

Dutch Network Science Summer Symposium 24 June 2026



Universiteit
Leiden



Extended programme

9:00 Walk-in coffee and registration

9:30 Welcome

9:40 **Ieke de Vries** (Leiden University)

Ego Networks, Crime Exposure and Victimization Experiences

Who becomes a victim of crime, and why? Victimization is rarely random. Beyond individual risk factors and neighborhood disadvantage, the people we are connected to shape our exposure to risk in ways that aggregate-level analyses cannot capture. This talk addresses how direct exposure to crime in proximate ego networks, encompassing household, family, school, neighborhood, and work ties relate to the likelihood of criminal victimization, using commercial sexual exploitation (CSE) as a critical case.

CSE represents an extreme and underexplored form of victimization in which social network processes are theoretically central yet empirically understudied. Using a population-based dataset of minors and young adults in the Netherlands (2016–2023), linked to police-recorded CSE victimization and large-scale administrative ego-network data, we identify latent profiles of network-level crime exposure, capturing the density of offending and prior victimization within individuals' immediate social environments.

To isolate network effects from individual and structural confounders, we use matching weights combined with doubly robust logistic regression, comparing CSE victims against other sex crime victims, other crime victims, and the general population. Across all comparisons, individuals embedded in high-exposure network profiles face substantially elevated victimization risk.

These findings reframe victimization as a relational phenomenon. Rather than locating risk solely in individual characteristics or spatial context, they point toward the crime-embeddedness of one's immediate social network as an independent and persistent risk pathway. The implications for follow-up analyses examining indirect ties through overlapping ego networks will be briefly discussed.

10:15 **Matteo Marsili** (ICTP Trieste)

Absolute abstraction: a renormalisation group approach

Abstraction is the process of extracting the essential features from raw data while ignoring irrelevant details. It is well known that abstraction emerges with depth in neural networks, where deep layers capture abstract characteristics of data by combining lower level features encoded in shallow layers (e.g. edges). Yet we argue that depth alone is not enough to develop truly abstract representations. We advocate that the level of abstraction crucially depends on how broad the training set is. We address the issue within a renormalisation group approach where a representation is expanded to encompass a broader set of data.

We take the unique fixed point of this transformation -- the Hierarchical Feature Model -- as a candidate for a representation which is absolutely abstract. This theoretical picture is tested in numerical experiments based on Deep Belief Networks and auto-encoders trained on data of different breadth. These show that representations in neural networks approach the Hierarchical Feature Model as the data get broader and as depth increases, in agreement with theoretical predictions.

[Reference: Carlo Orientale Caputo, Elias Seiffert, Enrico Frausin, Matteo Marsili, <https://arxiv.org/abs/2407.01656>]

10:50 Break

11:10 **Maksim Kitsak** (Delft University of Technology)

Inferring shortest and nearly shortest paths under network uncertainty.

Many dynamical processes on networks, from routing on the Internet to signal propagation in biological systems unfold along shortest or nearly shortest paths. When the underlying network is fully known, identifying shortest paths is a classical problem with a rich arsenal of efficient algorithms. In practice, however, our maps of large real-world networks are often incomplete due to measurement limitations, network dynamics, or both, rendering traditional shortest path methods inefficient.

In this talk, I will present recent and ongoing work by my group on shortest path inference in partially observed networks. We find that shortest paths in diverse real networks, including protein interaction networks and the Internet at the autonomous system level exhibit a latent-geometric organization. When nodes are embedded into latent hyperbolic spaces, shortest paths tend to align closely with geodesic curves connecting their endpoints.

This observation opens the door to a new generation of geometry-based pathfinding methods that can operate even when network maps are substantially incomplete. I will discuss recent advances toward understanding the theoretical limits of shortest-path alignment in geometric network models, the computational capabilities and limitations of network embedding approaches, and potential practical applications in cybersecurity and network medicine.

