

CSS/ITALY 2025

Monday 15 September 2025 - Wednesday 17 September 2025

Centro Polifunzionale Studenti Università di Bari



CSS/ITALY

ITALIAN CHAPTER OF
COMPLEX SYSTEMS SOCIETY



Book of Abstracts

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Heterogeneity of household stock portfolios in a national market

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Venice long data

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FROM LEGO TO TRANSCRIPTOMES: EMERGENT STATISTICAL LAWS IN COMPONENT SYSTEMS

Many complex systems exhibit a modular structure: genomes are composed of genes, books consist of words, and technological systems like LEGO sets can be broken down into elementary building blocks. Representing these as component systems—collections of discrete elements—reveals a range of quantitative regularities, often shared across domains. Among these, Zipf's law is perhaps the most well-known. In this talk, I will explore the statistical patterns that emerge in such systems and discuss possible common generative mechanisms underlying these regularities, as well as the relationships between different statistical laws. I will review several examples across domains and show how simple null models can help distinguish between universal features and system-specific behaviors. As a case study, I will focus on the cell transcriptome, treating it as a component system, and demonstrate how large-scale statistical analysis can yield biologically meaningful insights.

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On the stability of competitive ecological communities with pairwise and higher-order interactions

The emergence of biodiversity in ecological communities remains a major open question in theoretical ecology, leading to a fundamental inquiry: what mechanisms support the stability and coexistence of species within these ecosystems? Traditional ecological models have largely been based on the assumption that species primarily engage in pairwise interactions. However, interactions in ecological systems may involve groups of three or more individuals—i.e. higher-order interactions. As a result, the question of how the combined effects of pairwise and higher-order interactions shape the stability of large ecological communities remains unresolved. With this work, we address this gap by analyzing a model of competitive communities that incorporates both types of interactions at the same time. Using analytical techniques and numerical simulations, we find that higher-order interactions alone are not always sufficient to foster and maintain coexistence. When species are identical (i.e., have the same physiological rates), even a small proportion of higher-order interactions can stabilize their dynamics. However, when more realistic factors—such as heterogeneous birth and death rates or complex interaction structures—are introduced, even a large fraction of higher-order interactions may not be sufficient to achieve stable coexistence. Our findings challenge the role of higher-order interactions as a universal stabilizing mechanism in ecological communities and open new avenues for research into the interplay of different factors that underpin biodiversity and ecosystem stability.

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Complexity and data science for food security

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Integrating social and mobility information in epidemics

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Pathogen evolution in epidemics & emerging fitness landscapes

Pathogen mutations are widely understood to play a significant role in the long-term outcome of epidemics [1,2]. At the same time, the heterogeneous nature of social and mobility networks [3,4] can affect the evolution of pathogens by boosting or restraining availability of diverse hosts over different time scales. We report the results of our study on the interaction between these two dynamics with complementary approaches.

Firstly, we analyse scenarios in which evolution and epidemic spreading unfold over comparable time scales. In fact, when the two time scales are well separated, the corresponding dynamics disentangle, greatly simplifying analysis [5]. However, time scale separation does not always hold: indeed, the full complexity of these phenomena is revealed only as evolution and spreading are considered as coupled and fully dynamical processes. Thus, we propose a minimal model for within-host mutation of pathogens during epidemics, and study how the evolutionary dynamics and the spreading process affect each other. We show how the interplay of multiple time scales leads to the emergence of non-trivial patterns, comparing the qualitative predictions of our model to the empirical phenomenology of real-world pathogens' spreading.

Secondly, we focus on modelling within-host viral evolution under immune pressure as a metapopulation dynamics [6,7] on dynamical fitness landscapes [8]. Here, the landscape is represented by a random network whose nodes correspond to viable viral sequences, with links between nodes describing mutations. Moreover, each node viability will decrease sharply with its population, mimicking host immune response. We explore the phenomenology of this minimal framework, translating prior empirical and theoretical knowledge on both viral mutation and immune system [9] into model's constraints, defining the validity limits of this approach and of the insights it reveals.

