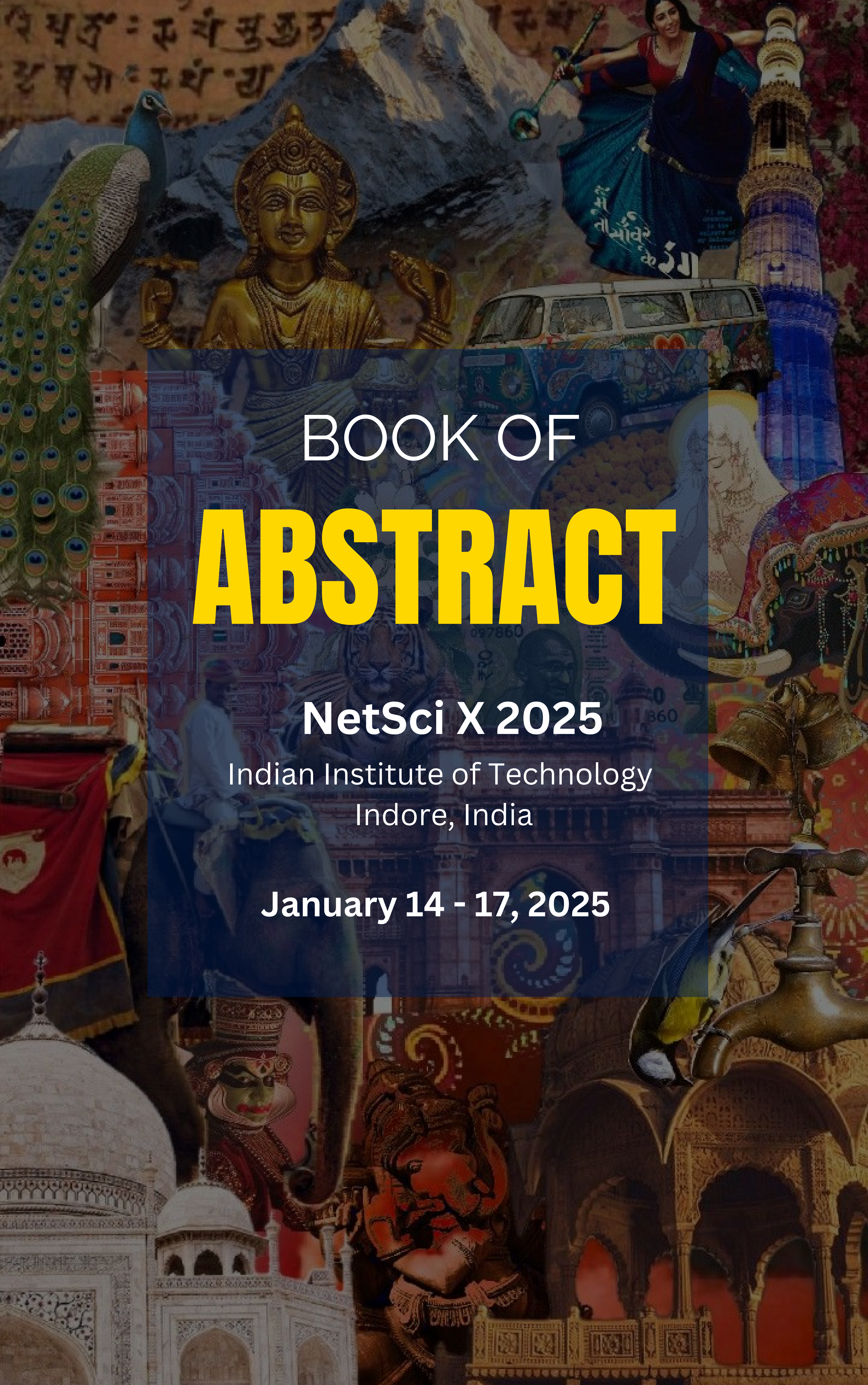

BOOK OF
ABSTRACT

NetSci X 2025

Indian Institute of Technology
Indore, India

January 14 - 17, 2025

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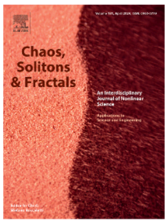

Chaos,
Solitons
& Fractals

An Interdisciplinary
Journal of Nonlinear
Science

CENTRO RICERCHE
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MINISTRY OF SCIENCE AND TECHNOLOGY

सत्यमेव जयते

जैवप्रौद्योगिकी विभाग
DEPARTMENT OF
BIOTECHNOLOGY

Table of Contents:

Plenary Talks

Inaugural Talk

Networks and Dynamical Systems

M. Lakshmanan
Department of Nonlinear Dynamics
School of Physics
Bharathidasan University
Tiruchirappalli, India.

In my talk, I will make a brief overview of the following aspects.

- Network of Fermi-Pasta-Ulam anharmonic lattice and the emergence of concepts of solitons and Hamilton chaos.
- Bifurcations and chaos in dissipative oscillators and collective dynamical states in coupled oscillator networks.
- Neuronal dynamics and artificial neural networks.
- Coupled nonlinear circuits and cellular neural networks.

I also hope to indicate the contributions of Indian scientists in the above context.

Keynote Talks

Network dynamics and the shape epidemics

Samuel Scarpino
Northeastern University, USA

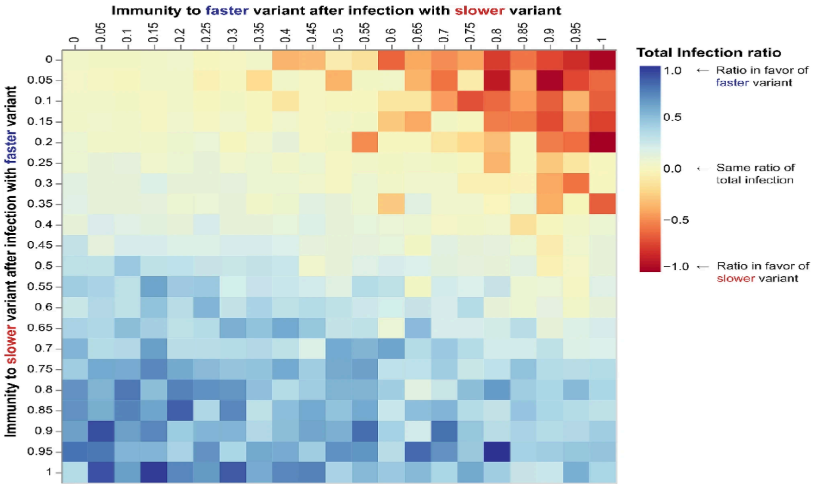
Epidemics emerge from the interaction of host and pathogen. Despite the complicated nature of these interactions, relatively simple network-based models have broad explanatory power across a range of host\pathogen systems. Using high-resolution human population, mobility, and infection data, I discuss the mechanisms underlying both the regularity and breakdown in predictability we see in epidemic dynamics. Next, by studying the neural network embeddings of over 60,000 historical infectious disease outbreaks, I describe the shape of past epidemics and determine how they map onto the network models discussed earlier in the talk. Finally, I outline a research agenda focused on creating a universal classification framework for epidemics and leveraging that framework to mitigate the risk of future pandemics.

Using an interaction-driven contagion model to understand the temporal dynamics of disease spread

Osnat Mokryn
Information Systems, University of Haifa, Israel

In this keynote, I will explore how interaction-driven models enhance our understanding of the temporal dynamics in disease spread, with a focus on airborne pathogens like SARS-CoV-2. By analyzing the timing and duration of social interactions, we show that temporal distancing strategies, such as time dilation, can more effectively slow transmission compared to traditional spatial methods. Incorporating in the model factors such as meeting duration and individual susceptibility to disease progression, we provide new insights into viral competition and asymptomatic transmission, highlighting the value of interaction-driven approaches in developing more effective public health interventions.

Keywords: Interaction-driven; Temporal dynamics; airborne pathogens; distancing strategies;



The transition to synchronization of networked dynamical systems

Stefano Boccaletti
CNR Institute for Complex Systems, Rome, Italy

From brain dynamics and neuronal firing, to power grids or financial markets, synchronization of networked units is the collective behavior characterizing the normal functioning of most natural and man-made systems.
As a control parameter (typically the coupling strength in each link of the network) increases, a transition occurs between a fully disordered and gaseous-like phase (where the units evolve in a totally incoherent manner) to an ordered or solid-like phase (in which, instead, all units follow the same trajectory in time). The transition between such two phases can be discontinuous and irreversible, or smooth, continuous, and reversible. The first case is known as Explosive Synchronization and refers to an abrupt onset of synchronization following an infinitesimally small change in the control parameter. The second case is the most commonly observed one and corresponds to a second-order phase transition, resulting in intermediate states emerging in between the two phases. Namely, the path to synchrony is here characterized by a sequence of events where structured states emerge made of different functional modules (or clusters), each one evolving in unison.

In my talk, I will assume that, during the transition, the synchronous solution of each cluster does not differ substantially from that of the entire network and, under such an approximation, I will introduce a (simple, effective, and limited in computational demand) method which is able to:
i) predict the entire sequence of events that are taking place during the transition,
ii) identify exactly which graph's node is belonging to each of the emergent clusters, and
iii) provide a well approximated calculation of the critical coupling strength value at which each of such clusters is observed to synchronize.
I will also demonstrate that, under the assumed approximation, the sequence of events is in fact universal, in that it is independent of the specific dynamical system operating in each network's node and depends, instead, only on the graph's structure.

Collective dynamics and path navigation of active particles

Punit Parmananda
Indian Institute of Technology, Bombay, India

Active particles harvest energy from the environment and convert it into directed motion. Examples include biological systems like bacteria, insects, animals, or synthetic systems of self-propelled rod, discs, light-induced active particles, and chemically driven systems. An elegant manifestation of chemically driven systems are Marangoni Surfers at the air–water interface. The motility of these surfers is attributed to underlying Surface Tension gradients. In this talk the collective dynamics, observed experimentally, of such systems in different network configurations will be discussed. Furthermore, the ability of these active system to exhibit pathway selection in the presence of different asymmetries will be explored.

Understanding the role of physicality in networks

Albert-Laszlo Barabasi
Northeastern University, USA

I will explore the applications of the network science toolset to physical networks, like the brain or metamaterials, which are networks whose links are physical entities that cannot cross each other. Link physicality affects both the evolution and the structure of a network, in a way that is not captured by current graph-based approaches. Yet, the existence of an exact mapping between physical networks and independent sets allows us to derive the onset of physical effects and the emergence of a jamming transition, demonstrating that physicality impacts the network structure even when the total volume of the links is negligible.

Research supported by the European Union's Horizon 2020 research and innovation program under grant agreement No 810115 - DYNASNET,.

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The geometry of dynamics on networks

Ernesto Estrada
Institute of Interdisciplinary Physics and Complex Systems, Spain

I will explore the geometry induced by dynamical processes, mainly diffusive ones, on networks. I will show how the conservative/non-conservative nature of these processes induce different types of embeddings of the networks into Euclidean spherical spaces. Using this approach and a geometrization of networks I will show how certain mechanisms of network generation, like Watts-Strogatz and Barabasi-Albert ones, create bypasses between nodes which facilitates the navigability of networks. I will show how these mechanisms complexify the structure of networks by providing several examples in the

real-world, from traffic in cities to the human brain.

Invited Talks

Emergent Networks and Hypernetworks in Electrochemical Systems

Istvan Kiss

Saint Louis University, USA

The analysis of network interactions among dynamical units and the impact of coupling on self-organized structures is a challenging task with implications for many biological and engineered systems. We explore the coupling topology that arises in electrochemical systems through various means, i.e., through coupling resistors, through external delayed feedback, and through the potential drops in a flow channel in lab-on-chip devices that accommodate chemical reactions on electrode arrays. The networks are revealed by an analysis of the synchronization patterns using an oscillatory chemical reaction (nickel electrodissolution) and are further confirmed by direct decoding through phase model analysis. Various coupling schemes, both uni- and bidirectional, positive or negative, were identified, depending on the type of physical coupling, feedback gain and delay, and the relative placement of the electrodes in the cell. The advantage of using network representation is demonstrated with a realization of heterogeneity-induced synchronization, where differences in chemical reaction properties can be leveraged to design systems that synchronize due to, and not in spite of, heterogeneities. We also show that coupling through a nonlinear delayed feedback, which is based on pairwise interactions, can be designed to induce hypernetworks, which are dependent on triplet phase differences. The findings open new avenues for network and hypernetwork based description and engineering of complex systems with heterogeneous frequencies and nonlinear interactions.

Energy efficiency of the synchronization dynamics in complex networks

Francesco Sorrentino

The University of New Mexico, USA

Synchronization occurs in many natural and artificial systems, which are often described as networks. Although synchronization requires communication between the individual systems or oscillators that form the network, the communication strategies that are responsible for synchronization are not always well understood. Most models of network synchronization assume that the individual systems that are connected are either permanently or intermittently communicating with one another. However, in most biological systems communication occurs when the individual oscillators reach a particular state, for example neurons in the brain transmit signals to the other neurons after they "fire". We investigate analytically, numerically, and experimentally network synchronization strategies that depend on the "transverse reactivity" of a synchronous oscillation, i.e., the instantaneous rate of growth of a perturbation about an oscillation. We show great advantage of such strategies both in terms of coupling expenditure and energy efficiency and propose possible application of such strategies to enhance the synchronization of technological systems.

Data-driven analysis of collective memory and attention on online social media

Yukie Sano
University of Tsukuba, Japan

With the widespread use of online social media, research on collective behavior, such as collective memory and attention, has made significant progress. Collective memory and attention play crucial roles in understanding social phenomena and cultural events. In this study, we introduce new mathematical models and indicators for quantitatively analyzing the dynamics of collective memory decay and attention through two case studies. First, we present a two-phase model using English Wikipedia page view data, capturing the shift in collective memory dynamics from exponential to power-law decay over time. This model reveals a “switching point” in memory decay, occurring 10 to 11 days after significant events with substantial societal impacts, such as obituaries or earthquakes.

Second, we propose a new indicator of collective attention derived from Twitter (now X) data related to Nippon Professional Baseball fans. This indicator quantitatively measures the diversity and focus of fan attention. It demonstrates how both positive (e.g., championships) and negative (e.g., player injuries) events influence fan attention, shedding light on fan interactions and the underlying mechanisms of collective behavior.

Finally, we compare these findings and discuss the future potential of data-driven approaches in collective behavior research, emphasizing the societal significance and applications of studying collective memory and sports fan dynamics.

Acknowledgments
This research was supported by JSPS KAKENHI Grant Number 23K28192.

Modeling Social Networks: Control, Energy, Zealots, and Statistical Dynamics

Yong Ee Hou
Nanyang Technical University, Singapore

In recent decades, complex networks have been extensively studied due to their valuable applications in modeling social systems, biological systems, and various man-made technological systems such as the internet. These networks are often represented as coupled systems of ordinary differential equations, where the state vector elements correspond to nodes or vertices in a graph, and the interactions between these elements are depicted as links or edges. The state vectors in such equations can represent a wide range of quantities, depending on the specific dynamical system being examined. In this talk, I will delve into how we can use complex networks to model social systems. I will discuss several topics such as the energy required to control a complex network, optimizing control energy with respect to target nodes, conformity behavior, the influence of zealots, and cooperative behavior in social insects.

Exploring Structural Inequalities and Collective Behaviors

Eun Lee
Pukyong National University, South korea

Structural inequality profoundly influences collective behaviors, impacting both public opinion formation and collaboration practices in academia. Specifically, correlated structures between individuals' attributes and their connectivity properties can shape the dynamics of(on) a network. We have studied how structurally correlated inequality affects various collective systems such as social contagion, perception bias, collaboration patterns, and faculty hiring networks. To address this, we apply network science using network modeling along with survey and data analysis. Our findings indicate that attribute-correlated network structures play a crucial role in social contagion, gendered gaps in collaboration patterns, and perception biases regarding minority group sizes, which can arise under extremely homophilic- (or heterophilic-) networks.

As a practical example of the cumulative effects of structurally correlated inequality, we explore faculty hiring networks, which exhibit steep hierarchies and reinforce epistemic inequalities in academia. We investigate adaptive rewiring network models that reinforce institutional prestige, and the results show that structural inequalities in real hiring networks are best reproduced by a mechanism of global placement power, where new hires are drawn from institutions based on their overall hiring influence. Conversely, network measures of biased visibility are better explained by a mechanism of local placement power, where new hires are drawn from institutions based on the number of previous hires already present at the hiring institution. This results demonstrate how the individual attribute and correlated preferences can increase the structural inequality, reinforcing the gaps between institutional prestiges. We will briefly present an extended analysis of an emerging country's higher education system to examine its reliance on Western high education, illustrating another example of how structural inequality influences collective behaviors.

Special Evening Talk

Complexity in the spotlight: Evolving Networks and their Dynamics

Ram Ramswami
IIT Delhi, India

In the past few years, prominence has been given to the study of complex systems and the study of networks, not just as a result of the award of major prizes, but more because these are of crucial importance to diverse communities of biologists, statistical physicists, social scientists, engineers, and mathematicians. It is widely accepted that complexity arises from the interplay of randomness and order both in the dynamics as well as in the interactions of the various elements of the underlying network. Temporal networks are essential if we are to address the big challenges in the coming years, especially in problems where social interactions will play a role.

