

LECTURE SERIES & WORKSHOPS 2022 / HYBRID
**NEXT-GENERATION OF MULTI-OMICS
RESEARCH: GOING TO THE SINGLE CELL**
INFECTION & IMMUNITY

23 FEB.
2022

* Wednesday

45' (talk)

11.00 - 11.45 am



AI for understanding molecular complexity in precision medicine

ABSTRACT

We are faced with a flood of molecular and clinical data. We are measuring interactions between various bio-molecules in and around a cell that form large, complex systems. Patient omics datasets are also increasingly becoming available. These systems-level network data provide heterogeneous, but complementary information about cells, tissues and diseases. The challenge is how to mine them collectively to answer fundamental biological and medical questions. This is nontrivial, because of computational intractability of many underlying problems on networks (also called graphs), necessitating the development of approximate algorithms (heuristic methods) for finding approximate solutions.

We develop artificial intelligence (AI) methods for extracting new biomedical knowledge from the wiring patterns of systems-level, heterogeneous biomedical networks. Our graphlet-based and other methods uncover the patterns in molecular networks and in the multi-scale organization of these networks indicative of biological function, translating the information hidden in the network topology into domain-specific knowledge. We also introduce a versatile data fusion (integration) machine learning (ML) framework to address key challenges in precision medicine from the wiring patterns of biomedical network data: better stratification of patients, prediction of driver genes in cancer, and re-purposing of approved drugs to particular patients and patient groups, including Covid-19 patients. Our new methods stem from novel network science algorithms coupled with graph-regularized non-negative matrix tri-factorization (NMTF), a machine learning technique for dimensionality reduction, inference and co-clustering of heterogeneous datasets. We utilize our new framework to develop methodologies for performing other related tasks, including disease re-classification from modern, heterogeneous molecular omic data, inferring new Gene Ontology relationships, aligning multiple molecular networks, and uncovering new cancer mechanisms.



SPEAKER

Prof. Dr. Natasa Przulj

ICREA Research Professor at Barcelona Supercomputing Center and a Full Professor of Biomedical Data Science at University College London (UCL) Computer Science Department

HOSTS:

Department of Infection and Immunity (LIH)
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RESPONSIBLE SCIENTISTS:

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