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Functional Adaptations of Diatoms to Different Environments in TARA Oceans Data

Diatoms (Bacillariophyta) are key contributors to marine ecosystems and global biogeochemical cycles. Using data from the TARA Oceans project, we analyzed the environmental responses of a diatom subspecies across diverse oceanic regions. Community detection on metatranscriptomic datasets identified three distinct clusters corresponding to regions with varying temperature profiles. These clusters represent distinct ecological niches influenced by environmental gradients. To further investigate functional adaptations, we performed a cross-grained analysis by focusing on PFAM domains. Using a multinomial null model, we identified PFAM categories enriched in metagenomic (metaG) and metatranscriptomic (metaT) data within each temperature cluster, revealing differential functional dynamics. Principal Component Analysis (PCA) was applied to explore the displacement from metagenomics to metatranscriptomic data. By analyzing angular distributions within the PCA space, we uncovered associations between specific functional profiles and environmental parameters, shedding light on the mechanistic foundations of diatom adaptability across thermal gradients. This integrative approach highlights the power of combining community detection, functional analysis, and multivariate statistics to elucidate the ecological and functional strategies of marine microorganisms. These findings contribute to our understanding of how diatoms adapt to environmental changes, providing insights into their role in ocean ecosystems under varying climate scenarios.

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Calliope e health impact assessment of air pollution on health outcomes

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Explainable AI highlights pesticide pollution as a critical driver of West Nile Virus outbreaks in Italy: A One Health perspective

West Nile Virus (WNV) is a mosquito-borne zoonotic disease increasingly recognized as a public health concern across Europe, particularly due to its complex transmission dynamics influenced by climatic, environmental, and anthropogenic factors. In this study, we implemented a predictive machine learning framework integrating Random Forest classifiers and explainable artificial intelligence (XAI) techniques, specifically SHapley Additive exPlanations (SHAP), to identify critical environmental drivers of WNV outbreaks across Italian provinces from 2012 to 2024. The model incorporated diverse environmental datasets, including climatic variables, land-use patterns, pesticide

residues in surface waters, and epidemiological surveillance data. Our results demonstrated robust predictive performance, especially in temporal cross-validation (accuracy = 0.71 ± 0.01), highlighting the model's effectiveness in forecasting disease incidence. Crucially, SHAP analysis underscored the significant influence of pesticide contamination in surface waters, alongside landscape features such as grasslands and topographic flatness, in determining WNV risk. These findings emphasize the pivotal role of agricultural pesticide runoff, suggesting ecological disruptions that may facilitate mosquito proliferation and virus transmission. This research reinforces the necessity of incorporating environmental pollution data within a One Health framework to enhance early-warning systems and inform targeted public health interventions.

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Unraveling the temporal dependence of ecological interaction measures

Species interactions—ranging from direct predator-prey relationships to indirect effects shaped by environmental factors—are fundamental to maintaining ecosystem balance and biodiversity. Although various empirical measures of these interactions have been proposed, their interpretability, informativeness, and limitations in ecosystem analysis remain challenging. In this study, we focus on the empirical interaction matrix, a widely used tool, and investigate its temporal variability. Using analytical approximations, we demonstrate that fluctuations in interaction measures—often interpreted as shifts between competition and facilitation—may instead arise intrinsically from the temporal dynamics of populations with fixed ecological roles (Fig. 1, left). We further show that, while interaction measures initially reflect direct species couplings, they increasingly capture environmentally mediated effects and experimental biases over time. Thus, assessing interaction measures at multiple time points offers a richer perspective on ecosystem dynamics. This time-resolved approach enables a systematic separation of direct and indirect species relationships (Fig. 1, right). Finally, we propose a model inference method based on interaction measures, which leverages multiple short time series instead of the extended longitudinal datasets typically required.

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Antimicrobial resistance

Antimicrobial resistance (AMR) is one of the most urgent and cross-cutting challenges to public health, society and the environment, due to the increasing ability of pathogens to develop resistance to drugs. This world-spread resistance is making infections harder to treat, raising the risk of higher and higher mortality.

The One Health framework, which acknowledges the interconnectedness of human, animal and environmental health, provides an integrated approach to tackle this phenomenon on a global scale. In this context, machine learning and explainable artificial intelligence (XAI) offer powerful tools to analyze large datasets and uncover complex patterns underlying the emergence of AMR. However, to fully harness their potential, it is crucial to ensure a comprehensive and harmonized data collection at national, regional and local levels, accounting for territorial and socio-economic differences. In our research, we employ a XAI approach to identify the most influential factors driving antimicrobial resistance in diverse territorial contexts, which vary significantly in terms of climate, economic conditions and social structures. Specifically, we use a wide set of indicators defined within the One Health framework to predict country-level mortality associated with antimicrobial resistance to five key pathogens: *Acinetobacter baumannii*, *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Streptococcus pneumoniae*. Our analysis highlights the critical role of water accessibility and quality indicators in determining AMR-related mortality across countries, pointing to their potential as valuable tools for decision support and ongoing monitoring efforts.