In recent years the toolbox of network science has developed tremendously by including multi-layer and higher order networks Access to reliable data is a challenge. Beyond static networks, we need to understand temporal and multilayer interactions. These are essential if we are to study dynamic processes arising from time-dependent connections. The challenge of coming to grips with this complexity thus needs a multidisciplinary approach combining nonlinearity, network science, machine learning and artificial intelligence with branches of the natural sciences.

Network of Ideas

Adilson Motter
Northwestern University, USA

Over the past 25 years, network science has shown us that everything is connected: entities, people, and fields. Through the lens of networks, a growing community has been able to extract coherent understanding from complexity. In this talk, I will reflect on key developments in the network science community, highlight promising directions, and explore open research questions. Drawing from my own work, I will share perspectives on the opportunities ahead. Ultimately, I will argue that the study of networks advances our understanding of emergent phenomena and drives foundational discoveries across science, mathematics, and engineering.

Focus Session Talks

Focus session1: Multilayer and Temporal Networks

Multidimensional political polarization in online social networks: A 2-layer analysis

János Kertész [1*] , Antonio F. Peralta [1] , Gerardo Iñiguez [1] Pedro Ramaciotti [2]
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Quellenstrasse 51, 1100 Vienna, Austria
[2]CNRS, Complex Systems Institute of Paris Ile-de-France (ISC-PIF), Sciences Po médialab
84 Rue de Grenelle, 75007 Paris, France

Political polarization in online social platforms is a rapidly growing phenomenon worldwide. Despite their relevance to modern-day politics, the structure and dynamics of polarized states in digital spaces are still poorly understood. We analyze the community structure of a two-layer, interconnected network of French Twitter users from 2019, where one layer contains Members of Parliament and the other one regular users. We obtain an optimal representation of the network in a four-dimensional political opinion space by combining network embedding methods and political survey data. We find structurally cohesive groups sharing common political attitudes and relate them to the political party landscape in France. The distribution of opinions of professional politicians is narrower than that of regular users, indicating the presence of more extreme attitudes in the general population. We find that politically extreme communities interact less with other groups as compared to more centrist groups. We apply an empirically tested social influence model to the two-layer network to pinpoint interaction mechanisms that can describe the political polarization seen in data, particularly for centrist groups. Our results shed light on the social behaviors that drive digital platforms towards polarization and uncover an informative multidimensional space to assess political attitudes online.

Keywords: Multidimensional political opinions, Polarization in OSNs, Communities in multilayer networks, Opinion dynamics

Reference:

1. Antonio F. Peralta, Pedro Ramaciotti, János Kertész, and Gerardo Iñiguez: Multidimensional political polarization in online social networks, Phys. Rev. Res. 6, 013170 (2024)

Deriving Dynamical Model Equations from Temporal Network Data Using a Graph Rewriting Framework

Hiroki Sayama[1,2*], Naoki Masuda[3,4]
[1]Binghamton Center of Complex Systems, Binghamton University, Binghamton, NY 13902-6000, USA
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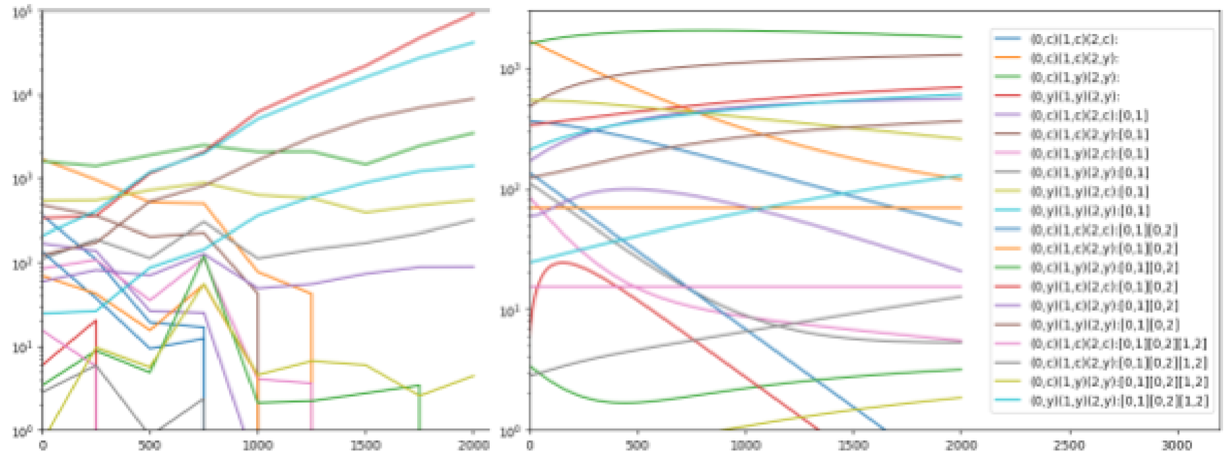
Many real-world networks dynamically change over time. Such networks are collectively referred to as temporal networks [1]. A wide variety of methods have already been developed and used for temporal network analysis, but they are predominantly descriptive so that they cannot provide dynamical, mechanistic explanation of observed network behaviors. To address this gap, here we propose a novel modeling method that derives dynamical model equations of temporal network behaviors directly from real-world temporal network data. We expect that this will help generate a more mechanistic



"understanding" of what happened in the network under investigation, offering interpretable explanations of "how" and "why" the observed temporal network behaviors occurred. The proposed method is based on an unconventional approach by describing temporal network dynamics as repeated extraction and replacement of subgraphs across time [2,3]. The dynamics of the subgraph densities and interactions are then formulated into dynamical model equations. If successful, this project will produce a novel framework with which to analyze and interpret temporal network data. We have implemented a prototype of the proposed method and tested its functionalities with small-scale synthetic temporal network data generated from a hypothetical social evolution model starting with Zachary's Karate Club (ZKC) labeled graph. The results showed that the proposed algorithm was able to successfully generate meaningful linear dynamical equations, and that the behaviors of the generated equation-based model captured aspects of the actual behavior of the temporal network (Fig. 1). The results also highlighted several limitations of the current implementation, most notably the lack of an ability to capture nonlinear interactions between (potentially overlapping) subgraphs. Strategies for overcoming these limitations and future directions will be discussed.

Figure 1: Subgraph density dynamics. Left: Actual behaviors observed in provided temporal network data (synthetic data from a simulation of a hypothetical social evolution starting with the ZKC graph). Right: Predicted behaviors using the dynamical equation-based model obtained automatically from the temporal network data. The horizontal axes show time, and the vertical ones show subgraph frequencies. Each colored line corresponds to a subgraph. While the predicted behaviors (right) differ from the actual ones (left), the subgraph densities at the end of simulation generally showed positive correlations between these two.

Keywords: Temporal networks; dynamical equations; graph rewriting systems; automatic model construction

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Robustness and Vulnerability Assessment of Multilayer Networks

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Complex networks, such as social, communication, transportation, and biological systems, are robust to random failures. If a few nodes of the system fail randomly, the network can still function effectively because the connections between the remaining nodes provide sufficient redundancy. However, these networks are typically more vulnerable to targeted attacks [1]. A targeted attack is one in which specific, critical nodes (e.g., hubs, central nodes) are attacked to disrupt the system. If these important nodes fail, it can lead to a cascade of failures or a significant degradation of performance. The vulnerability stems from the structure of the network, where some nodes play a larger role in maintaining connectivity [2, 3, 6, 9]. Real-world systems are typically not single-layered but rather consist of multiple interconnected layers. These interdependencies can be modelled as multilayer networks, where each layer represents a different set of relationships or interactions, but they all influence each other [4, 8, 7]. Multilayer networks are more complex and typically more vulnerable than single-layer networks because failure of a node or connection in one layer can lead to cascading failures across other layers. The interconnectedness between layers can amplify the effects of an attack, making the system less resilient to disturbances. In this way, multilayer networks exhibit a greater susceptibility to disruptions compared to single-layer systems [10, 11, 12]. In addition, real-world networks are often heterogeneous. This heterogeneity amplifies the vulnerability of the network, as attacks on the hubs can have a disproportionate impact on the system's performance [12]. One of the major challenges in network robustness studies is the variety of metrics used to evaluate the efficiency of different attack strategies [5]. Attack strategies are often compared using different criteria, such as disruption to connectivity, network efficiency or size of the largest connected component. Different attack strategies may prioritise different properties of the network, making it difficult to compare their effectiveness across studies. Percolation theory helps quantify network resilience, but the challenge remains in comparing various attack strategies due to differing metrics of efficiency used in the literature. This indicates that a critical and unified analysis of network robustness measures is essential.

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Information Control Systems & Technologies (ICST 2024) Odesa, Ukraine, September 23–25, 2024.

Focus session 2: Asian Network Science

Networks Down Under: Applications of Network Science in Australia

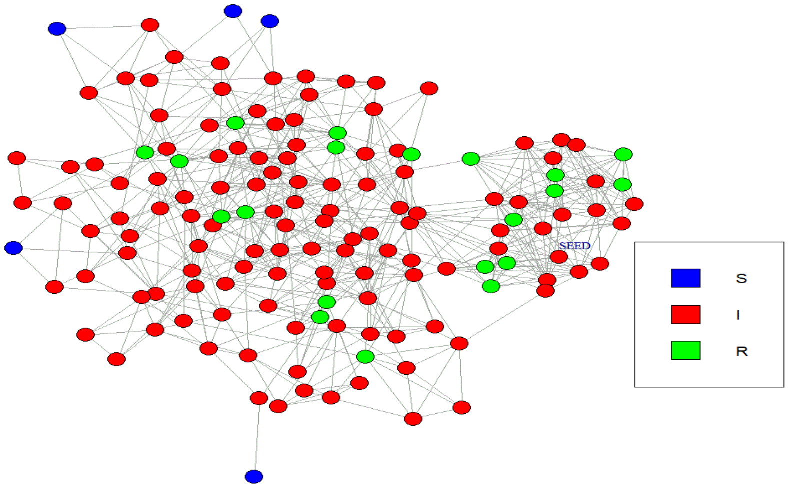
Michael Small
The University of Western Australia (UWA), Australia

This talk will provide a brief summary of some of the more interesting applications of network science being undertaken in collaboration with the Australian government and industry. Applications include modelling of disease transmission in remote and regional environments (Western Australia is one of the largest and most sparsely populated administrative region on Earth), team dynamics in Australian sport (Australian Rules Football is a rather idiosyncratic code which lends itself rather nicely to this analysis), and organisational structure in primary mental health care. These varied applications have also led to significant novel work in the ways in which we are able to model network structure and dynamics from data. This talk will also describe some of these new methodological results.

Navigating Social Networks: Insights from Viral Spread to Film Industry Dynamics

Fatimah Abdul Razak
National University of Malaysia, Malaysia

We explore the versatile applications of network analysis across various domains. First, we examine how network analysis can inform reopening strategies during the COVID-19 pandemic by modeling the complex interconnections between individuals, communities, and public health measures. Next, we analyze student friendships and peer tutor networks, revealing insights into peer learning dynamics. Additionally, we highlight the significance of animation in the Malay language film industry by mapping the interconnected web of actors. These case studies illustrate how social network analysis can provide actionable insights and guide decision-making processes in diverse real-world applications in Malaysia.



Phase Transitions in Growing Complex Networks and Their Applications

Seong Woo Son
Hanyang University, ERICA, Korea

Complex networks are ubiquitous in diverse real-world systems, from co-authorship social networks to protein interaction biological networks. Many empirical networks grow over time, increasing in both nodes and links, a characteristic shared by the first scale-free network model, Barabasi-Albert model. The percolation transition of growing random networks exhibits an infinite-order phase transition, where the giant cluster emerges continuously with infinite-order critical behavior. However, when large cluster growth is suppressed, as in the Achlioptas process, the transition type changes to the second-order. Further, when global information suppresses large cluster growth, the continuous percolation transition becomes discontinuous, with an abrupt jump in the order parameter at a delayed transition point. Consequently, infinite-order, second-order, and first-order transitions all occur within a single framework when the infinite-order phase transition of growing networks is suppressed. We present a simple argument explaining the underlying mechanism of these anomalous transition behaviors and derive an analytic form as a function of a control parameter representing suppression strength, using scaling ansatz. Finally, we discuss several applications and variations of the growing network model.

Gravitational Graph as a New Approach to Converting Spatio-Temporal Data into Complex Network

G.Cigdem YALCIN[1] and M.Berk ONDER[2]
[1]Department of Physics, Istanbul University, Istanbul, Turkiye.
[2]Institute of Graduate Studies in Sciences, Istanbul University, Istanbul, Turkiye.

Very recently, we introduced a method called "Gravitational Graph" that we developed for converting spatio-temporal data series into a complex network representation [1,2]. By analyzing spatio-temporal datasets from complex natural and human-made systems, we present a physics-based method to transform spatio-temporal data into complex network representations.
Our focus in this presentation will be on illustrating in varies fields on why there is a strong need develop a method converting spatio-temporal data series into a complex network representation. To illustrate the application of our proposed method "Gravitational Graph" in various disciplines, we will

highlight complex human-nature interacting systems. On the other hand, to better understand the underlying properties of these complex systems, for which we analyze spatio-temporal data, we will discuss topics such as interaction, adaptation, and self-organization.

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1. G.Cigdem Yalcin, Berk Onder, "Uncovering the complex network structure from spatial-temporal air quality data: A case study of Istanbul" XXXV IUPAP Conference on Computational Physics (CCP2024), Aristotle University, Thessaloniki, Greece, 7-12 July, 2024.
2. G.Cigdem Yalcin, Berk Onder, "A transformation journey of spatio-temporal data from an environmental complex system into complex network" Conference on Complex Systems 2024, Data & Complexity Science in Climate and Finance (DCSCF), Exeter University, UK, 2-6 September, 2024.

Network Structure of Transitions in Thermo-fluid Systems in Nature & Engineering

R. I. Sujith[1,2]

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[2]*Department of Aerospace Engineering, IIT Madras, Chennai 600036, India*

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Critical phenomena in natural systems such as extreme rainfall, or in engineering systems such as the occurrence of oscillatory instabilities are the result of complex interactions between several variables. We use complex networks to understand critical phenomena in nature and engineering.

The interaction of hydrodynamic, acoustic and heat release rate fluctuations in a turbulent combustor of a rocket or aeroengine leads to ruinously large amplitude periodic oscillations. This phenomenon leads to increased thermal and vibrational loads that result in structural damage causing shutdown in powerplants and mission failure in rockets [1]. We use complex networks to identify the emergent patterns during the transition from stable operation to thermoacoustic instability. Using network construction schemes such as visibility algorithm [2], recurrence networks [3] and phase space cycle networks [4], we encode the time series data of acoustic pressure onto a network. We show that the complex networks constructed during the low amplitude chaotic oscillations during the stable operation (known as combustion noise in thermoacoustics parlance) have a scale-free structure. The scale-free nature of the pressure fluctuations during the state of combustion noise disappears giving way to the emergence of order in the complex network topology as the thermoacoustic system transitions from combustion noise to thermoacoustic instability.

We construct spatial networks from flow field data. Using multilayer networks, we study the interactions between the vorticity dynamics and thermoacoustic power generated due thermoacoustic interactions in a turbulent combustor [5]. Using network measures, we identify the hubs, which are ideal locations for implementing passive control strategies. Injecting micro-jets at hubs, we succeeded in reducing the amplitude of the pressure oscillations to the levels observed during stable operation [6]. This approach paves the way for new strategies to control instabilities in thermo-fluid systems.

Extreme events such as cyclones wreak havoc on the population where landfall occurs. Using complex networks, we studied the merger of two co-rotating cyclones in the vicinity of each other to form a super-cyclone [7]. We used time-evolving unweighted directed networks constructed by quantifying the induced velocity at each location. We use *in-degree* and the *out-degree* to characterize the different stages of interaction between the two cyclones. The network measures provide precursors to the cyclone merger well before its occurrence.

The intertropical convergence zone (ITCZ) is a narrow tropical band of deep convective clouds, intense precipitation, and monsoon circulations girdling our planet. Complex interactions between the ITCZ and local geophysical dynamics result in high climate variability, making weather forecasting and predicting extreme rainfall or drought events challenging. We use complex network analysis and community detection to decipher the teleconnection patterns resulting from the complex spatio-temporal dyanmics of the ITC. We classify the tropics into seven regions based on the ITCZ dynamics.

Keywords: Extreme events, emergent order, thermoacoustic instability, climate

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Focus session 3: Noise, Networks, and Biology

Network Structure of Transitions in Thermo-fluid Systems in Nature & Engineering

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Motivated by the wide presence of multilayer networks in both natural and human-made systems, within a random matrix theory (RMT) approach, in this study we compute eigenfunction and spectral properties of multilayer directed random networks (MDRNs) in two setups composed by M layers of size N: a line and a complete graph (node-aligned multiplex network). First, we numerically demonstrate that the normalized localization length β of the eigenfunctions of MDRNs follows a simple scaling law given by $\beta = \frac{x^*}{(1+x^*)}$ with $x^* = \gamma\left(\frac{b_{eff}^2}{L}\right)^{\delta}$ with $\gamma, \delta \sim 1$ and b_{eff} being the effective bandwidth of the adjacency matrix of the network of size $L = M \times N$. Here, b_{eff} incorporates both intra– and inter–layer connectivity. Then, we show that other eigenfunction and spectral RMT measures (the inverse participation ratio of eigenfunctions, the ratio between nearest- and next-to-nearest-neighbor eigenvalue distances, and the ratio between consecutive singular-value spacings) of MDRNs also scale with x^*.