11:45 **Lightning Talk session 1**

Robbert van der Burg	Bayesian Recovery of Dependence Structures on Networks
Sámuel Balogh Gáspár	Geometric alignment and inference of shortest paths in Soft random geometric graphs
Alexander Ferraro	Aggregation Sampling Biases in Temporal Networks
Rachel de Jong	Fuzzy k-anonymity in complex networks
Elizaveta Evmenova	Country composition of Network Science
Benedetta Giovannelli	Influence of self-infection on the Markovian epsilon-SIR on the complete graph
Federico Ravazzolo	RIMA: Recursive Isolation Mean-field Approximation of SIS epidemics on networks
Kamiel Gulpen	The Cost of Interaction Aggregation in Models of Complex Contagion
Matteo D'Alessandro	Non-Markovian dynamics in COVID-19: evidence from Cyprus contact tracing data

12:30 Lunch

14:00 **Javier Garcia-Bernardo** (Utrecht University)

The Impact of Intersecting Social Contexts on Socioeconomic Outcomes

Decades of sociological research have extensively examined factors impacting socioeconomic outcomes, often emphasizing social contexts such as families, schools, or neighborhoods. However, understanding their relative importance is challenging because individuals are embedded in complex networks of these social contexts, which interact with each other and with individual characteristics to constrain or facilitate opportunities. Here, we study how children's social contexts around age 12--before tracking into secondary school--are linked to educational attainment and later income. We treat individuals as part of a multiplex network of families, classmates, schools, and neighbors, and use statistical models of increasing complexity, from linear models to graph neural networks, to examine how these contexts contribute to prediction. We then ask when these associations can be interpreted causally, using mover-based variation in peer exposure to study network effects on intergenerational mobility.

14:35 **Clelia de Mulatier** (University of Amsterdam)

Uncovering robust high-order structures in noisy data with spin models: simplicity matters!

Finding the model that best captures patterns hidden within noisy data is a central problem in science. In this context, the Ising model has been widely used to infer pairwise patterns in binary data. In recent years, attention has been brought to high-order patterns of data and the question of how to detect them. We will discuss the use of (classical) spin models with interactions of order higher than two to extract such patterns in binary data, and why this problem is challenging. The ideas and results discussed in this talk can also be extended to spin models for discrete data.

By analyzing the information-theoretic complexity of spin models, we will see that, despite their appearance, models with high-order interactions are not necessarily more complex than pairwise models. We identify changes of representation of the binary variables that map a spin model to another one, while preserving all its statistical properties. These models are different representations of the same abstract statistical model. This opens the path towards equivariant approaches to modeling data and underscores the importance of developing a comprehensive high-order framework for statistical inference.

We will then focus on a sub-family of spin models with minimal information-theoretic complexity, which we call Minimally Complex Models (MCMs). These models have interactions organized in a community-like manner, and we will see how this can be used to identify groups of highly correlated variables in binary data. Uncovering such community structures in noisy data is crucial to understanding emergent phenomena in many complex systems, such as the brain, or health or social systems. So far, many existing techniques rely solely on the pairwise correlation patterns of the data; in contrast, our approach takes into account all higher-order data patterns. We will demonstrate the capabilities of our approach against pairwise community detection on artificial data with built-in high-order community structures. Finally, we will discuss applications of MCMs in the context of neuroscience. Using Minimally Complex Models opens up new ways to tackle high-dimensional data modeling.

15:10 Break

15:30 **Lightning Talk session 2**

Irene Martínez	Resilience of compound road networks
Robert Jankowski	Benchmarking Hyperbolic Graph Embeddings for Link Prediction and Topology Reconstruction
Ella Has	Unlearning removed connections in random-walk-based dynamic network embedding
Yongdin Tian	Topology of Low-Loss Regions in Neural Networks

Lightning Talk session 2

Gabriella D. Franco	Impact of network adaptation driven by homophily and triadic closure on long-term opinion dynamics
Elena Candellone	Understanding political preferences and behavioural patterns across issues on DerStandard: a network embedding approach
Yunming Hui	How Users Gain Attention in Online Social Networks: Evidence from Reddit's Meme Coin Communities
Hediyeh Zabolinezhad	Identification of Hate Amplifiers in UK Immigration Discourse on Reddit Using LLMs and Network Influence Analysis

16:15 **Mike van Santvoort** (Eindhoven University of Technology)

Modelling cell-cell interactions with random graphs: a journey from biology to math and back

We present and study a mathematical framework to model cell-cell interactions in cancerous tissue. This framework is called the Random Cell-cell Interaction Generator (RaCInG) and builds random graphs that represent cellular communication based on bulk RNA-seq data. In this talk we will first formalize the framework as a Monte-Carlo algorithm, and then show that consistent biological properties can be derived from it despite relying on some random choices to generate its output. Then, we analyze this framework mathematically and show it is asymptotically equivalent to a specific version of the inhomogeneous random digraph model. Finally, we will use this asymptotic equivalence to extract a large number of biological properties from a real-life dataset and show that RaCInG is able to predict immunotherapy response within this dataset.

16:50 Best Lightning Talk Award and closing remarks

17:00 Drinks and borrel at De Fusie bar