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Laplacian lens on complex and signed networks and the onset of the spin glass behavior

Heterogeneous and complex networks represent the intertwined interactions between real-world elements or agents. Determining the multi-scale mesoscopic organization of clusters and intertwined structures is still a fundamental and open problem of complex network theory. By taking advantage of the recent Laplacian Renormalization Group [1-4] approach, we scrutinize information diffusion pathways throughout networks to shed further light on this issue. Based on inter-node communicability, our definition provides a clear-cut framework for resolving the multi-scale mesh of structures in complex networks, disentangling their intrinsic arboreal architecture. Then we move to adapt the LRG framework to signed networks up to show its usefulness to tackle the issue connected with balancing, frustration and spin glass transition [5]

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Topic modelling methods for the analysis of multi-omics data

Topic models are a set of algorithms originally developed to extract latent variables from texts corpora. The most popular of these algorithms is the so-called Latent Dirichlet Allocation (LDA) which has been successfully applied in these last years not only in texts analysis but also in bioinformatics. In fact algorithms which try to identify the topic of a given document from the word usage have to face the same type of challenges we usually face when studying gene expression data. In this analogy the cancer samples play the role of the documents, the words are the genes, the number of times a particular word is used in a given document is the analogous of the expression level of a particular gene in a given sample and the topics are the gene sets (the “signatures”) we use to cluster samples into subtypes. The goal of topic modeling is to identify the topic of a given document from the word usage within that document and exactly in the same way our goal is to identify the cancer subtype from the gene expression pattern. The major advantage of topic modeling methods with respect to standard clustering approaches is that they allow a “fuzzy” type of clustering. The output of a typical topic modeling algorithm is a probability distribution of membership i.e. the probability of a given document to be composed by a given topic and at the same time the probability of a word to characterize a given topic. In our context this means that we have as output of our analysis a set of values which quantify the probability of a given sample to belong to a particular cancer subtype

and the relevance of a given gene in driving this identification.

In this talk, after a general introduction to topic modeling and LDA I will discuss a new set of algorithms, based on a hierarchical version of Stochastic Block Modeling (hSBM) which have been recently proposed to overcome some of the problems of LDA and show a few application to cancer gene expression and multi-omics data.

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Archetypal Decomposition of Metagenomic Profiles for Cross-Study Diagnostic Classification

Shotgun metagenomics enables the quantitative profiling of microbial communities in biological samples, providing a rich, high-dimensional description of microbiota composition. These microbial profiles are increasingly used to investigate associations with host health. However, the high dimensionality of such data—thousands of microbial or functional features per sample—and the heterogeneity introduced by cross-study aggregation pose significant challenges for data analysis and interpretation.

In this work, we explore the use of Archetypal Analysis (AA) as a geometry-aware dimensionality reduction method to extract interpretable low-dimensional structure from metagenomic data, with particular application to inflammatory gastrointestinal conditions. AA approximates each sample as a convex combination of a small number of archetypes, corresponding to extreme points in the data cloud. Compared to PCA, which captures directions of maximal variance, AA emphasizes the boundary geometry of the dataset, enabling the identification of meaningful data directions in terms of compositional extremes.

We apply AA to an aggregated dataset of metagenomic profiles drawn from multiple independent studies, uniformly reprocessed through a common pipeline. Archetypes specific to individual studies can be removed to improve cross-study comparability, allowing for the construction of a robust shared representation that preserves biologically relevant information. In this reduced space, the healthy/diseased status of samples emerges naturally as a prominent axis of separation, enabling the training of a classifier with good generalization performance across studies.

These results suggest that archetypal geometry can serve as a powerful tool in microbiome-based diagnostics, particularly when data integration across studies is necessary.

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Machine-enhanced reconstruction of functional connectomes unravels discriminative brain sub-systems in health and disease

The human brain is a complex system of 100 billion neurons, each one connected on average to 10,000 other neurons to exchange electrochemical information. It is possible to coarse-grain this system by considering the average activity of large neuronal aggregates into Regions of Interest (ROIs), acting as fundamental areas in functional Magnetic Resonance Imaging (fMRI), and their co-activation patterns, providing a map of the underlying functional connectivity. The main difficulties with this approach relate to the choice of the statistical technique and arbitrary thresholds for pruning the correlation network obtained from fMRI signals. Here we tackle this challenge by switching the focus from statistical to functional pruning: instead of considering the significance of co-activation signals separately, we consider the collective co-activation patterns of whole sub-networks to choose which links to drop.

Being a hard combinatorial problem, we boost the search for solutions by means of geometric deep learning coupled to a suitable explainer. Using fMRI data from healthy and ASD subjects, we build multilayer network representations from a multi-frequency decomposition of the signals and provide robust evidence that the machine-learned sub-systemic co-activation patterns significantly improve the identification of affected individuals. Our results demonstrate how functional pruning—which is based on collective, rather than individual, co-activation patterns—provides mechanistic insights that can be reliably used to characterize brain disorders, at variance with statistical pruning. Our approach—depicted in Figure 1—is general and can be applied to find task-based biomarkers, as we demonstrate in panel H, where ASD-affected subjects show, for instance, a significant increase in the connectivity of the sub-systems related to the default mode network, which is known to be involved in the pathophysiology of the disease.