Linking Exposome and Health by leveraging Network Science

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Characterising the exposome beyond the genome is crucial for understanding the environmental factors influencing human health and disease. In this talk, I will present our research to link the chemical exposome to health effects via a systematic compilation, curation and exploration of the existing information contained in published toxicological studies on diverse groups of environmental chemicals including endocrine disrupting chemicals, environmental neurotoxicants, human milk contaminants, fragrance chemicals in children's products, vitiligo-triggering chemicals, heavy metals, plastic additives and petroleum hydrocarbons. Notably, there is recent recognition of the need to leverage data / network science, specifically, computational and systems biology approaches, in exposome research. I will present our results from such data-driven computational analyses on the compiled toxicological information for the diverse groups of environmental chemicals. One of our toxicogenomic resources and associated research on endocrine disruptors has already enabled a prominent European agency in framing chemical regulations.

Design principles of gene regulatory networks: a Boolean modeling perspective

Claus Kadelka
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Gene regulatory networks (GRNs) describe how a collection of genes governs the molecular processes within a cell. Understanding how GRNs perform particular functions and do so consistently in the face of ubiquitous variability constitutes a fundamental biological question. A clear, theory-based understanding of the mechanistic principles underlying the structure of GRNs and how the specific structure helps the regulatory networks in our cells to maintain a stable phenotype is still lacking.

In this talk, I will address these questions in the context of discrete dynamical systems, e.g. Boolean and multistate network models, which have become a popular modeling framework in the last few decades. By combining data and network science with rigorous theoretical and computational analysis, I and others identified a number of features, in which GRNs differ from “random” networks. However, all these features are correlated and interrelated, which raises the important question: which features does evolution actively select for, and why? To conclude, I will properly motivate this question and attempt to partially answer it.

Understanding and Addressing Complex Diseases through Network Based Approaches

Anshu Bhardwaj
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AB-Data Science Lab focuses on developing methods to understand complex phenotypes with specific focus on infectious and mitochondrial diseases. These methods include prediction of potential drug targets for drug resistant pathogens using network based approaches, molecular function correlations among known drug-target pairs to predict novel drug-target interactions for drug repurposing, utilizing the concept of structural alphabets towards improving genome annotation and other methods in systems biology and machine learning to elucidate the complex interplay of genotype-phenotype correlations. The talk will discuss these methods and resources and their significance in the current context. We shall also discuss novel methods of teaching like video games to simplify scientific concepts with the objective of generating awareness on some of the most pressing health challenges in the world today.

Focus session 4: Recent advancements in Network Science

How complex is to be a hub? Complexity as a proxy for the network degree distribution

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The relationship between topology and dynamics along the path to synchrony in complex networks has been thoroughly explored, and the knowledge gathered so far has driven crucial applications. However, there are cases in which the system operates in a partially or weakly synchronized regime to maintain the balance between functional integration and parallel processing, while full synchronization is pathological. Even in this incoherent state, each unit encodes the signature of its structural role in its own dynamics. We explore how this feature can be used to extract information about the network without referring to pairwise correlations, which is particularly useful when the structure is unknown [1,2].

For this purpose, we study the evolution of the k-class statistical complexity C_k in large complex networks of dynamical units. After coupling, the complexity becomes a strongly hierarchical function of the degree, persisting until system synchronization, where all nodes return to the complexity of the uncoupled state. This suggests a way to rank nodes based on time series complexity and to potentially use this correlation as a proxy for the degree sequence. The correlation between C_k and k persists across a wide range of coupling, making this method applicable in natural systems [3]. Similar results have been obtained in various other systems, and the method is robust against node heterogeneity, noise, and dynamical and topological changes, which make this approach potentially useful in fields such as neuroscience, econophysics, and power grids.

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Network Science Enhances Our Understanding of the Interplay between Epidemics and Human Mobility

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The COVID-19 pandemic significantly reshaped societal norms and mobility behaviors. In this talk, we utilize network science to demonstrate the reciprocal relationship between mobility and epidemics. Our first study examines aggregated park mobility data from Washington State, USA, analyzing a constructed visitation network and exploring its properties and the impact of socio-economic factors before and during the pandemic. Our findings underscore that high-income residents expanded their recreational activities both locally and regionally, while low-income residents limited their recreational choices. [1].

The second study introduces a mathematical framework for epidemic dynamics, integrating intra-population and inter-population mobility within a meta-population network. This framework,

termed the "Big Bang" model, allows us to identify the origin of epidemics in time and space through a novel definition of effective distance. Validated against empirical data from the COVID-19 and H1N1 outbreaks, the model reveals a universal contagion geometry, enhancing our understanding of epidemic spread [2].

Keywords: Mobility Network; Meta-population Network; Epidemics; Effective Distance;

References:

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Emergent dynamics of networks of quantum oscillators

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Understanding emergent dynamics in dissipative quantum systems has recently been a topic of extensive research. The well known dynamical manifestations of emergent dynamics of coupled oscillators, such as synchronizations and symmetry breaking are well understood in the classical domain, however, they behave differently in the quantum regime. This may be attributed to the fact that quantum oscillations are bounded by several constraints of quantum mechanics such as Heisenberg uncertainty principle and quantum mechanical entanglement. Studies on this problem require formalism from open quantum system that rely on the construction and solution of quantum master equations, which are nontrivial and thus challenging. In this talk I will systematically introduce the concept of quantum limit cycle using the open quantum formulation and discuss some intriguing emergent dynamics such as symmetry-breaking transitions [1] and quantum aging transition [2] in a network of coupled quantum oscillators.

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UNFOLDing Biological Paradoxes: Insights into Robustness, Plasticity, and Multifunctionality of Gene Regulatory Networks

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This study investigates the fundamental paradox of biological systems: their capacity for phenotypic conservation and evolutionary innovation. We address this question through computational analysis of gene regulatory networks, specifically examining the dynamics of all possible three-gene circuits. Our comprehensive simulations encompassed over 190 million distinct circuit configurations, enabling systematic classification of their functional behaviours. Our principal finding reveals that three-gene regulatory circuits are constrained to twenty distinct functional patterns despite their structural diversity. The analysis demonstrates that these circuits predominantly evolve toward stable states following a perturbation. Furthermore, each circuit exhibits multifunctional potential, capable of performing between 2 and 17 distinct functions depending on parametric conditions. We introduce UNFOLD (UNified FramewOrk for reguLatory Dynamics), a novel analytical framework for examining four critical biological properties: robustness, plasticity, evolvability, and functional canalisation. Through this framework, we demonstrate that 93.5% of network structures exhibit plasticity, while robustness can be achieved across all network structures given appropriate parameters. These findings provide significant insights into the mechanisms underlying biological systems' ability to maintain functional conservation and innovation, fundamental characteristics essential for survival and evolution.

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Community detection on geometric graphs

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In many real-world networks, such as co-authorship and social networks, the graph structure is correlated with the locations of the nodes. The geometric dependence is typically evidenced by the absence of long-distance edges and the abundance of triangles. Detecting latent communities on such geometric graphs has been an important direction of research. We consider the community recovery problem on a random geometric graph where every node has two independent labels: a location label and a community label. A geometric kernel maps the locations of pairs of nodes to probabilities. Edges are drawn between pairs of nodes based on their communities and the value of the kernel corresponding to the respective node locations. Given the graph so generated along with the location labels, the latent communities of the nodes are to be inferred. In this talk, we will look into the fundamental limits for recovering the communities in such models. Additionally, we propose a linear time algorithm (in the number of edges) and show that it recovers the communities of nodes exactly up to the information-theoretic threshold.

Networks' dependency studies in complex data sets and their financial applications

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In this talk I will discuss how tools used within Econophysics might be useful to study dependency in complex data sets [1,2]. I will introduce correlation-based information filtering networks tools, and I will show that these are powerful tools to study complex datasets, valuable tools for risk management and portfolio optimization too [3] and they allow to construct probabilistic sparse modeling for financial systems that can be used for forecasting, stress testing and risk allocation [4,5]. Finally, I will show functional hypergraphs as a further step from pairwise type of dependences' studies by providing a higher-order representation of financial market data [6].

Keywords: Econophysics; Complex systems; Complex networks; Dependency.

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Disorder in aid of Order in Networks

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We demonstrate how a collection of chaotic systems can be tamed by random coupling connections, heterogeneity in the constituent chaotic sub-systems and asynchronicity in dynamical evolution, i.e. disorder and asymmetry can induce ordered behaviour. We will discuss this phenomena in a wide class of systems, ranging from coupled oscillators to biochemical, neural and infection spreading networks. We will also show how dynamically switched random links can prevent blow-ups in coupled nonlinear systems suffering from unbounded growth. Lastly we will demonstrate that random connections can destroy chimeras, yielding more homogeneous and ordered states.

Focus session 5: Hypergraphs and Higher-order networks

Turing patterns: from network to higher-order structures

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Self-organised phenomena are widespread in Nature and have been studied for a long time in various domains, be it physics, chemistry, biology, ecology, neurophysiology, to name a few [1]. Despite the rich literature on the subject, there is still a need for understanding, analysing and predicting their emergence and behaviour.

Patterns are commonly based on local interaction rules that determine the creation and destruction of the entities, say species, at given spatial positions; on top of this, a diffusion process is at play that determines the migration of species. For this reason reaction-diffusion systems are a common framework for modelling such systems [2].

In a pioneer article, Turing considered a two-species model of morphogenesis [3]. For the first time, he established the conditions for a stable spatially homogeneous state, to migrate towards a new heterogeneous, spatially patched, equilibrium under the driving effect of diffusion, at odd with the idea that diffusion is a source of homogeneity. Even though the explanation for morphogenesis has evolved and now relies more on genetic programming, many actual results are grounded on this pioneering work. Nowadays, Turing instability goes beyond this initial framework and it can be used to explain emergence of self-organised collective patterns.

The geometry of the underlying support where the reaction-diffusion evolve, plays a relevant role in the patterned outcome, it can be because of the non flat geometry [4] (possibly growing) [5] or because of its anisotropy [6]. In several applications the underlying domain can be supposed to be divided into local patches where reactions occurs and diffusion across patches is realised via the links existing among the latter; this framework leads naturally to the introduction of reaction-diffusion systems defined on complex networks [7].

The aim of this talk is to introduce some of the recent developments we obtained with my collaborators concerning the emergence of Turing patterns on complex networks and their generalisation, such as multiplex [8, 9], time varying networks [10,11] or simplicial complexes [12]. We will focus in particular on hypergraphs [13,14] and the recently defined m-directed hypergraphs [15].

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Triadic percolation induces dynamical topological patterns in higher-order networks

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Triadic interactions are higher-order interactions that occur when a set of nodes affects the interaction between two other nodes. Examples of triadic interactions are present in the brain when glia modulate the synaptic signals among neuron pairs or when interneuron axon-axonic synapses enable presynaptic inhibition and facilitation, and in ecosystems when one or more species can affect the interaction among two other species. On random graphs, triadic percolation has been recently shown to turn percolation into a fully-fledged dynamical process in which the size of the giant component undergoes a route to chaos. However, in many real cases, triadic interactions are local and occur on spatially embedded networks. Here we show that triadic interactions in spatial networks induce a very complex spatio-temporal modulation of the giant component which gives rise to triadic percolation patterns with significantly different topology. We classify the observed patterns (stripes, octopus, and small clusters) with topological data analysis and we assess their information content (entropy and complexity). Moreover, we illustrate the multistability of the dynamics of the triadic percolation patterns and we provide a comprehensive phase diagram of the model. These results open new perspectives in percolation as they demonstrate that in presence of spatial triadic interactions, the giant component can acquire a time-varying topology. Hence, this work provides a theoretical framework that can be applied to model realistic scenarios in which the giant component is time-dependent as in neuroscience.

Renormalization and Higher-Order Interactions: Bridging Structure and Dynamics in Complex Systems

Giovanni Petri
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I will explore the interplay between renormalization techniques and higher-order correlations in both structural and dynamical models. By examining how renormalization can be extended to capture higher-order interactions in complex systems, I aim to highlight the crucial role these correlations play in shaping emergent phenomena.

Through recent advancements in higher-order network theory and models of dynamical systems, I will demonstrate how incorporating higher-order structural correlations refines our understanding of collective dynamics.

This synthesis provides a pathway to unify topological insights and renormalization group methods, offering a deeper framework for analyzing systems that exhibit both strong interdependence and hierarchical organization.

The implications for both theoretical approaches and empirical models will be discussed, with an emphasis on future research directions.

Hypermodularity and community detection in higher-order networks

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Trakia University, Bulgaria

The presence of network communities has been detected in a large number of real-world systems, such as protein networks, social networks and food webs, as well as in synthetic models of complex systems of diverse nature. In general, a community structure affects the behaviour of the system, and often one can trace a direct correspondence between the communities and structural units responsible for a specific function.

For example, communities in metabolic networks correspond to biochemical pathways. As a result, a large number of algorithms and methods have been developed to detect communities in networks [1–3]. A particularly successful approach is the maximization of a quality function that measures how pronounced a partition of a network into communities is by computing the difference between the density of the observed intra community links and that of a suitably chosen null model. One of the most celebrated such function is itself called modularity [4].

Recently, however, it has become increasingly clear that dyadic interactions only constitute a part of the important relationships that occur in many complex systems. In fact, researchers have recognized the relevance of collective interactions for the functioning of systems as diverse as social groups, neural networks and multi-species assemblages of microorganisms, sparking a new interest in higher-order structures [5, 6].Thus, the main type of structural backbone that is currently generating considerable attention is no longer that of a graph, but rather that of a hypergraph. In hypergraphs, edges do not necessarily connect pairs of elements, but rather they can connect triplets, quadruplets, or sets of nodes of any other size [7].

Unfortunately, the landscape of research on the subject of community detection in hypergraphs is not well developed, with only a few methods available, mostly dynamical [8], or based on stochastic block models [9] or using projections and extensions of exponential random graphs as a null model [10, 11]. This is probably due to the inherent difficulty of operating on a structure that requires tensor methods without projecting it. Thus, the use of a modularity measure that maintains its original sense in hypergraphs is still an open problem. Here, we introduce and characterize one such new quantity to measure and detect community structure in hypergraphs.

In a fully general case, a hypergraph H may contain edges involving different numbers of nodes. However, each edge order is independent from all the others, and they all correspond to different specific orders of many-body interactions. Thus, one can independently consider each sub-hypergraph consisting of the edges of a single order. In turn, this consideration also applies to the task of finding the structure of communities of H, since, for example, a group of nodes may form strong 3-body interactions but no significant pairwise ones. Therefore, we consider the problem on uniform hypergraphs, since a solution on them is also a solution in the general case. The idea behind classic network modularity is to exploit a measure based on the difference between the number of observed edges between two nodes and the one that would be expected if the placement of all the edges in the graph were randomized whilst keeping the degrees of the nodes unchanged. Given a partition of a network with N nodes and m edges into a set of communities, this approach results in the following expression for the modularity Q [4]:

$$Q = \frac{1}{2m}\sum_{i=1}^{N}\sum_{j=1}^{N}\left[\left(A_{i,j} - \frac{d_i d_j}{2m}\right)\delta_{C_i C_j}\right],$$

where A is the adjacency matrix, d_i is the degree of node i, δ is Kronecker's symbol and C_i is the community to which node i has been assigned. Applying the same ideas to a k-uniform hypergraph, we derive an expression for the hypermodularity of a partition:

$$Q = \frac{1}{k!m}\sum_{\{\nu_1,\nu_2,\ldots,\nu_k\}}\left[\left(A_{\nu_1,\nu_2,\ldots,\nu_k} - \frac{(k-1)!}{(km)^{k-1}}\prod_{i=1}^{k} d_{\nu_i}\right)a\prod_{i,j=1\ i\neq j}^{k}\delta_{C_{\nu_i},C_{\nu_j}}\right]. \qquad (1)$$

In the formula above, A is the adjacency tensor of the hypergraph, the combinatorial factor before the inner product accounts for the number of ways available to join nodes of given degrees in an edge, and the sum is on all the possible choices of k nodes, allowing for repetitions. Note that if the hypergraph is simple, as it is often the case in real-world structures, then one can write $A_{\nu_1,\nu_2,\ldots,\nu_k} = 1_{(\nu_1,\nu_2,\ldots,\nu_k)\in H}$, where 1 is an indicator variable whose value is 1 if the edge $(\nu_1, \nu_2, \ldots, \nu_k)$ belongs to H and 0 otherwise. Also note that, for $k = 2$, the expression reduces to that of graph modularity, which becomes therefore a special case of this more general formulation, as desired.

