's Hospital

"Targeting Microglial Metabolic Dysfunction to Halt Chronic Central Nervous System Inflammation"
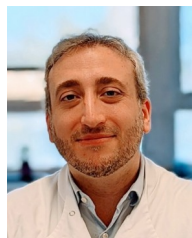
Abstract. Central nervous system (CNS) inflammation, necessary for initial injury repair, can become detrimental if unresolved, promoting a chronic inflammatory microenvironment and contributing to progressive neuropathology. Microglia, the primary resident immune cells of the CNS, are key mediators of this sustained inflammatory state in the brain. However, the precise molecular mechanisms governing the transition of microglia to chronically activated, pro-inflammatory, detrimental phenotypes remain incompletely elucidated. We have identified a critical role for mitochondrial metabolism in this process. Specifically, we demonstrate that chronically activated microglia exhibit significant mitochondrial dysfunction characterized by impaired oxidative phosphorylation efficiency, dysregulated mitochondrial complex expression, and perturbations in tricarboxylic acid cycle metabolism resulting in the release of intermediate metabolites. Importantly, we demonstrate that targeted pharmacological modulation of microglial mitochondrial function at multiple regulatory sites can effectively re-establish normal microglial functions. This novel immunometabolic approach offers a novel avenue for therapeutic intervention in debilitating neuroinflammatory and neurodegenerative diseases.

George Vassiliou – Professor of Haematological Medicine at the University of Cambridge, Cancer Research UK Senior Fellow and Consultant Haematologist at Cambridge University Hospitals

"Clonal haematopoiesis and leukaemia prevention"

Abstract. Each day humans produce more than 200 billion mature blood cells from 50,000-200,00 hematopoietic stem cells (HSCs). Like all somatic cells these long-lived HSCs inexorably acquire somatic mutations over time. Most mutations have no conspicuous consequences, but a small minority impart their host HSC with a fitness advantage and drive it to expand clonally. This phenomenon, known as clonal haematopoiesis (CH), becomes ubiquitous with advancing age and is associated with an increased risk of blood cancers, as well as several non-haematological diseases.

Over the last few years, we have been working to decipher the causes and consequences of CH, with a particular focus on **i)** understanding the basis of clonal expansion, **ii)** quantifying the risk of progression to blood cancer and **iii)** developing approaches to prevent such progression.

In my talk, I will describe our progress and our hope that we can make blood cancer prevention a clinical reality in our lifetime.

Irina Mohorianu – Head of Bioinformatics/ Scientific Computing @ CSCI, University of Cambridge

"RoSignOL: robust signature of Life"

The rapid development of high throughput approaches generated vast quantities of data. However, these are often underutilised due to computational or time constraints. Within the Core Bioinformatics group at CSCI, we generated a set of tools (named after birds); in this last talk, we will discuss about future projects which underline how essential a thorough computational perspective is for the analysis of biological high throughput datasets.