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Brain networks for clinical purposes

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Principal Component Analysis and Generalized Eigenvector Decomposition of the neurophysiology of auditory memory

Magnetoencephalography (MEG) is a neuroimaging technique that captures the magnetic fields generated by neuronal activity, offering millisecond-scale temporal resolution and fine-grained spatial information, making it ideal for exploring the complex dynamics of the human brain. In cognitive neuroscience, event-related experimental designs are commonly used to investigate how the brain processes sensory stimuli and performs cognitive tasks. However, MEG data are inherently high-dimensional and characterized by intricate spatiotemporal patterns, overlapping neural sources, artifacts, and noise, which pose significant challenges for analysis. This study addresses these challenges by developing and validating efficient, data-driven strategies to decompose and interpret complex MEG signals, with a focus on their spatiotemporal structure. Principal Component Analysis (PCA) and Generalized Eigenvector Decomposition (GED) are applied to MEG recordings from a melody recognition task designed to probe auditory memory across age groups. PCA is used to extract broadband brain networks from data averaged across participants and experimental conditions, with robustness confirmed via statistical randomization and single-subject analyses. GED isolates frequency-specific components, allowing the tracking of oscillatory mechanisms involved in memory processes, particularly those that vary with aging. A Morlet wavelet-based time-frequency analysis, followed by statistical testing, reveals consistent neural patterns across conditions and age cohorts. PCA uncovers networks in auditory cortices, medial cingulate, hippocampus, and prefrontal

areas. GED highlights age-sensitive frequency components, especially in the alpha and beta bands, frequencies linked to cognitive decline and memory efficiency. By systematically comparing results with existing neuroimaging literature and testing the methods under various computational settings, this work provides a robust framework for analyzing biologically complex, high-dimensional neurophysiological data. Importantly, the present approach avoids reliance on predefined regions of interest, allowing for an unbiased exploration of brain networks. The results show the potential of linear decomposition techniques in unveiling the biomedical relevance of spatiotemporal dynamics in MEG data, offering insights into aging-related changes in brain function.

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A collective intelligence model for swarm cooperation

The capacity of groups to accomplish complicated tasks that exceed individual skills is acknowledged in natural and human environments [1]. Animals that live in groups demonstrate complex collective behaviours that allows to fulfil fundamental biologic functionalities, such as foraging or defence from predators. In this connection, the collective intelligence of animal swarms can be mimicked by artificial systems, made of physical or virtual agents, to achieve superior performance in optimization problems [2].

Merging ingredients from meta-heuristic optimization approaches and consensus-driven methods, we introduce a collective intelligence model for the cooperation of a vehicle swarm. The model is formulated as an overdamped Langevin equation, with minor tuning parameters. The model, governing the balance between social interactions, cognitive stimuli and stochastic fluctuations leads the swarm to accomplish complex tasks, such as the optimization of multimodal functions.

The effectiveness of the model as optimization tool is tested against several static landscape functions, as well as in a simulated marine environment, where a small swarm of underwater vehicles are required to localize a pollutant source in the open sea.

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WiFi Footprints; Tracing Campus Life Through Temporal Networks

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A complex systems approach to One Health: from cells to societies

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Unveiling Complex Patterns: An Information-Theoretic Approach to High-Order Behaviors in Microarray Data

The information-theoretic framework provides valuable insights into the dynamics of correlated groups within networks. Although established methodologies exist for measuring new information, storage, and transmission, accurately quantifying changes in information remains challenging. Information change in networks pertains to redundancy and synergy among systems that collectively contain information about a specific target. Redundancy refers to the overlapping information accessible through individual source systems independently, while synergy describes information accessible only when multiple systems are jointly considered.

Partial Information Decomposition (PID) is an advanced method designed to differentiate unique, redundant, and synergistic components of shared information. These distinctions, however, cannot be directly captured through traditional information-theoretic measures alone. In this research, we utilize the PID approach on publicly accessible microarray gene expression datasets from two separate studies involving patients diagnosed with Hepatocellular Carcinoma (HCC) and Autism Spectrum Disorder (ASD).

Through comparative analysis of gene and sample synergy clusters with conventional correlation clusters, our approach reveals higher-order patterns, including differentially expressed genes and significantly enriched biological functions directly associated with disease phenotypes. These insights demonstrate how the PID approach applied to gene expression data can enhance our understanding of genetic underpinnings related to the physiological manifestations of complex diseases.