The principal difference between the hypermodularity of Eq. 1 and modularity for graphs is in the fact that the latter can be cast into a pure matrix equation, whereas such a manipulation is not possible in the hypergraph case. Thus, one cannot directly use the same spectral methods employed in the graph case to produce a bipartition of the network, which is a fundamental step in many community detection algorithms. However, we prove that the same information can be extracted in hypergraphs by treating the whole term within the round brackets in Eq. 1 as a data tensor B, and using higher-order singular-value decomposition methods on it. In fact, we demonstrate that the results of such methods are actually exact, and they constitute the best possible binary community assignment of the nodes in a higher-order network. Incidentally, this proof also finally provides a mathematical explanation of the success that higher-order singular-value decomposition has had when used for classification tasks in machine learning. These techniques depend on the standard flattenings $E^{(i)}$ of the tensor $\boldsymbol{B}$, which, for the specific case of hypermodularity, take the form

$$E^{(i)}_{\left(\nu_1,\nu_2,\ldots,\nu_k,\nu_1,\nu_2,\ldots,\nu_k\right),\nu_1,\nu_2,\ldots,\nu_k} = 1_{(\nu_1,\nu_2,\ldots,\nu_k)\in H} - \frac{(k-1)!}{(km)^{k-1}}\prod_{j=1}^{k} d_{\nu_j}.$$

It is straightforward to verify that the sum of all the elements of any $E^{(i)}$ vanishes. Additionally, we prove that, for simple hypergraphs, all the k possible flattenings are equal to each other, which eliminates the difficulty of a motivated choice of the specific flattening to use.

With these results, we build an iterative procedure that starts with the construction of an initial partition into two communities that maximize the value of Q. This starting point is then refined via a multi-step algorithm that includes both local and global optimization steps to efficiently search for the best overall community structure. We apply this new algorithm to both synthetic and real-world higher-order networks, demonstrating its versatility and its effectiveness in finding the best partition of a hypergraph into communities. To the best of our knowledge, our work introduces the first purely structural measure of hypergraph modularity that does not rely on projections or reductions to traditional graphs, or on the construction of simple related networks.

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Contributed Talks

Effects of edge weights on evolutionary dynamics

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1 Introduction

In constant-selection evolutionary dynamics, network structures can either amplify or suppress the spread of a fitter mutant throughout a population [1]. Most undirected and unweighted networks typically act as amplifiers under common updating rules and initial conditions [2]. This study examines how edge weights influence selection in undirected networks. We find that edge weights often reduce amplification in networks, frequently converting them into suppressors of selection [3], adding to similar suppressing effects of known variations of networks such as directed, temporal and multilayer networks, and hypergraphs (e.g., [4]).

We model the population on a static undirected weighted network with N nodes, in which each node is occupied by either a resident or a mutant. Residents have a fitness of 1, while mutants have a fitness of r. Initially, a single node, chosen uniformly at random, hosts the mutant, while the remaining $N-1$ nodes are occupied by residents.

We analyze the Birth-death (Bd) process on networks, which is commonly used in the literature [1]. In each step, a node ν reproduces with a probability proportional to its fitness, and its type replaces a neighbor ν', chosen with a probability proportional to the edge weight (ν, ν'). We also examine the death-Birth (dB) updating rule [2], where a randomly selected node ν dies, and its type is replaced by that of a neighbor ν', chosen based on fitness and edge weight.

2 Results

We analyzed fixation probabilities in six-node connected networks, exhaustively considering 112 non-isomorphic undirected connected networks. For each network, we assigned random edge weights from a uniform distribution on (0,1], generating 100 weighted networks per unweighted network. We evaluated fixation probabilities under the Bd rule with uniform initialization, classifying each as an amplifier, suppressor, or neither. Notably, we found that 3862 out of 11200 weighted networks (34.5%) were suppressors, contrasting sharply with the unweighted case, where only one of the 112 networks was a suppressor.

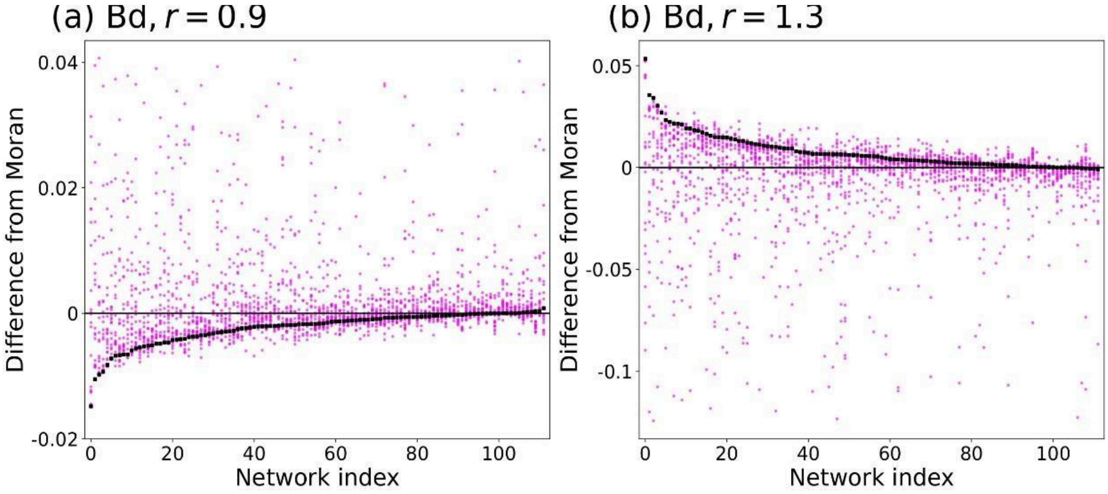

Figure 1: Fixation probability of weighted networks on six nodes for the Bd updating rule. The horizontal axis represents the index of the 112 non-isomorphic unweighted networks on six nodes. The vertical axis represents the difference from the Moran process in terms of the fixation probability. (a) r = 0.9. (b) r = 1.3. A magenta circle represents a weighted network. A black square represents the corresponding unweighted network.

Figure 1 shows that many weighted networks exhibit a positive difference in fixation probability at $r = 0.9$ (45.0%; Fig. 1(a)) and a negative difference at $r = 1.3$ (43.8%; Fig. 1(b)). These networks are strongly suggested to be suppressors of selection. In summary, adding random edge weights to undirected networks generally increases the likelihood of the network becoming more suppressing, contrasting with unweighted networks where amplifiers are more common [2]. The same trend also applies to five of the six larger empirical networks we studied. For synthetic networks with high symmetry, results are more nuanced, with weighted complete and star graphs either amplifying or suppressing depending on edge weight parameters. Overall, introducing edge weights is an effective approach to making networks more suppressing than their unweighted counterparts or the Moran process. This method aligns with other variations, such as directed, temporal and multilayer networks, and hypergraphs, which also tend to induce suppressors of selection (e.g., see [4] for temporal networks).

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Characterizing H5N1 Spread Among Cattle in the United States Using Temporal Network Modeling and Analysis

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As of August 15, 2024, Highly Pathogenic Avian Influenza (HPAI) H5N1 infections have been documented in 192 dairy cattle herds across 13 states in the U.S., spreading from Texas in the south to states in the north such as Michigan and Iowa[1]. The virus may spread within a herd on a dairy premises with an infected cow through various routes, including contaminated milking equipment or contaminated floors and bedding where animals rest[2, 3]. The drop in milk quality and production in cows following H5N1 infection and the visible sickening up to 15% of a herd raises concerns about significant losses to the dairy industry and increased risk of infection of farm workers, and the potential for the virus to evolve, increasing the risk of a human pandemic[4]. Cattle movements play a crucial role in the spread of H5N1 between dairy premises[5]. Understanding how temporal fluctuations in cattle trade movements between dairy premises in the United States impact the spatio-temporal dynamics of H5N1 is crucial for effective control of its spread while averting heavy losses to the dairy industry.

We adapt the temporal network-based SIR model described in Bajardi et al. [6], which utilized livestock displacement data in Italy, to analyze the spread of H5N1 in the United States. In our model, each dairy premises is represented as a node in a directed temporal network $G = (V,E(t))$ where V is the set of premises. We aggregate cattle trade movements on a weekly timescale ($\Delta T = 7$ *days*), where an edge $e = (u, v) \in E(t)$ between nodes $u, v \in V$ exists if cattle are moved from u to v during week t. We introduced a notion of *premises recovery period* dependent on herd size. We used 1,000 dairy network realizations from Sellman et al. (2022) [7] and simulated 1,000 epidemics per dairy network for various parameter settings, including seed infected nodes, transmission probabilities, and recovery periods. We analyzed the simulations to calculate infection risk over time (Figure 1), and evaluated the spreading potential of premises to identify temporally central nodes at different stages of the epidemic.

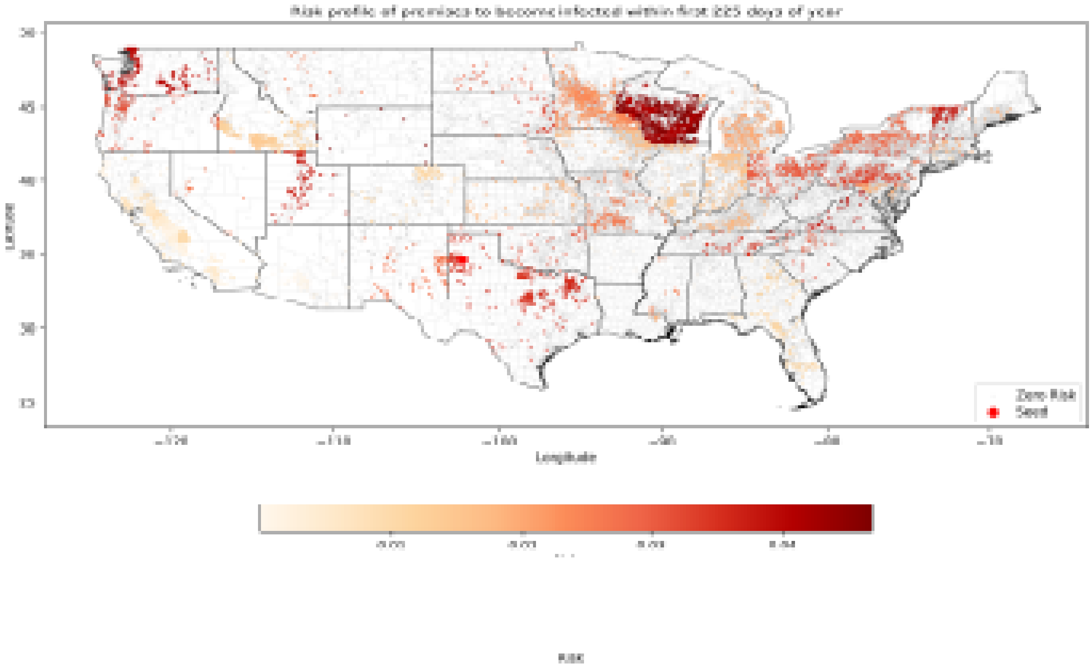

Figure 1: Risk profile of dairy cattle premises under various epidemic scenarios, starting from seed premises in Texas on January 28, 2024. Risk is shown as the fraction of simulations where a premises gets infected within 225 days. The large red circle marks the seed premises, grey dots indicate premises that remained uninfected, and other premises are color-coded by infection risk.

Keywords: temporal network epidemiology; network models; animal movement networks; H5N1

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Overlapping Communities Detection by Hypergraph Constructing

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Over the past decade, numerous methods for discovering clusters in complex networks have been developed. The primary approach focuses on defining clusters as subnetworks with a link density that is higher than average. On the other hand, in social networks, actors can define the communities they belong to without considering the network as a whole. A community is a group of actors who have formed connections within the community. Communities can be identified through an analysis of the attributes of near-neighbor actors. An actor can belong to more than one community. In a well-established community, the joint activity of actors results in a high number of triads, which leads to a high clustering coefficient. This allows communities to be detected based solely on link correlation analysis.

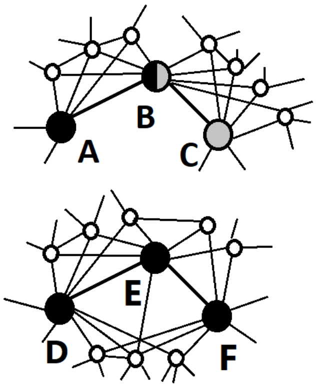

Fig. Network fragments. Depicted three nodes and all their common neighbors. c(A,B)=3/7, c(B,C)=4/10, c(A,C)=1/13, c(D,E)=4/11, c(E,F)=3/11, c(D,F)=4/13.

Let $N(i)$ be an actor i with his neighborhood. Commonality $c(i,j)$ of two actors i and j is a function of $N(i)$ and $N(j)$ so that if $c(i,j) > c_0$ these actors "for sure" belongs to the same community. The simplest commonality can be fraction of common neighbors, Jaccart index of $N(i)$ and $N(j)$.

The validity of commonality has been verified through a statistical analysis of intra- and inter-community links in real social networks with known community structures (the Karate Club, YouTube users, and DBLP authors).

In Fig. (A,B), (B,C), (D,E), (E,F) are "for sure" inner links, so these couples belongs to the same community. In Fig. actors A, C belong to distinct communities, and actor B belongs to both overlapping communities. Conversely, actors D and F belong to the same community. The threshold value c0 needs to be selected depends on links density of the network and is typically close to network's clustering coefficient value.

The simplest method to detect communities is by hypergraph constructing. Each three actors having big mutual commonality are one hypernode. (D, E, F) is a hypernode. Two hypernodes having two nodes in common are linked in hypergraph. Each connected component in the constructed hypergraph is a community.

Based on this approach, we have developed an overlapping communities detection algorithm. Starting with arbitrary chosen actor, by links commonality calculation and hypergraph constructing, can be detected all communities overlapping with the actor's community. The algorithm was applied to different real world social networks and to big networks with communities generated for testing. The effectiveness and efficiency of the algorithm has been investigated. Advantages of this approach are locality (no need for information about the entire network to detect a community) and stability (even after randomly changing a certain number of links, the same communities remain recognizable).

Keywords: overlapping communities; hypergraph; commonality; social networks.

The Evolution and Formation of Indian Political Debate Networks

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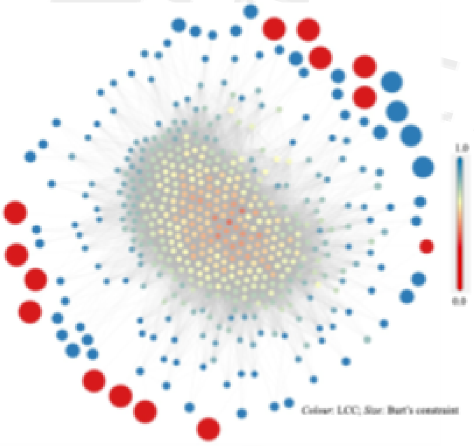

Recent studies have used tools from network science to model voting behaviour in parliaments. In this work, we explore the structure and formation of a network of debating members in the Rajya Sabha, the upper house of the Indian Parliament, for all debates between 2010 and 2021. Two members are connected if they participate in a debate during a parliament session. We implement the valued-Exponential Random Graph Model (valued-ERGM) (Krivitsky, 2012), which accounts for the frequency of debates between two members of the Rajya Sabha between 2010 and 2021. The figure presents the networks of debaters.

The input variables are the network configurations, including the *k*-core index, Burt's constraint measure, local clustering coefficient (LCC), nodal attributes of gender and educational qualification (highest degree achieved), and the homophily effects. The valued-ERGM, defined as the probability distribution function of valued link formation between Rajya Sabha members, is given as:

$$Pr\,(Y = y) = h(y)(1/\kappa)exp(\theta_1 NonZero(y,x) + \theta_2 Sum(y,x) + \theta_3 k_{core}(y,x) + \theta_4 Constraint_{Burt}(y,x)$$

$$+ \theta_5 LCC(y,x) + \theta_6 Nodefactor_{Gender}(y,x) + \theta_7 Nodematch_{Gender}(y,x) + \theta_8 Nodefactor_{HighestDegree}(y,x) + \theta_9 Nodematch_{HighestDegree}(y,x))$$

In the above valued-ERGM, the *NonZero* variable accounts for the situation where the count of debates between two members would be relatively high, even if the network were sparse. The constant term of *Sum* accounts for the likelihood of strength of two debating members without any knowledge about their nodal attributes.

We observe that the effect for Professional Graduate and Intermediate degree holders is positive and significant ($p<0.001$), while a weak significant effect exists for Post Graduates ($p<0.05$). On the contrary, strong negative effects are seen for Matriculation and Professional Post Graduates ($p<0.001$), while weak negative effect exists for Doctorate and members with no formal degree ($p<0.05$). Interestingly, no significant impact was observed among the graduate members ($p>0.05$). Focussing on members with Professional Graduate degrees, the expected number of debates between two Professional Graduates is 1.086 ($e^{0.083} = 1.086$) times those between members without any

Professional Graduate degrees. We also observe a negative coefficient for the homophily term ($p<0.01$), suggesting that debaters with similar educational qualifications are less likely to debate.

Our findings suggest that homophily of the highest educational degree has higher statistical power than gender homophily in the upper house of the bicameral parliament of India. Our research questions have policy implications for government bodies that emphasise gender diversity in decision-making.

