

SEMINAR ANNOUNCEMENT

Tuesday, 15th April 2025, at 10:30 am

Room "U24 – C02" - Zephyrum Building (ex U24)

Computational challenges and innovations in constructing and validating individual-specific networks for precision medicine

Speaker: Professor Kristel Van Steen, University of Liège (Belgium)

Abstract

Detailed patient characterization is fundamental to precision health, enabling targeted prevention, diagnosis, and treatment strategies. As humans function as complex biological systems, network theory provides a powerful framework for modeling personalized interactions and capturing individual variability. With the increasing availability of omics profiling and large-scale population datasets, the construction of individual-specific networks from reference population data (ISNs) has emerged as a promising approach for integrating patient-specific molecular and biological interactions. However, several computational challenges arise in constructing, validating, and implementing ISNs for AI-driven inference, clinically meaningful patient stratification, and personalized drug repurposing. One major challenge is defining the system's boundaries—selecting biologically and clinically relevant nodes that contribute to informative network structures for individuals where such granularity is necessary. This selection process can be guided by AI models, such as visible neural networks or multi-view learning approaches, which use higher-order importance scores to prioritize key variables. Additionally, the choice of ISN construction methods may influence downstream analyses, raising questions about the balance between network accuracy and practical applicability for specific tasks. Addressing these challenges—particularly scalability, statistical robustness, and the impact of construction choices on downstream analyses—will be essential for advancing ISNs as a computationally feasible and biologically meaningful tool in precision medicine, offering an intermediate solution between population-level generic models and digital twins.

Short bio

Kristel Van Steen is a Professor at the University of Liège (Belgium), where she leads the BIO3 (Biostatistics, Biomedicine, Bioinformatics) group within the Molecular and Computational Biology Research Unit at the GIGA Institute. Her research positions at the intersection of translational science and systems medicine, focusing on the development and application of advanced quantitative methods to address major health challenges. Her academic journey began with a mathematics degree from the University of Ghent (Belgium) and expanded across multiple disciplines, including biostatistics (Hasselt University), statistical genetics and network medicine (Harvard University), systems medicine (KU Leuven), and genetic epidemiology - machine learning (University of Liège). Holding two PhDs—one in Exact Sciences (Geometry) and another in Biomedical Sciences (Biostatistics/Statistical Genetics)—she brings an interdisciplinary approach to precision health, integrating data science with biological insights to advance systems health. A key focus of her work is the detection of gene-gene and gene-environment interactions, as well as the development and analysis of individual-specific networks (ISNs). These networks, which capture unique biological interactions, are instrumental in understanding complex diseases such as cancer, neurodegenerative, and inflammatory disorders while offering new opportunities for drug repurposing and personalized therapies. Her research is driven by a clear multifold objective: to align biological and statistical evidence, integrate large-scale population data with individual-level precision, and translate scientific discoveries into real-world applications. With extensive training in leadership and project management, along with a strong track record in leading national and international research projects, she remains dedicated to advancing precision public health and digital health, pushing the boundaries of data-driven medicine.