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Modeling Gentrification as a Relocation Flow-Based, Spatio-Temporal Process

Gentrification, “the rapid increase in cost and standard of living in a disadvantaged neighbourhood” , causes the relocation of lower-income inhabitants in favor of wealthier citizens[1]. Relocation is caused by socio-economic inequalities and may be influenced by the presence of amenities and infrastructures. In this work, we focus on relocation trajectories and develop an agent-based gentrification model. We model society as a mixture of agents belonging to three (Low-, Middle-, High-) income profiles, with different needs and possibilities to improve their living conditions [2]. We represent the urban system as a regular lattice, in which each cell represents a neighborhood. Agents of different types base their choice of whether to move (relocate) on the current cost of living at different spatio-temporal scales. For example, high-income agents have access to temporal information regarding the fluctuations of cost-of-living across the cells, i.e., their rate of change. These relocation strategies align with two primary socio-economic gentrification theories: the economical “Rent-Gap” theory, which attributes gentrification to the disparity between a property’s actual value and its potential rent under a more lucrative use, and the sociological “Demand-Side” theory, which suggests that middle-income residents exploring new neighborhoods attract high-income individuals. The overall model outcome is a collection of relocation trajectories of the three types of agents over time, which can naturally be translated into the framework of temporal networks. Our model does not have a specific termination condition. In fact, we model gentrification as a continuous process over time to capture its emerging and reoccurring spatio-temporal patterns. Ultimately, we introduce a temporal, directed, multilayer network-based gentrification indicator, $G_i(t, \Delta)$ of a neighborhood defined as the product of the out-flow of L agents leaving the neighborhood, and the coordinated in-flow of M and H agents observed in a time window of length Δ . We thus define gentrification of neighborhood i as a period of increase of $G_i(t, \Delta)$ followed by a local maximum and decline, indicating an increase in the number of incoming M and H agents, and simultaneous increase of displaced L agents, until both flows relax to zero: the relaxation corresponds to the completion of the gentrification process in the neighborhood.

We show how such flow-based measure allows us to capture the emergence of gentrification patterns, defined as transient peaks of $G_i(t, \Delta)$, well in advance compared to other, node-wise measures, such as the ratio between the fractions of M and L income agents populating the neighborhood.

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Species Vulnerability and Ecosystem Fragility: A Dual Perspective in Food Webs

Ecosystems face intensifying threats from climate change, overexploitation, and other human pressures, emphasizing the urgent need to identify keystone species and vulnerable ones. While established network-based measures often rely on a single metric to quantify a species’ relevance, they overlook how organisms can be both carbon providers and consumers, thus playing a dual role in food webs. Here, we introduce a novel approach that assigns each species two complementary scores—an importance index quantifying their centrality as carbon source and a predatory index capturing their vulnerability. We show that species with high importance index are more likely to trigger co-extinctions upon removal, while high-predatory index species typically endure until later stages of collapse, in line with their broader prey ranges. On the other hand, low predatory index species are the most vulnerable and susceptible to extinctions. Tested on multiple food webs, our method outperforms traditional degree-based analyses and competes effectively with eigenvector-based approaches, while also providing additional insights.

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Emergence of scaling and organization in microblogging platforms: the emblematic examples of BlueSky and Truth Social

We present an analysis of the complex network structure of some microblogging platforms, comparing their internal organizations and, for the case of BlueSky, its growth during a period of massive migration from X/Twitter. Topological differences are the result of platforms’ functionalities and of individuals’ behaviors. At the same time, the sudden increase of users in BlueSky acts as a large perturbation to the platform’s dynamics and provides a unique opportunity to explore how the mesoscale organization in a decentralized environment changes, giving rise to scaling laws. Using a dataset of 21 million users, we investigate the differences introduced by the migration “shock” and compare BlueSky’s network features with those of other platforms, including Truth Social, Gab, Mastodon, Parler, and X/Twitter, as well as a previous snapshot of BlueSky updated to March 2024. Notably, BlueSky’s use of “starter packs” facilitates connectivity and may significantly impact user behavior and collective behavior. Preliminary results reveal the emergence of scaling relations between the number of followers and followees, such as $k_{in} \sim k_{out}^\mu$, which is of interest due to its effect on the bursty dynamics of online collective attention[1]. Additionally, we report on higher-order topological correlations, conveying information on the hierarchical structure[2], and (dis)similarities in mesoscale organization, such as community structure and network robustness, specifically comparing Truth Social with BlueSky. This ongoing study contributes to understanding how users behavior impacts the emergence of network topology and how the decentralized microblogging platforms adapt to external, large-scale, shocks and evolve under non-equilibrium conditions, offering insights into the interplay between structure and dynamics in complex social networks. structure of the mobility network varies depending on the approach used to model the spreading process.