Keywords: Network science; Political debates; Homophily; valued-ERGM

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Biologically Meaningful Regulatory Logic Enhances the Convergence Rate in Boolean Networks and Bushiness of their State Transition Graph

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Boolean models of gene regulatory networks (GRNs) have gained widespread traction as they can easily recapitulate cellular phenotypes via their attractor states. Their overall dynamics are embodied in a state transition graph (STG). Indeed, two Boolean networks (BNs) with the same network structure and attractors can have drastically different STGs depending on the type of Boolean functions (BFs) employed. Our objective here is to systematically delineate the effects of different classes of BFs on the structural features of the STG of reconstructed Boolean GRNs while keeping network structure and biological attractors fixed, and explore the characteristics of BFs that drive those features. Using 10 reconstructed Boolean GRNs, we generate ensembles that differ in BFs and compute from their STGs the dynamics' rate of contraction or 'bushiness' and rate of 'convergence', quantified with measures inspired from cellular automata (CA) that are based on the garden-of-Eden (*GoE*) states. We find that biologically meaningful BFs lead to higher STG 'bushiness' and 'convergence' than random ones. Obtaining such 'global' measures gets computationally expensive with larger network sizes, stressing the need for feasible proxies. So we adapt Wuensche's Z-parameter in CA to BFs in BNs and provide four natural variants, which, along with the average sensitivity of BFs computed at the network level, comprise our descriptors of local dynamics and we find some of them to be good proxies for bushiness.

Finally, we provide an excellent proxy for the ‘convergence’ based on computing transient lengths originating at random states rather than *GoE* states.

Keywords: gene regulatory networks (GRNs); network sensitivity; *G*-density; *Z*-parameter

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Who is driving the conversation? Analyzing the nodality of British MPs and journalists on online platforms

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In political science, *nodality* —the capacity to share and receive information—is one of the key tools that government uses to make policy [1]. Nodality used to be something that government possessed almost by virtue of being government, as the “water mill” at the centre of society’s information networks. But in a digital era, governmental actors face greater competition for nodality. Widespread use of the internet means that journalists, public figures and even citizens themselves can acquire nodality, which can challenge the government’s capacity to capture public attention and to communicate efficiently with society at large [2]. In every policy related conversation, there is constant jostling for position, the nodality of an agent needs to be seen *with respect* to the other agents, and governmental actors have no monopoly on nodality.

Framed within the context of policy making in the UK, we seek to analyse the nodality of actors on online platforms to determine how they fare in the competition for public attention. Specifically, we compute the nodality scores of individual actors —581 MPs and 8606 journalists on Twitter (now X) in conversations related to four policy-related topics: 1) the Russia-Ukraine War, 2) the cost-of-living crisis, 3) brexit and 4) the COVID-19 pandemic. As a first step, we observe the information networks and find that some actors (with senior parliamentary positions) consistently appear central in all four conversations, while some other actors (with less prominent roles in the parliament) sporadically appear central in some networks (e.g., Zarah Sultana, a back-bench Labour MP, appears central only in the cost-of-living crisis network). Thus we hypothesise that nodality can have multiple dimensions where it can either be: (i) inherent to an actor —transferable across topics and typically reflects their institutional status, or it can be gained through (ii) topic-related activity (termed active nodality). To capture both dimensions of nodality, we construct an information network for each topic and a corresponding null network that captures remaining interactions between the actors, and we perform a PCA using node measures across both networks (Fig 1). We use an eigenvector test to ensure that PC1 captures the inherent nodality of actors, and PC2 captures the residual topic-related nodality and a k-means++ clustering is used to group actors into 3 clusters [3]. Plotting the networks with the cluster memberships, we find that each cluster forms a tier in the network. Specifically, we find that information flows from the central *Leaders* (with high inherent nodality), through the intermediate *Funnelers* to the peripheral *Receivers*. This result is further supported by a transfer-entropy analysis of their activity time-series where we observe that *Leaders* consistently have the highest share of influence over the activity of others across all four topics. Finally, we bring our findings together in a regression model where we show that the capacity of a group to influence the activity of others and to drive a conversation is significantly (and positively) related to their mean inherent and active nodalities.

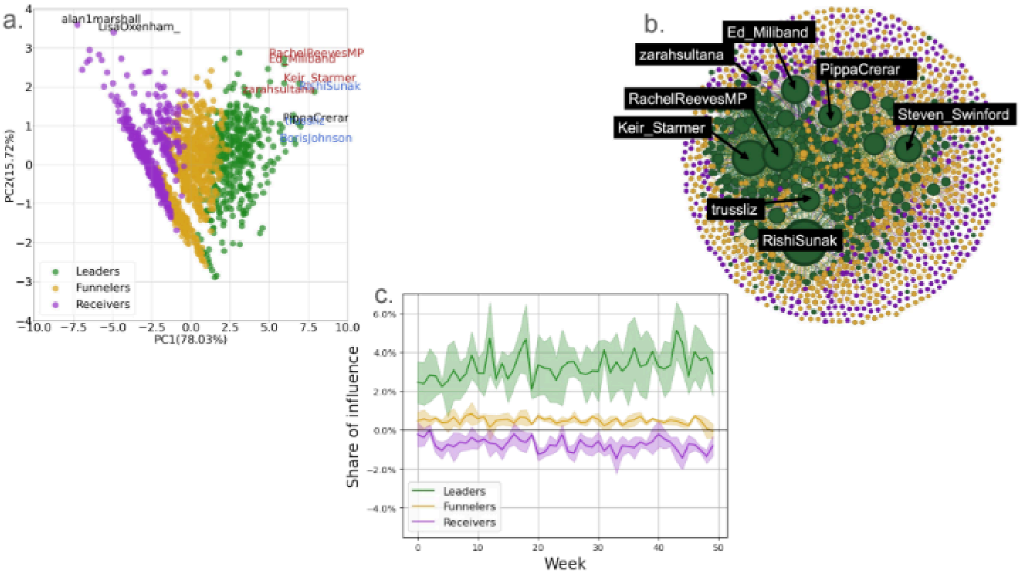

Figure 1: Figure showing (a) the PCA results for the cost-of-living crisis topic, (b) the information network for the cost-of-living crisis topic where the colour of the node represents the cluster membership (whether the node belongs to *Leader*, *Funneler* or *Receiver* cluster) and node size is representative of the out-degree of the node (i.e. how often the actor is engaged with —retweeted/ mentioned/replied to), and (c) results of the transfer entropy analysis that shows the influence of each cluster on the activity of the rest of the population across all four topics (the line plot represents the mean across all topics while the shaded region represents the standard deviation).

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Epidemics on Evolving Scale-free Graphs are Critical

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The evolution of epidemics and other contact processes depends on the interaction network between individuals. However, realistic networks are typically dynamic and change over time. Here, we show that taking into account random shuffling of the network, a SIR-like epidemic becomes critical. Specifically, in any scale-free graph with infinite variance, periodic redrawing of degrees and the underling graph, leads, in the limit of an infinite graph and with probability one, to a reproduction number that, averaged over time, converges to one. In other words, the dynamics evolve into the critical threshold between exponential expansion and decay. Criticality is obtained through a self-organization mechanism and does not require any feedback between the state of the epidemic and the behaviour of individuals. Consequently, asymptotically the entire population is infected. This dynamic occurs for all parameter values. Our results provide a new possible explanation why some epidemics, in their final stages, do not decay exponentially as expected, but rather appear endemic over long timescales.

Keywords: SIR model; Random graphs; Dynamic networks; Criticality.

Firm-level systemic risk on reconstructed production networks

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Production networks are formed by firms that purchase goods from other firms as input for their own production. These networks amplify economic growth and technological improvements [3, 11] and are at the basis of our society's well-being. However, they also play a crucial role in the propagation and amplification of economic shocks, and their fragility has been highlighted by several recent crises – the paramount example being the Covid-19 pandemics [1, 10, 8, 2]. Measuring the resilience of production networks and assessing the large-scale effects of supply chain disruptions requires detailed data on who supplies what to whom. Such comprehensive and disaggregated data is, however, usually confidential and thus seldom available [4]. Reconstruction methods can overcome this problem by predicting the most likely configurations of the network starting from the aggregate information that is easier to obtain [12].

In this work we test whether network reconstruction methods rooted in the Maximum Entropy framework, appropriately formulated for production networks, can correctly infer the economic systemic risk generated by individual firms. In particular we consider the density-corrected Gravity Model (dcGM) [5], the Input-Output scGM (IO scGM) and the stripe-corrected Gravity Model (scGM) [9], which require increasingly detailed information about the network. As case study we consider the Ecuadorian production network, accessed through a unique dataset provided by the Ecuadorian Tax Office. We measure the economic systemic risk index (ESRI) [6], a shock propagation dynamic on the production network based on a generalized Leontief production function, quantifying the total disruption on the economy caused by the failure of each individual firm.

We show that to statistically reproduce the systemic risk properties of the Ecuadorian network, the reconstruction method must constrain the input and output relationships of firms aggregated by sector (as the scGM does). The latter information can also be estimated using flows between industrial sectors to rescale firms' aggregate exposures (as in the IO scGM). Thanks to this (very limited) information on the system, we obtain a remarkable agreement between empirical and reconstructed ESRI of each firm (Figure 1). In particular, we are able to reconstruct the ESRI plateau, namely the set of firms whose failure would constitute a major threat to the economy. Notably, the agreement between empirical and reconstructed ESRI improves when we aggregate firms into sectors, while using directly aggregate input-output data to obtain sector-level risk leads to largely incorrect estimates [7]. Our findings shed light on the minimum amount of information that firms should disclose to regulators, in order to generate realistic synthetic production networks capable of capturing the systemic risk of an economy.

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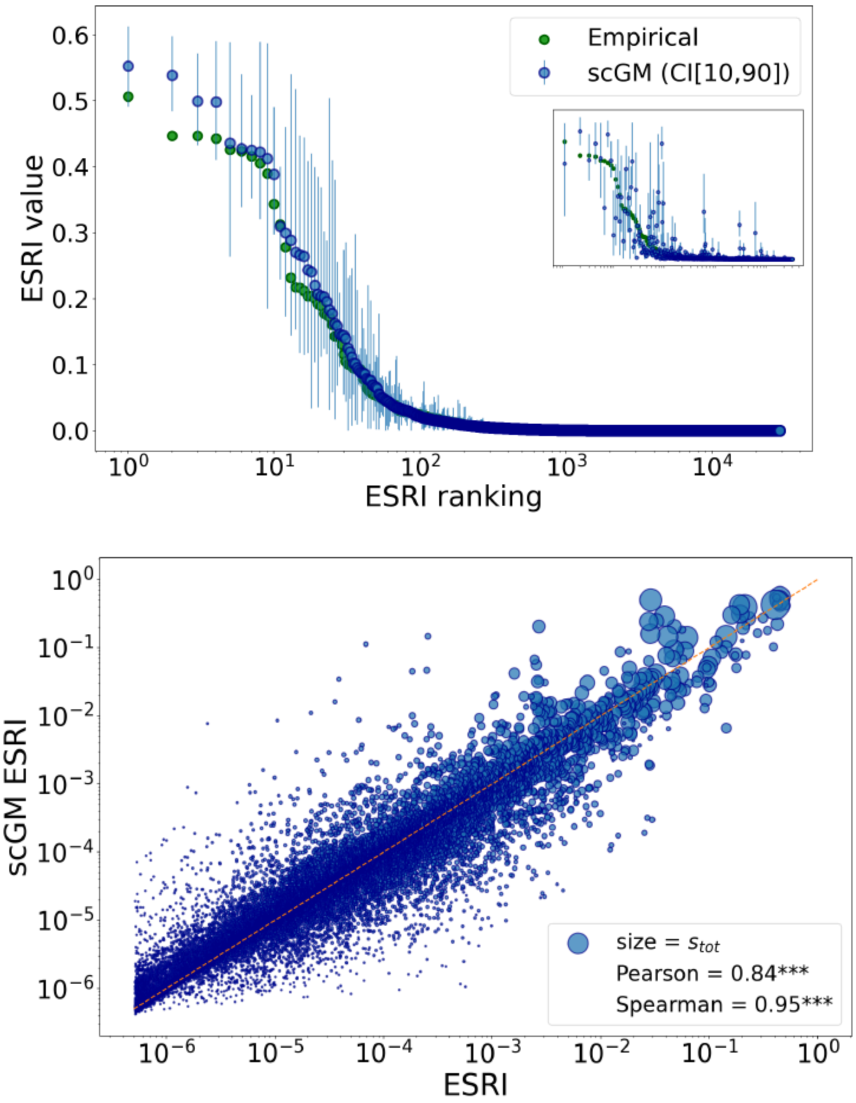

Figure 1: (Top) Empirical ERSI values versus those reconstructed by the scGM, for all the firms in the network. The two quantities are highly correlated, both in terms of values (Pearson = 0.84) and, particularly, in terms of rankings (Spearman = 0.95). (Bottom) Empirical and scGM values of ESRI ordered with their ranking. The model correctly predicts the presence of a plateau composed by the most risky firms, which is very close in value to the empirical one. Additionally the model is able to recover 7 out of the top 10 firms of the empirical plateau – as evident when reordering the scGM ESRI values according to the empirical ranking (inset).

Network Analysis of Odour Experiences in Urban Environments: Insights from the Smell Vancouver Project

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Urban odours are more than a nuisance; they significantly impact health, well-being, quality of life, and the economic value of properties. However, addressing odours and their impacts poses challenges due to differences in individual sensitivity and perception, atmospheric dynamics, and the emissions of odours as mixtures of odorous contaminants. The Smell Vancouver (SmellVan) project leverages crowdsourced data to map the urban odour landscape. Over a 4-year period, the SmellVan web application (https://smell-vancouver.ca/) has collected over 3000 odour reports from residents across Metro Vancouver. These reports include spatiotemporal information, descriptions of odours (O), symptoms experienced (S), actions taken in response (A), suspected causes (C), and demographic details. This study aims to unravel the complex OSAC networks in the SmellVan data.

Here, we conducted thematic analysis by coding the descriptive text for OSAC, generating high-level OSAC categories based on the text. Then, we conducted textual pairwise correlation analysis and hierarchical (divisive) clustering analysis for trinary (e.g., co-occurrence of an odour, a symptom, and a suspected cause) and quaternary associations (e.g., co-occurrence of an odour, a symptom, an action, and a suspected cause). To better understand the binary (e.g., co-occurrence of an odour and a symptom) and higher order relationships of OSAC categories, we decided to visually represent the binary relationships across OSAC as intricate 2-D networks of vertices (OSAC categories) and linear edges (binary relationships). We placed OSAC categories in a higher number of combinations closer together and represented the strength of the binary associations by the thickness of the edge connecting them with other OSAC categories. We call these new visual representations of environmental exposures "constellation plots" (Figure 1).

We observe hundreds of trinary and quaternary associations of odours, symptoms, actions, and probable causes. Our correlation analysis reveals odour- and cause- connections to actions and symptoms (Figure 1). For example, we find that suspected causes (fires, smoke, and burning, FSB) are often linked to specific symptoms (respiratory irritation, REI) through the experience of specific odours (burning, BRN). However, suspected causes (garbage and compost, GAC) are linked to symptoms (neurological, NEU) and actions (making a complaint, MAC) without odour mediation. We think these examples show that odours can affect health and well-being, either directly by making people aware of a harmful source due to the smell or due to the psychological effect of a potentially harmful odour source nearby. These findings have implications for environmental injustice with regards to urban planning (siting of odour sources) and for understanding the mechanisms of smell impacts (epidemiology), highlighting the potential value of incorporating odour landscapes in decision-making. Overall, crowdsourcing provides a rich, real-time dataset that captures the subjective nature of odour experiences and their complex linkages to health and well-being via OSAC networks.

In conclusion, this study shows that the application of network analysis adds substantial value to crowd-sourcing studies collecting data on environmental exposures such as odours, turning even qualitative data into a quantitative ensemble. We hope that this study serves as a proof of concept for further development of such analytical approaches.

Keywords: OSAC linkages; crowd-sourced science; spatiotemporal variability; odour.