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Modelling Response of Brain Activity to Perturbations

Understanding the brain's response to transcranial magnetic stimulation (TMS) is crucial for advancing both basic and clinical neuroscience. This study applies neural mass modelling to analyze TMS-evoked potentials (TEPs) through electroencephalography (EEG). Building on Momi et al. (2023) [1], who used source-localized TMS-EEG analyses to disentangle local from network dynamics, we aim to replicate and extend these findings by modelling the response from the resting state. We adopt the whole-brain Hopf model proposed by Ponce-Alvarez and Deco (2024) [2], adapting it to EEG data [3]. Our results show that this model can reproduce resting state activity in the Fourier domain, while the TMS-evoked dynamics are accurately captured in the EEG trajectory space. This highlights the model's potential in bridging spontaneous and perturbation-driven brain activity. Current efforts focus on integrating site-specific effective connectivity into the model, estimated for different TMS stimulation targets. This approach aims to capture how local connectivity profiles shape both spontaneous and evoked activity. By combining resting state dynamics with region-dependent effective connectivity, we aim to predict perturbation responses more accurately across stimulation sites. This direction holds promise for informing stimulation strategies and improving individualized neuromodulation protocols.

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A statistical study of precipitation data in Sicily: looking for signatures of climate change

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The TvL model legacy: exploring success in economics, science and sports

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Assessing the robustness of the U.S. power grid under extreme wind events

In this work we address the problem of assessing the network robustness of transportation networks due to external stressors, such as natural events. Here we focus on US power grid, but the same framework can be applied in a system where there is a physical quantity flowing through the nodes, as current in the power lines. As a stressor, we consider daily wind gust data at 10 meters above ground level, spanning from 2014 to 2023, as an external field that drives node failures as in Fig. 1 (left), according to the probability function proposed in [1].

For the dynamical model, we adopt a non-Markovian spreading mechanism introduced in [2], which we simulate over the U.S. power grid topology, denoted as W_{ij} :

$$c_i(t+1) = \sum_j T_{ij} c_j(t) + j_i^{\pm}$$

where $T_{ij} = W_{ij} c_i$ is the transfer matrix, $c_i(t)$ represents the outflow current per unit weight from node i and the last term account for possible source $j+$ or sink $j-$ contributions.

At each time step, the directed current from i to j is computed as $L_{ij} = c_i W_{ij}$, with the total load on the line is given by $C_{ij} = L_{ij} + L_{ji}$, following the mechanism proposed in [2]. In power grids, the redistribution of load following an initial failure can trigger secondary failures, potentially leading to cascading failures. To model this, we impose that each line has a maximum capacity $C_{ij}^{\max} = (1 + \alpha) C_{ij}^0$, which is proportional to the initial load on the line C_{ij}^0 and to a tolerance parameter α . If a power line fails due to strong wind, the transfer matrix in Eq. (1) is updated accordingly, and the dynamics evolve until equilibrium is reached.

Finally, we validate our approach using a dataset of historical power outages in the U.S. We apply our framework to predict the number of people affected by outages during extreme weather events, as shown in Fig. 1 (right). Our model achieves a significant Spearman correlation of 0.37, demonstrating that, despite its simplicity, it aligns with real-world observations. This framework has potential applications in real-time network control and optimization, particularly for large-scale systems where using more detailed models would be computationally unfeasible.

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Quantifying biases in reconstructed brain networks

Brain network reconstruction from neuroimaging data is subject to sources of systematic bias. One can arise from the arbitrariness introduced by thresholding procedures used in typical structural and functional network reconstruction techniques. The produced connectivity matrices exhibit variable density, which has been shown to impact the evaluation of many graph metrics [1]. Additionally, potential biases in the estimation of network descriptors may arise depending on the type of statistical approach used to handle the variability across subjects, particularly when attempting to estimate quantities from systems with probabilistic or fluctuating characteristics. In statistical mechanics, the evaluation of a metric can be seen as the application of a highly complex and non-linear function f of the adjacency matrix. In such a case, there is a difference between the exact equation for the model on a sparse network and its mean-field approximation, according to the so-called Jensen's inequality [2].

Here, we quantify how different types of bias impact network measures at macro-, meso-, and micro-scales, analyzing their dependence on network density.