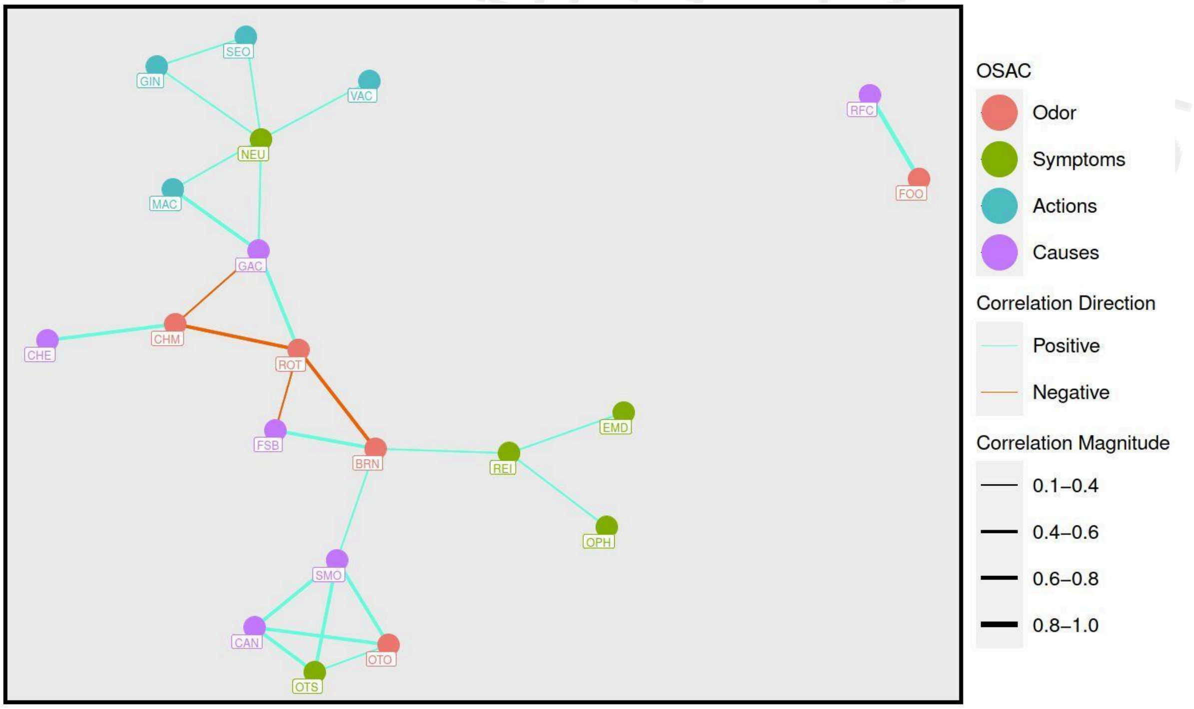

Figure 1 OSAC associations based on the descriptions reported in SmellVan (Dec 2020–Dec 2021). Specific values of OSAC are represented as three-letter shorthands summarized here: Odors: CHM = "Chemical", ROT = "Rotten", FOO = "Food", BRN = "Burning", OTO = "Other odours". Symptoms: EMD = "Emotional disturbance", REI = "Respiratory irritation", NEU = "Neurological", OPH = "Ophthalmological", OTS = "Other symptoms". Actions: VAC = "Ventilation and air cleaning", GIN = "Gone inside", SEO = "Stopped exercising outdoors", MAC = "Made a complaint". Causes: RFC = "Restaurants and food cooking", FSB = "Fires, smoke, and burning", CHE = "Chemicals", GAC = "Garbage and compost", SMO = "Smoking", CAN = "Cannabis facilities".

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Solution and Coarse-graining of Second Order Random Networks Solution and Coarse-graining of Second Order Random Networks

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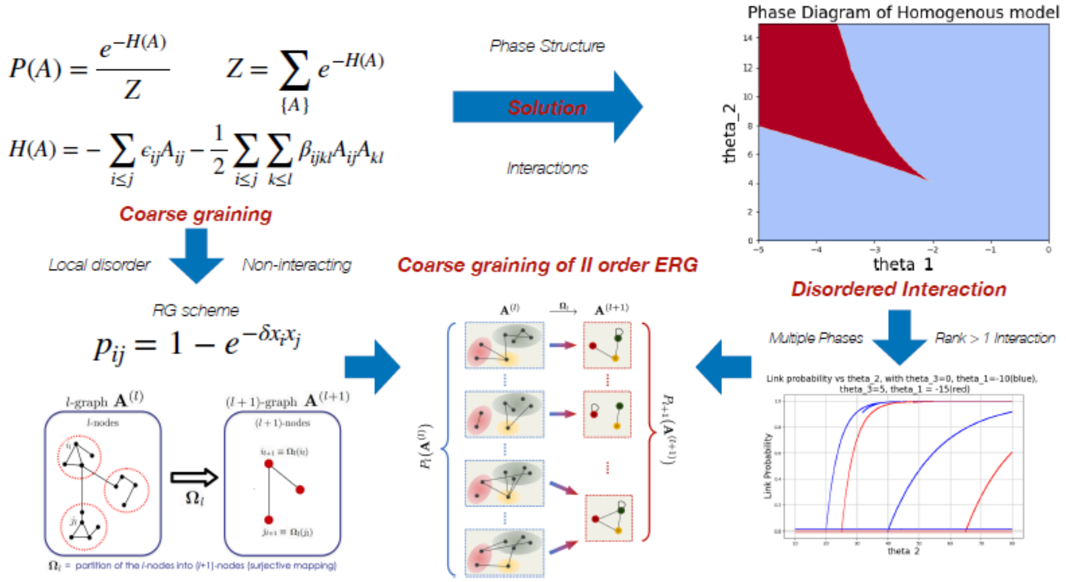
We show a solution pipeline for any second order Exponential Random Graph.We then explicitly compute the solution for some models of interest in the large size limit to describe the separation of phases behaviour. When the interaction structure is far from homogeneous we show multiple phases emerge, and provide a criteria, based on the rank of the interaction, to assess if the mean field approximation can still be valid or not. As a byproduct of the solution of these models we can write an effective single-link probability, taking into account the phase the graph is in and the spectral separation of the interaction. We show then how these models can be mapped into a (multivariate) fitness model that is designed to be scale-invariant. Finally we show how some second order models can be arbitrarily coarse-grained.



Explosive Cooperation in Social Dilemmas on Higher-Order Networks

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Keywords: Game-theory, Higher-order networks, Dynamical systems, Social dilemmas

The pervasiveness of cooperation in our world has long puzzled researchers. In a competitive world, driven by Darwinian selection, costly altruistic cooperative behaviours seem inappropriate, since they do not bring any immediate advantage to the cooperators. It is instead more profitable for a self-interested individual to defect, free-riding the benefits coming from the cooperators' actions. Such situations, where the self-interest behaviour/strategy yields to higher payoff, but if everyone adopts this more profitable strategy then everyone suffers, are known as social dilemmas. Social dilemmas are typically studied using pairwise symmetric games such as the Prisoner's Dilemma (PD), on structured populations modelled as networks. Networks are however limited in their representation of real-world systems. The links of a network can indeed only describe pairwise interactions, while the units of a complex system can also interact in groups of more than two. Thus, networks do not allow to accommodate more realistic and general forms of higher-order social interactions.

To overcome this major limitation, we propose modelling the population's interaction structure as a hypergraph, moving beyond pairwise interactions. In our model [1], the players are the nodes of a hypergraph and are involved, at the same time, in both pairwise (PW) and higher-order (HO) games as represented by hyperedges of different sizes. In particular, we focus on the case of hypergraphs with a fraction $1 - \delta$ of hyperedges of size two (2-hyperedges) and a fraction δ of three (3-hyperedges), respectively corresponding to classical pairwise games (2-games) and games played in groups of three players (3-games). The complete payoff structure of 2 and 3-game is shown in Fig. 1(a).

In particular, we observe that for the 3-player social dilemmas, we have two new payoffs: W, for defection against a cooperator and another defector, and G for cooperation against a defector and another cooperator. G and W represent higher-order effects, completely absent in pairwise games. We found that the presence of HO interactions has a profound impact on the model outcome. By comparing the results of extensive numerical simulations of the evolutionary dynamics on random hypergraphs to mean-field analytical results, we find that beyond a critical fraction δc, we observe the emergence of a discontinuous first-order explosive transition to a bi-stable state, where full defection coexists with ρ_{+}^{*}, a non-trivial stationary state where a finite fraction of the population cooperates, see Fig. 1(b). The presence of bistability, however, indicates that the survival of cooperators is not guaranteed: a critical mass of initial cooperators ρ_{-}^{*}, is needed for the system to converge to ρ_{+}^{*}, see Fig. 1(c). This is in agreement with empirical observations regarding the critical mass of initiators required to trigger social and cultural changes. Our findings show that higher-order interactions can foster cooperation in competitive settings, offering a novel solution to social dilemmas.

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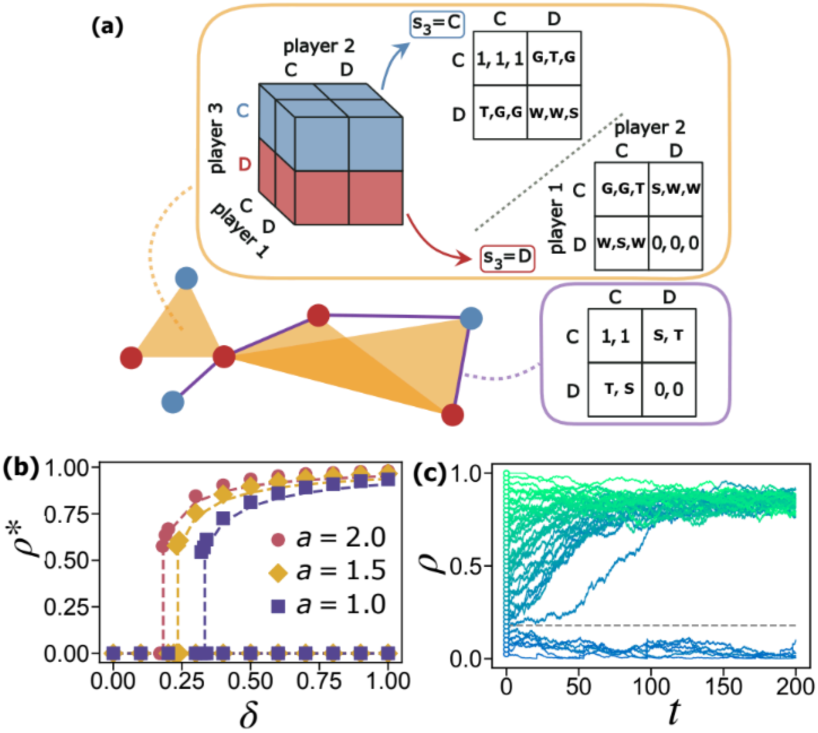

Figure 1: (a) Higher-order games on a hypergraph schematic. The payoffs for the respective games are denoted by payoff matrix and payoff cube. (b) Fraction of cooperators at equilibrium (ρ_+^*) for the Prisoner Dilemma on random hypergraphs with N = 1500 and average hyperdegree k = 20, with a tunable ratio δ of three-body interactions for different values of $a = 2(G - W)$. (c) Temporal trajectories of cooperation levels for various initial values of cooperation $\rho(0)$. We see a bifurcation into two stable states based on the critical initial mass ρ_-^*.

Correlation tensor spectra for crypto asset transaction networks

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Crypto assets, such as XRP, are digital or virtual assets that use cryptography for security and operate on decentralized networks, offering innovative solutions for financial transactions and services. We develop a novel method of correlation tensor spectra for the dynamical XRP networks, which can indicate XRP price [1, 2]. A weighted directed weekly transaction network among XRP wallets is constructed by aggregating all weekly transactions. A vector for each

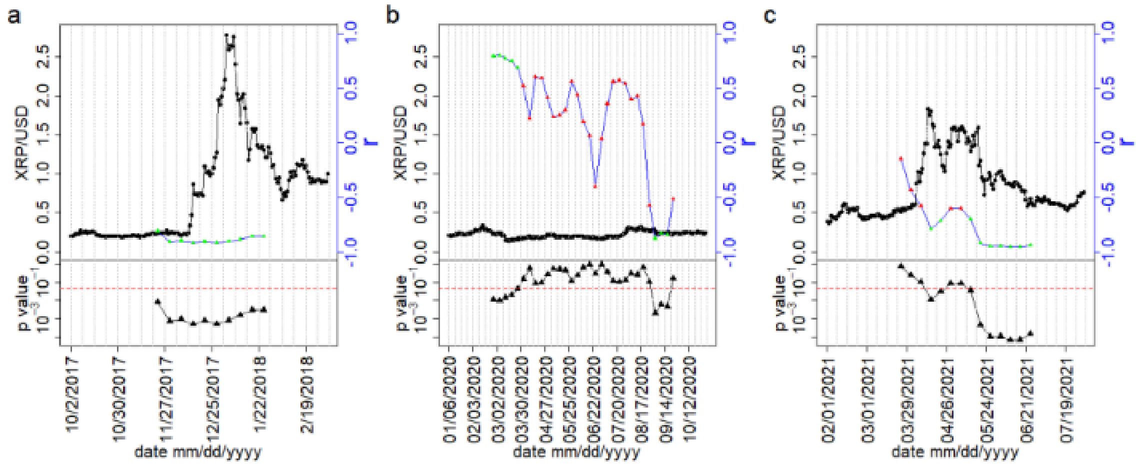

Figure 1: The comparison of daily XRP/USD price with the correlation *r(t)* between the weekly XRP/USD price, and the largest singular value using a moving window of 9 weeks for three different periods - (a) October 2, 2017- March 4, 2018, (b) January 6, 2020 - November 1, 2020 and (c) February 1, 2021- August 1, 2021. The blue curve with green and red triangles represents correlation *r(t),* where the green triangles indicate significant correlations (p-value < 0.05) and the red triangles indicate no significant correlations (p-value > 0.05). The three lower panels show the p-values for the corresponding Pearson correlations. The dotted grey vertical lines represent the weekly windows.

node is then obtained by embedding the weekly network in continuous vector space. We construct a correlation tensor from a set of weekly snapshots of node vectors. A double singular value decomposition of the correlation tensors gives its singular values. We calculate and compare the distribution of the largest singular values of the correlation tensor using the random matrix theory with the largest singular values of the empirical correlation tensor. We investigate the correlation between the XRP price and the largest singular values for a period spanning two years. We also uncover the distinct dependence between XRP price and the singular values for bubble and non-bubble periods [Fig. 1]. The significance of the time evolution of singular values is shown by comparison with the evolution of singular values of the reshuffled correlation tensor. Furthermore, using singular vectors, we identify a set of driver nodes in the transaction networks that drive the market during the bubble period. Our correlation tensor spectra method is highly versatile and can be readily applied to transaction networks involving various other crypto assets.

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Bipartite networks: tools from Economic Complexity

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Bipartite networks are ubiquitous, as many systems can be represented as a user-item interaction; examples range from social to biological systems. Consequently, many approaches have been developed to study the evolution of bipartite networks; a typical example is the projection into one of the two layers to obtain a monopartite network.

A prominent application of these methodologies is the field called *Economic Complexity* (EC), an innovative framework that borrows concepts and tools from statistical physics and network science to study development economics. A key concept of EC is *relatedness*, used to define either the affinity between a location and a human activity or the similarity between human activities, e.g. industrial, technological, or scientific sectors. Being a measure of how much, for instance, a country is far from being able to produce a target product, relatedness is a key tool for institutions and policymakers. Many different definitions of relatedness coexist in the literature, most of them based on networks of co-occurrences; in this case, two products are related if relatively many countries export both. We build a testing framework that can be used to compare and scientifically validate these different approaches in a coherent and systematic way: an out-of-sample prediction task [Albora et al., 2023b]. In particular, we predict which country will be competitive in which product in five years – an information of key importance from a policy perspective. We compared supervised algorithms with the co-occurrence networks and semi-trivial benchmarks, finding that tree-based models, such as random forest and boosted trees, outperform the other methods [Tacchella et al., 2023]. We obtain similar results when we apply these methods to the patenting and exporting activity of companies [Albora and Zaccaria, 2022].

Given these results, we investigated how to improve the explainability and interpretability of our machine learning methods [Fessina et al., 2024]. These efforts led to the introduction of the *Sapling Similarity* [Albora et al., 2023a], a minimal bipartite to monopartite projection method, which preserves the prediction performance of machine learning methods but with a simple and intuitive interpretation. We believe that these methods are easily generalizable and applicable to other social and biological systems, as long as they can be represented as bipartite networks.

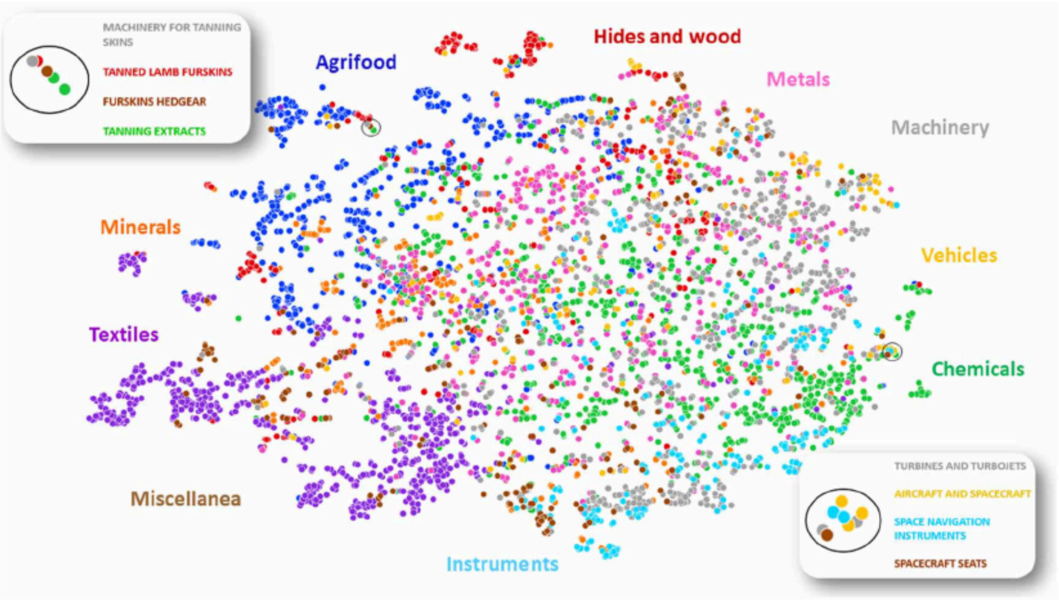

Figure 1: Machine learning methods show an excellent performance in predicting the evolution of bipartite networks. Moreover, their output can be used to represent the nodes of one of the two layers in an euclidean space. In the figure above, extracted from [Fessina et al., 2024], we show a metric projection of the space of products obtained from the prediction of the country-product network.

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From Spanning Trees to Antiphase: How Mixed Interactions Shape Oscillator Patterns

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This study explores how attractive and repulsive interactions in networks of limit cycle oscillators influence synchronization patterns, particularly antiphase synchronization, where adjacent nodes oscillate in opposition. We discover that selective negative control, applied through a spanning tree, is more effective than random negative connections in achieving this synchronization in bipartite networks. Our research also examines cluster synchronization in networks with mixed interactions, revealing practical implications for neural networks, social models, and ecological systems.

We introduce the universal 0-π rule, which simplifies the achievement of antiphase synchronization and extends to non-bipartite networks to predict and manage frustration levels. By analyzing cluster stability and formation with this rule, we offer new insights into controlling synchronization in complex systems, enhancing our ability to manage collective behaviors across various fields.

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Robustness of ecological communities driven by correlated perturbations

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Ecological communities face continuous perturbations due to fluctuations in environmental conditions. When the environment changes, similar species respond similarly, and therefore their vital rates change in a correlated way. Here we study the robustness of models of ecological communities challenged by correlated perturbations of their parameters, focusing on the probability that fluctuations are large enough to make coexistence impossible and thus trigger extinctions. We show that classic studies of robustness have concentrated on the case of independent perturbations of model parameters, and build a framework to extend these approaches to the case of correlated perturbations. We identify specific distributions of perturbations that are most or least conducive to coexistence, and prove that one can always find a distribution of perturbations that counters exactly the effect of species interactions---making population abundances behave independently of one another. Thus, given a matrix of interactions, we can find which correlated perturbations would most (least) likely result in extinctions, and give a simple ecological interpretation for the effects of fluctuations. The framework can be used to contrast the effect of different interaction structures on coexistence, and derive optimal interaction structures for simple families of interaction structures. Importantly, when moving from one interaction structure to the other, essential statistics on species abundances are kept constant, thus ensuring a fair comparison.

Keywords: robustness; feasibility; perturbations; coexistence

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Heterogeneous Popularity of Metabolic Reactions from Evolution [1]

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The orchestration of biochemical reactions in cellular metabolism is a cornerstone of life, intricately balancing the generation and consumption of matter and energy. Recent advancements in genome sequencing and annotation of numerous species have provided invaluable insights into the metabolic landscapes. Through computational inference and database structuring, the complex networks of biochemical reactions have been unveiled, which can shed light on the evolutionary trajectories of metabolic pathways across diverse species.

In this study, we investigate the distribution of reactions among different species to illuminate the underlying principles governing metabolic organization. The concept of reaction popularity, representing the frequency with which a particular reaction occurs across species, has emerged as a focal point of investigation. The studies including ours have revealed that reaction popularity follows a power-law distribution, suggesting non-random processes at play in shaping metabolic networks, while the number of reactions exploited in each species follows a homogeneous distribution [Fig. 1].

Delving deeper into the dynamics of metabolic evolution, we explore the coevolution of metabolism within the context of species phylogenies. By tracing the ancestral origins of metabolic reactions and their subsequent recruitment in descendant species, we elucidate how reaction popularity diversifies over evolutionary time scales. This approach offers valuable insights into the interplay between evolutionary forces and biochemical constraints in shaping metabolic diversity.

Building upon this foundation, we suggest a co-evolutionary model inspired by ecological network dynamics, by concretizing the stochastic recruitment of chemical reactions into the metabolism of different species at different times and their inheritance to descendants [Fig. 2]. Through meticulous calibration and validation against empirical data, we confirm that our suggested model succeeds in reproducing not only the primarily observed distributions [Fig. 1] but also other empirical features. Therefore this model can be utilized as a framework for understanding the complex interplay between genetic inheritance, environmental pressures, and stochastic processes in shaping metabolic diversity.

In conclusion, our study offers a window into the fundamental principles governing life’s chemical intricacies through interdisciplinary approaches integrating genomics, computational biology, and evolutionary theory. Further studies are desirable towards unraveling the mysteries of metabolic diversity and the large-scale evolutionary processes shaping life on Earth.

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Evaluating changes in attractor sets under small network perturbations to infer reliable microbial interaction networks from abundance patterns

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Inferring microbial interaction networks from microbiome data is a core task of computational ecology. An avenue of research to create reliable inference methods is based on a highly stylized view of microbiome data, starting from the assumption that the presences and absences of microbiomes, rather than the quantitative abundances, are informative about the underlying interaction network. With this starting point, inference algorithms can be based on the notion of attractors (asymptotic states) in Boolean networks. In principle, the Boolean network framework offers a computationally efficient method to tackle this inference problem [2, 3]. However, often existing algorithms operating under a Boolean network assumption, fail to provide networks that can reproduce the complete set of initial attractors (abundance patterns). Therefore, there is a need for network inference algorithms capable of reproducing the initial stable states of the system.

We study the change of attractors in Boolean threshold dynamics on signed undirected graphs under small changes in network architecture and show, how to leverage these relationships to enhance network inference algorithms. We use this information to generate an evolutionary algorithm that drives a partially inferred network towards a network that can generate the initial attractors and (in most cases) allows inference of the original network (depicted in Figure 1). As an illustration of this algorithmic approach, we analyze microbial abundance patterns from stool samples of humans with inflammatory bowel disease (IBD), with colorectal cancer and from healthy individuals to study differences between the interaction networks of the three conditions. The method reveals strong diversity in IBD interaction networks. The networks are first partially deduced by an earlier inference method called ESABO [2], then we apply the new algorithm developed here, EDAME, to this result to generate a network that comes nearest to satisfying the original attractors.

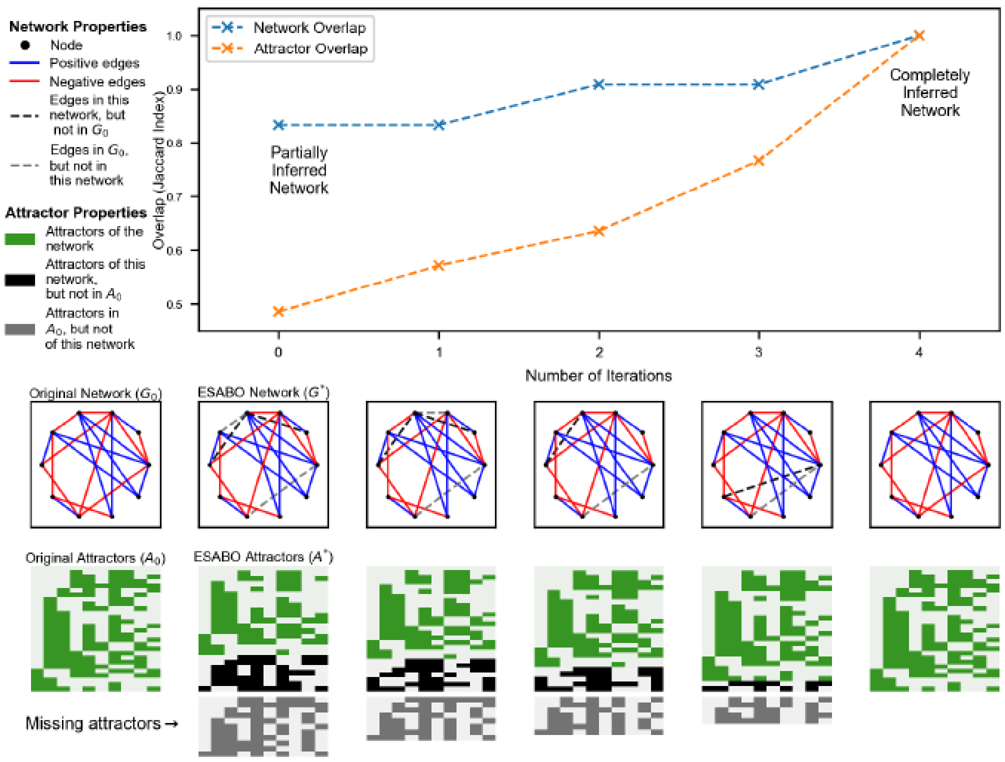

Figure 1: Evolution of partially inferred network, G_* (by an algorithm from [2]: ESABO), to a network with the same attractor set as A_0, which gives us the original network, G_0. Network parameters are $N = M+ = M- = 10$. Shown below the networks are the attractors of the networks with green: attractors matching to A_0; black: attractors absent in A_0; grey: attractors present in A_0 but missing in the corresponding attractor set. The algorithm takes 4 iterations to correct 4 edges (2 false positives, 2 false negatives), shown as dashed edges in the network G_*.

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Connecting inter-city mobility with urban welfare

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Keywords: *Human mobility, city science, transportation networks, science of success*

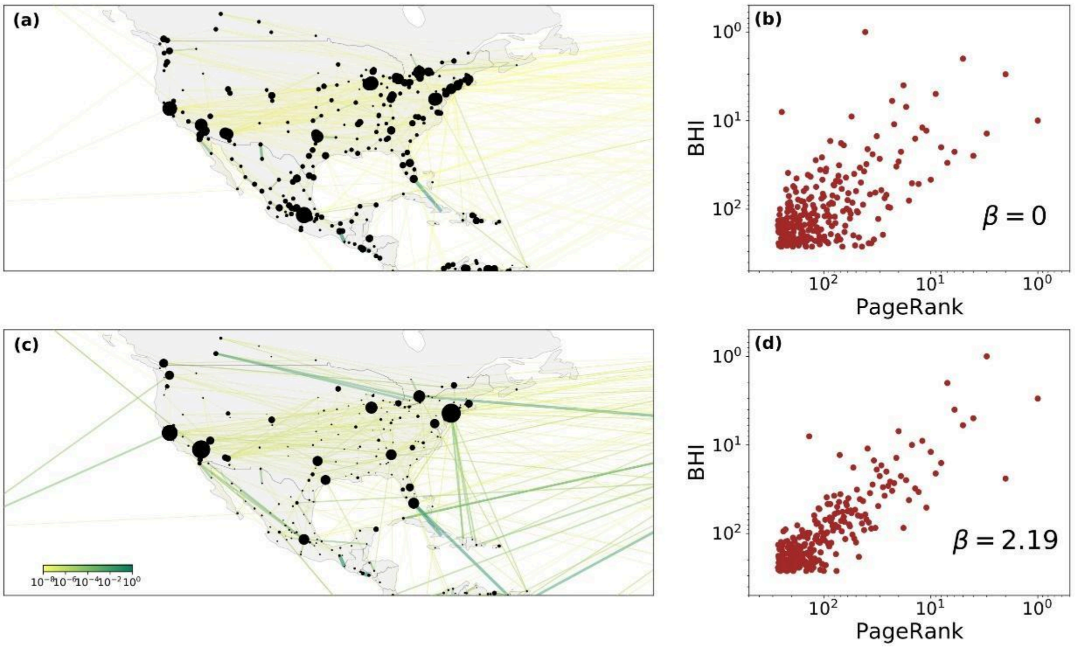

FIG. 1. **Connecting network position and welfare**. Weights of the global mobility network for **a** the raw mobility flows and **c** when incorporating the e_ect of distance in the weights, shown for North American cities. Node sizes are proportional to their PageRank in both maps. **b** The composite measure

of development (BHI) vs PageRank unweighted flows where the horizontal axis indicates the ordered ranking based on their PageRank values. **d** The same for the weighted network, yielding $\rho_s = 0:77$.

While significant effort has been devoted to understand the role of intra-urban characteristics on sustainability and growth, much remains to be understood about the effect of inter-urban interactions and the role cities have in determining each other's urban welfare. Here we consider a global mobility network of population flows between cities as a proxy for the communication between these regions, and analyze how it correlates with socioeconomic indicators.

We use several measures of centrality to rank cities according to their importance in the mobility network, finding PageRank to be the most effective measure for reflecting these prosperity indicators. Our analysis reveals that the characterization of the welfare of cities based on mobility information hinges on their corresponding development stage. Namely, while network-based predictions of welfare correlate well with economic indicators in mature cities, for developing urban areas additional information about the prosperity of their mobility neighborhood is needed. We develop a simple generative model for the allocation of population flows out of a city that balances the costs and benefits of interaction with other cities that are successful, finding that it provides a strong fit to the flows observed in the global mobility network and highlights the differences in flow patterns between developed and developing urban regions. Our results hint towards the importance of leveraging inter-urban connections in service of urban development and welfare. More details can be found in the published version of the paper [1]

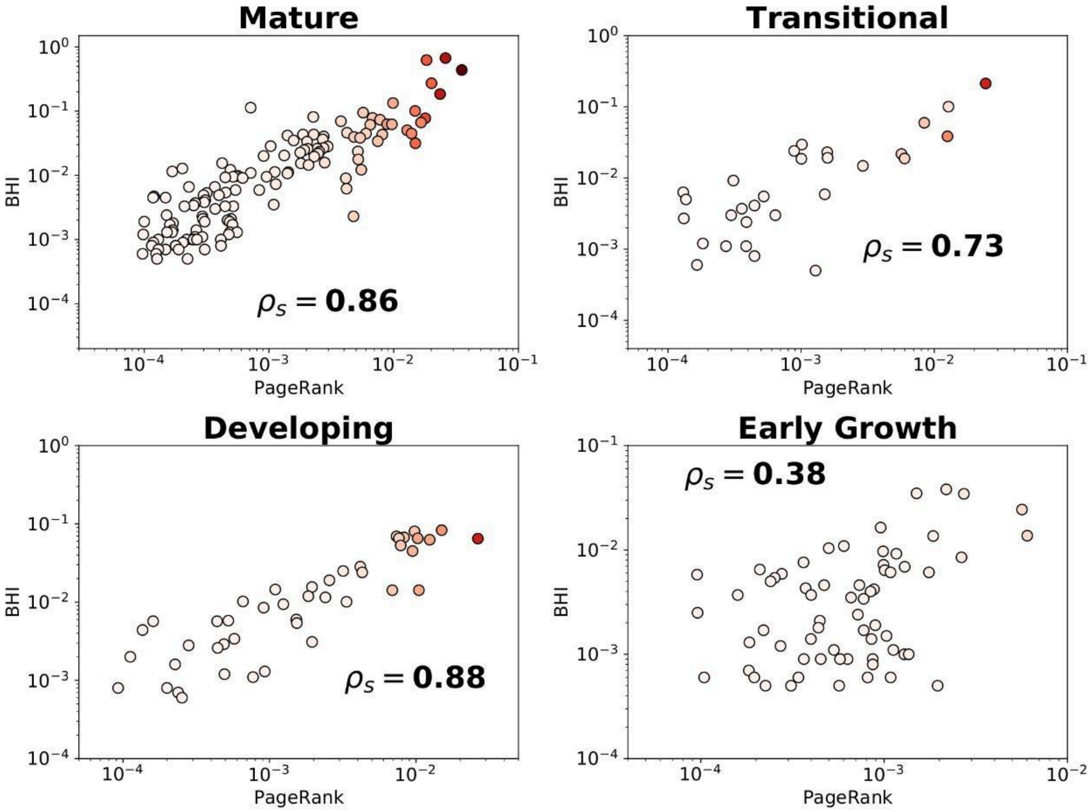

FIG. 2. **Disaggregating cities by development level.** Pagerank vs BHI when cities are grouped with respect to their development level. Spearman's correlation in each panel shows association level of the socioeconomic indicator and the network centrality measure. Colors represent the strength of connectivity for each city with dark red indicating higher levels of weighted-degree.

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Advances in Modularity-based Community Detection in Bipartite Networks

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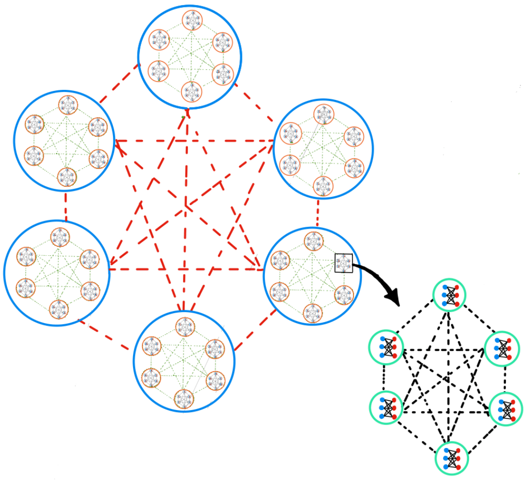
Bipartite networks, consisting of two distinct types of nodes with links only between unlike nodes, are prevalent in fields like citation networks and biomedical research. Community detection in these networks is crucial for understanding their underlying structures, such as revealing connections between diseases and symptoms or genes and their functions.

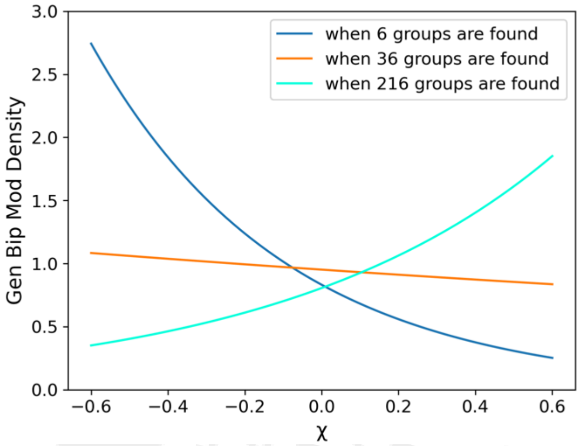
Traditional modularity-based methods for community detection in bipartite networks face challenges, including the resolution limit problem and the NP-complete nature of finding the optimal partition. To address these issues, we introduce **Bipartite Generalized Modularity Density (Q_{bg})**, a novel objective function that, like Generalized Modularity Density [Guo, Singh, and Bassler, J. Phys. Complex. 4 (2023) 025001] for unipartite networks, has a tunable parameter that allows for the detection of hierarchical structures by adjusting the scale of communities. When this parameter is set to zero, Q_{bg} simplifies to the traditional Barber Bipartite Modularity [Barber, Phys. Rev. E 76, 066102 (2007)].