Specifically, we analyzed a group mean approach, where a network descriptor is estimated from the average connectome, and an ensemble mean approach, where a network descriptor is evaluated from each individual connectome and then averaged (see Fig 1 A-B). For cases that can be treated analytically, we estimate the explicit dependence of topological metrics on network density and we assess the magnitude of the difference between the estimates obtained using different statistical methods. Our analytical results demonstrate that global clustering coefficient estimates have an explicit dependence on network density that is maintained regardless of the statistical approach. Results are confirmed and generalized for a set of measures at different scales through the analysis of neuroimaging data and synthetic network ensembles preserving specific features of real networks. In functional connectomes, we find that the statistical approach affects estimates for all the selected metrics and the difference depends on network density. Furthermore, for high-density values, the results are reconciled, but they are not statistically different from random networks (see Fig 1C). Our findings set limits on analyses based on the thresholding of connectomes – and more generally, of graphs where edges are defined by correlations – while calling for caution in interpreting results.

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Data-Driven Resilience Analysis of the Foggia Road Network under Targeted Bridge Attack Scenarios Using Complex Network Theory

This research applies complex network theory to investigate the resilience of provincial road networks, focusing on Foggia Province in southern Italy. Foggia was selected due to its critical role in regional logistics and its vulnerability to disruptions caused by environmental hazards such as earthquakes. Road infrastructure resilience is essential for sustaining economic and social systems, as these networks support goods and passenger transit. Bridges are often critical points in road networks, and their failure can severely impact connectivity [1]. This research implements a large segmented road network to examine localized disruptions and their impact on connectivity, even in small-scale failures.

Resilience is the network's ability to recover from localized disruptions while maintaining functionality. In this study, road segments are represented as edges, and their start and end points as nodes. To identify vulnerable bridges in the event of earthquakes, empirical fragility curves from the RISK-UE project were used [2]. These curves estimate damage probabilities based on material, span continuity, and seismic parameters. Road data were extracted from OpenStreetMap and preprocessed using the GeoPandas library, incorporating street hierarchies (highways, primary roads, local roads) and bridge data. The effects of failures were evaluated by monitoring changes in quantitative metrics like global efficiency and average shortest path length before and after edge removal.

This study highlights how localized disruptions, such as critical bridge failures, can have broader network-wide impacts. Preliminary results show that a few highways act as primary connectors in Foggia's network, while local roads play a crucial role in maintaining regional connectivity under stress. The methodology identifies network vulnerabilities and offers guidance for targeted infrastructure investments to improve resilience. The framework can be universally applied to different network topologies. Future work will expand this approach to include road quality, maintenance, and traffic congestion.

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Exploring the linkages between cancer incidence and socio-economic well-being with complex networks and machine learning

In recent years, network science predictive methods leveraging artificial intelligence have gained particular prominence in big data analysis. Among the various implementations of these tools, they have proven particularly useful for monitoring and predicting socioeconomic and health-related phenomena, uncovering intriguing and non-intuitive patterns [1]. In this way, a consensus began to prevail within the international community that global challenges can only be effectively addressed by mitigating factors such as poverty, inequality, and severe diseases on a global scale. This perspective underlies the establishment of the United Nations' 2030 Agenda for Sustainable Development, which sets forth the Sustainable Development Goals (SDGs) [2].

In this work, we explore the association of cancer incidence recorded by WHO in 2022 [3] and a variety of SDGs indicators about the social, economic, and environmental status of UN member states (UNMS). To choose relevant indicators for prediction, we construct a weighted complex network, where nodes are SDG indicators, and links correspond to statistically significant correlations between indicators, calculated from 2022 data recorded across UNMS. Applying the disparity filter [4], we reduce network complexity by preserving significant connections while eliminating statistically weak links. After performing community detection through modularity optimization [5], we select the most representative node in each community. We then develop a regression model using XGBoost to predict cancer incidence rates using as independent variables these selected indicators. Our model is able to explain 60% of the variance in cancer incidence (measured on the test set).

More interestingly, our results show how various social, economic, and environmental factors contribute to explaining cancer incidence. The SHAP analysis in Figure 1 highlights the SDG indicators that most influence the prediction of the WHO All Cancer incidence indicator. Some indicators as "Proportion of tariff lines applied to imports with zero-tariff (%)" (SDG 10) and "National Biodiversity Strategy" (SDG 9) reflect, respectively, the socio-economic status of a country and its strategic actions taken to control invasive species and protect ecosystems. Furthermore, several SHAP indicators are related to water resources (SDG 6). These SDG indicators underscore the importance of both natural and artificial water sources. Specifically, they measure changes in the surface water area of artificial reservoirs, a critical factor in preventing droughts, enhancing water resource management, and improving public sanitation and hygiene conditions.

We are now further analyzing these interesting but not necessarily intuitive results in order to gain a better understanding of these complex interactions. In future work, we also aim at applying this method to different types of cancers to investigate potential differences in the role of the various social, economic and environmental factors.

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Incorporating Structure of Interactions and Effective Learning in Random Neural Networks

The collective dynamics of complex systems such as neural circuits are shaped by how their units interact. Theoretical models of recurrent neural networks (RNNs) with random interactions have been investigated by dynamical mean field theory (DMFT) to derive fundamental properties of their dynamics such as the onset of chaos. However, the fully-interacting systems considered in previous studies diverges from the biological realism, as neural circuits exhibit a significant structural heterogeneity. In this work, we introduce degree-dependent connectivity structure in RNNs by drawing node degrees from a lognormal distribution, consistent with a large amount of empirical data [1]. We extend DMFT to account for both randomness in interaction strength and structured connectivity, deriving an effective dynamical equation for a neuron of given degree. Linear stability analysis reveals that the critical coupling strength for the transition to chaos depends inversely on the coefficient of variation of the degree distribution. Hence, greater degree heterogeneity lowers network stability. Moreover, the eigenvalue spectrum of the stability matrix reveals that heterogeneous networks exhibit nonuniform spectral density, with unstable modes localized in high-degree nodes that drive the dynamics of the network. Importantly, incorporating learning-induced positive symmetric weight correlations introduces a non-Markovian memory term to the dynamical equations. The effect on the dynamics is shown to be equivalent of effective recurrent self-interactions [2], with magnitude proportional to the number of connections of the nodes. Remarkably, a partially-symmetric and heterogeneous structure of interactions generates the emergence of a long-tailed distribution of intrinsic timescales as observed in cortical circuits [3], with temporal activity of high-degree nodes fluctuating over slower timescales. Our findings suggest that heterogeneous structure of interactions and effective learning provide a biologically plausible microscopic mechanism to explain the complex temporal dynamics spanning over multiple timescales, while providing a theoretical framework to predict the structural functional relation in real neural circuits.

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DECODING THE MIND: UNSUPERVISED LEARNING FOR MENTAL DISORDER DIAGNOSIS

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Diagnosing mental disorders remains one of the most intricate challenges in neuroscience and clinical practice. Unlike many physical illnesses, mental health conditions often lack well-defined biological markers or clear-cut diagnostic thresholds. Instead, diagnoses are typically informed by subjective assessments, behavioral evaluations, and social indicators, making the process highly dependent on the clinician’s experience and judgment. Compounding this complexity is the nature of the brain itself: a highly dynamic and interconnected system, where even subtle variations in neural activity can reflect significant cognitive or behavioral differences. Technologies like functional Magnetic Resonance Imaging (fMRI) allow researchers to capture snapshots of this activity, but the high-dimensional, noisy, and temporally complex data they produce require sophisticated analytical approaches to extract meaningful patterns.

In this study, we explore the use of unsupervised contrastive learning techniques to identify latent neural structures associated with mental health conditions, specifically autism spectrum disorder. The data consists of multiplex brain networks derived from fMRI scans [1], where each subject is represented as a 12-layer graph with 264 regions of interest (ROIs) as nodes. Unlike supervised approaches that rely on diagnostic labels—which are themselves subject to

ambiguity and inconsistency—our method seeks to uncover intrinsic patterns in the data without label information, thereby avoiding potential bias and enabling a more objective analysis.

A central innovation of our approach is the generation of positive sample pairs for contrastive learning in the absence of explicit features or labels. To this end, we employ a link prediction mechanism that operates mainly on the graph topology. Given a subject's brain network (represented as a node embeddings pooling in the latent space), we use a shared GAT to map nodes in the embedding space in order to identify links that are likely to exist within the same distribution, effectively synthesizing structurally similar yet independent graph instances. These positive pairs allow the model to learn representations that bring similar network topologies closer in the embedding space, while naturally pushing dissimilar ones apart.

This structure-aware training strategy enables the model to capture meaningful connectivity patterns that correlate with mental health conditions, without requiring hand-crafted features or domain-specific annotations. Additionally, the model's design ensures that the learning process focuses exclusively on the underlying graph structure, thus enhancing its generalizability to different data sources and mental health scenarios. Validation across multiple datasets, including real-world network collections and citation graphs like CORA, further demonstrates the method's robustness and versatility. In particular, embeddings generated from real-world networks show clear class separation, as illustrated in Figure 1, highlighting the ability of the model to learn discriminative representations even in an unsupervised setting.

Our findings suggest that unsupervised graph-based contrastive learning offers a promising direction for developing data-driven, interpretable tools to support mental disorder diagnostics, potentially contributing to more standardized and reproducible assessments in clinical neuroscience.

Figure 1: Plot of the embedding of the real world networks after the model training.

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