Additionally, to tackle the NP-complete problem, we employ a variant of **RenEEL** [Guo, Singh, and Bassler, Sci. Rep. 9, 14234 (2019)], a cutting-edge ensemble learning algorithm. RenEEL efficiently finds partitions that maximize Q_{bg} by considering an ensemble of partitions that is updated using extremal criteria until consensus within the ensemble is reached, which reduces computational complexity and improves accuracy.

Our approach, integrating Bipartite Generalized Modularity Density with RenEEL, effectively identifies sub-communities and hierarchical structures in artificial networks. This method enhances both the efficiency and accuracy of community detection in bipartite networks.

Keywords : Bipartite graph, Modularity.





(a) (b)

Figure: (a) Artificial hierarchical bipartite network. It includes four levels of hierarchy. The elementary level (level1) is a clique formed by fully connecting three blue nodes and three red nodes with links weighted 4. To construct a level 2 network, we use the clique network from level 1 as a generalized node with links weighted 3. Similarly for level 3 and level 4 networks, the links weights are 2 and 1 respectively. Link between two generalized nodes is achieved by connecting one link between any red node in one generalized node and any blue node in another.
(b) Objective function Q_{bg} for different partitions as a function of control parameter χ. A smaller value of χ finds 6 groups corresponding to the blue circles in (a). As the value of χ increases, it finds 36 groups corresponding to the orange circles, and eventually 216 groups to the elementary cliques.

Unraveling Vaccine Scare Dynamics in Populations Using Complex Network Models and Game Theory

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Rumours about adverse health outcomes—whether from infection or vaccination—significantly influence vaccination rates. The way these rumours spread is significantly influenced by the structure of social contact networks, leading to highly varied risk distributions across different population segments, ultimately affecting vaccination uptake. Therefore, understanding how contact network topology, risk evolution, and individual attitudes interact during a health scare is crucial. This insight can play a vital role in designing effective intervention strategies and informed policy making for public health programs.

In my presentation, I will utilize evolutionary game models for both homogeneous and heterogeneous populations to illustrate how human attitudes towards vaccination change during a health scare, drawing on empirical data on vaccination coverage of various childhood diseases. For instance, I will highlight the critical role of social-learning in understanding resilience in the dynamics of vaccine uptake. I will introduce the concept of vaccination games on social networks to examine the impact of rare but severe events on vaccination dynamics. For example, adverse events from vaccines (but not infections) can significantly extend the duration of an outbreak, or even a small risk of vaccine adverse events can lead to a sharp decline in vaccine coverage, particularly in scale-free networks. Moreover, the global dissemination of information can be more effective than local information in increasing vaccine coverage.

Keywords: Vaccination game, Vaccination scare, Complex network, Disease dynamics

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(sub) Optimal Resources Allocation in Complex Systems

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Recently, we explained the connection between the Fitness and Complexity algorithm (FC) to the Sinkhorn-Knopp algorithm used in matrix scaling [1]. This uncovered many properties of FC but most interesting it linked the entire framework of Economic Complexity to the Optimal Transport (OT) theory. Despite being a simple and fairly old theory, OT is largely unknown to physics and network communities. The Optimal Transport theory was initially devised for optimizing the movement of materials between locations with varying characteristics, such as the transportation of coal from mines to storage facilities. Its primary objective is to minimize the overall transportation cost, taking into account constraints related to coal extraction from mines (r_x), storage facility capacity (c_y), and transportation costs between locations (ϕ_{xy}). This optimization entails finding the matrix π_{xy}, which represents the total mass transported from

location x to location y, in order to minimize the total cost $C = \sum_{xy} \phi_x \pi_{xy}$, while complying with the constraints $\sum_{xy} \pi_{xy} = c_y$, $\sum_{xy} \pi_{xy} = r_x$. Interestingly, these two fundamental components, the constraint vectors (r_x, c_y) and the cost matrix ϕ_{xy}, are rarely considered together in complex systems, particularly in the context of economic complexity. The simplicity of the Optimal Transport theory makes it applicable across various fields. For instance, in international trade, it can be employed to model countries' resource constraints while maximizing export gains. In recent times, faster algorithms like the Sinkhorn algorithm have made Optimal Transport more accessible by solving an approximate problem. A well known property of OT solution is its network topology. In fact, it is easy to prove that the optimal structure is a tree. While a perfect tree-like network is never observed in real data, we study how the structure's properties change in sub-optimal solutions of the OT problem, assuming a finite temperature that drives the system away from the optimality. We study a random graph model that constraints the total resources of the system to fixed values and that tune the importance of the cost function with the parameter β (the inverse of a temperature). With this parameter we can go from a perfect OT problem ($\beta = \infty$) to a case of flat preferences ($\beta = 0$) where the cost function is negligible. In this work we study the 'sparsification' process of resources allocation as a function of the temperature, that, from preliminary results, shows a critical behaviour. Our order parameter is the mass share of the

Maximum Spanning Tree (MST share) observed in $\pi(\beta)$. This quantity starts from a small finite value in the dense regime, eventually going to zero for larger systems. With rising β, MST mass share reaches value 1 in the sparse regime, as expected for an OT problem. The transition becomes more abrupt with the size of the system as shown in the figure.

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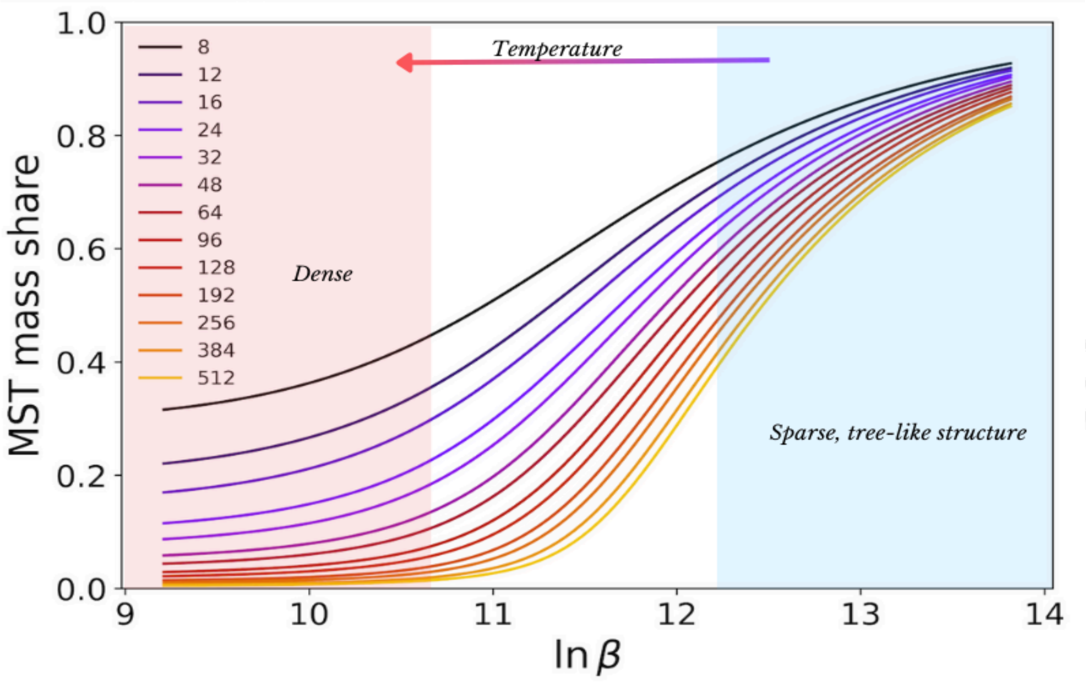

Mapping cultural evolution using complex networks. Quantitative insights from Wikipedia's interdisciplinary relationships over five centuries.

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The development of revolutionary ideas, cultural breakthroughs, or paradigm shifts typically emerges from complex interactions among many people, concepts, and objects that structure social, historical, and cultural spaces. These interactions are difficult to quantify, and the increasing number of cultural elements to be considered would eventually make it hard, if not impossible, to fully understand the cultural dynamics using traditional tools. To overcome these limitations, several quantitative methodologies have been proposed recently (Schich et al., 2014; Goldfarb et al., 2015; Brown et al., 2017), some of them using Wikipedia as a suitable source for data mining and quantitative cultural research. Based on the formalism of complex networks theory, it has been recently shown that it is possible to convert the network of internal links on Wikipedia into a meaningful network of knowledge

(Schwartz, 2021). Thus, we have shown in previous studies that the simple observation of what is connected to what, properly treated, can unveil relevant knowledge about the structure of cultural networks. The success of this methodology applied to specific events (Schwartz, 2021; Miccio et al., 2022) encourages us to move from particular cases to characterising entire historical periods. Thus, the present work aims to quantitatively analyse the interdisciplinary cultural networks that connect art, science, and philosophy along the last five centuries. In this way, we can understand the flow of knowledge among different disciplines and quantify the individual behaviour of nodes and the collective characteristics of clusters and networks. To achieve this challenge, we used the normalised Google distance to measure the structural relatedness between each pair of Wikipedia entries. Based on these metrics, we generated hundreds of undirected networks representing cultural maps of the Wikipedia articles related to the studied historical periods, allowing us to perform a multiscale analysis to understand the global, cluster and individual behaviours. Thus, we found how the average normalised modularity is increasing along the studied period, in good agreement with the well-known rise of the disciplinary specialisation in the last centuries. The detailed analysis of the inter-cluster interactions reveals a power law distribution of the links, whereas a lognormal distribution is observed for the intra-cluster connections. This approach allows a quantitative analysis of cultural networks, provides new insights into their structures, and boosts quantitative studies in cultural dynamics using complex network tools.

Keywords: Complex networks; Cultural analytics; Historical networks; Wikipedia.

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Topological and spectral properties of random digraphs

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In recent years, the use of networks to represent complex systems has grown significantly in diverse fields. This trend highlights the network’s effectiveness in capturing the properties of these systems, where vertices represent agents and edges their interactions. The study of network properties covers multiple aspects, focusing mainly on their topological and spectral properties.

Although numerous relevant studies of these properties have been conducted, most focus on networks without direction on their edges. However, in many cases, it is crucial to incorporate the direction of information flow to model specific realworld systems. Therefore, there is a growing interest in exploring the properties of directed networks, which motivates this study on the topological and spectral properties of directed random networks, specifically digraphs of the Erdős-Rényi type. We define these digraphs by two parameters: n, representing the number of vertices, and p, the connection probability, denoting them as $D(n, p)$.

First, we analyze topological properties, such as the number of arcs m, the number of nonisolated vertices $V_x(D)$, and closed cycles of length 2 C_2. We also study two topological indices based on the degree of vertices: the Randić index $R(D)$ and the summation connectivity index $\chi(D)$. Although these indices have been widely used in mathematical chemistry, we apply them to characterize the topological properties of networks.

Using a scaling analysis, we show that the average degree $\langle k \rangle$ acts as a scaling parameter for the average values of these quantities. We also formulate expressions relating these properties to the parameters (n, p) of the ER random digraphs.

As for the spectral properties, we start the analysis of the eigenvalues, observing two key behaviors: on the one hand, the largest eigenvalue is separated from the rest of the spectrum and is determined by the average degree of the network; on the other hand, the bulk of the spectrum converges to a circle whose radius, in analogy with the Ginibre law, is $\sqrt{np(1-p)}$.

Furthermore, we explore six alternative definitions of the concept of graph energy, initially proposed by Gutman for undirected networks, and we observe that these energies also scale with $\sqrt{np(1-p)}$ Finally, we reformulate a set of bounds previously reported in the literature for these energies as a function of (n, p). We also state phenomenological relations between these energies that allow extending previously known bounds.

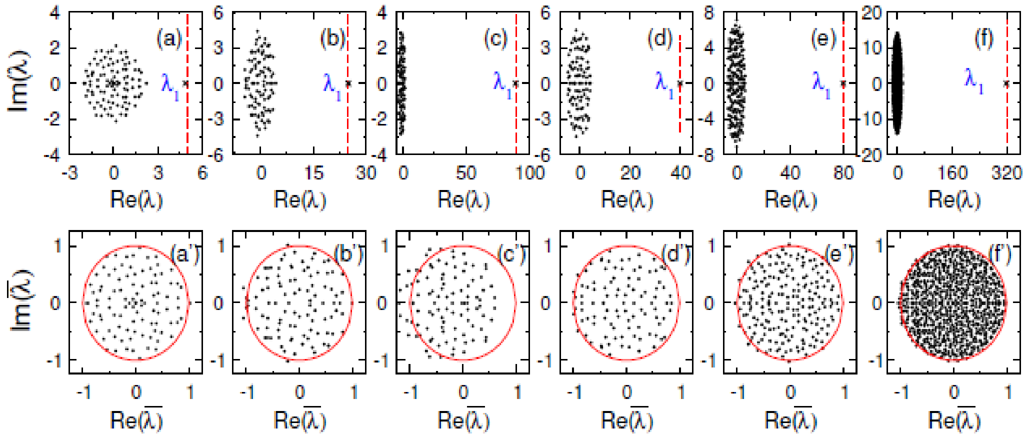

Figure 1: TOP: Eigenvalues λ of Erdős-Rényi digraphs of various combination of p and n. (a) p = 0:05 and n = 100, (b) p = 0:25 and n = 100, (c) p = 0:9 and n=100, (d) p=0:4 and n=100, (e) p=0:4 and n=200, (f) p=0:4 and n=800. The red dashed line corresponds to np. 11 indicates the largest eigenvalue.
BOTTOM: Eigenvalues λ (normalized to $\sqrt{np(1-p)}$ of the Erdős-Rényi digraphs of various combinations of p and n. The same data reported in the top panels, but normalized and removing the largest eigenvalue.

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Impact of Node Failures on Productivity in Multi-layered Supply Chain Networks: An Influence Network Analysis in the Indian Electronics Sector

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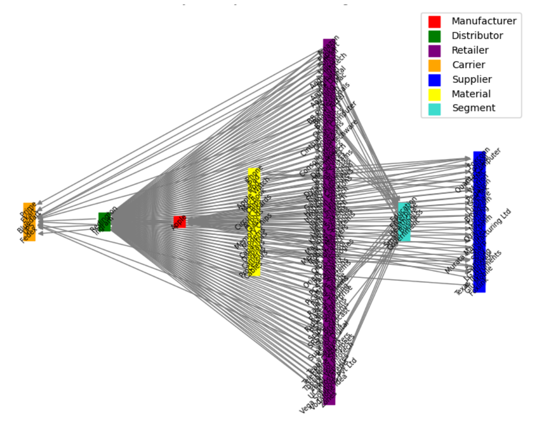
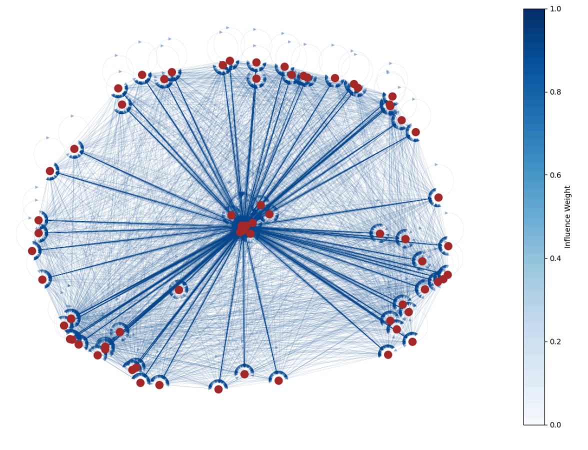
Supply chain networks are essential for delivering goods and information, but disruptions like natural disasters or trade embargoes can severely impact them (Mchopa et al. 2021). Resilience of entire networks under different types of disruptions when nodes or edges fail has been extensively studied (Zhao et al. 2022). However, failure of a particular company impacting another company of interest within a network and the extent of the impact has not been studied so far. In that direction, we created a multi-layered physical supply chain network (Figure 1.1) of companies in an electronics supply chain concentrated in India. We found through simulations how the productivity of a company *i* is affected when another company *j* is randomly removed from the network. Extending this simulation for all possible combinations of companies *(i, j)* gave us an influence network (Figure 1.2) that represents the interdependence amongst nodes in terms of productivity. We found that when a critical node *j-critical* was removed, productivity of node *i* can either increase or decrease. We articulate the reasons affecting the increase or decrease in productivity and the actions that supply chain managers can take to maintain productivity of their nodes in the supply chain network.

Keywords: Supply Chain Resilience, Influence Network, Node Failure, Productivity Impact



igure 1.1: The above multi-layered network represents ompany types (nodes) in various colors and the links edges) between the companies represent goods flow.



igure 1.2: In the above influence network, each node i s connected to every node j by productivity values vhen each node j is removed from the original network.

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Deterministic construction of typical networks in network models

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In many applications, particularly in machine learning, it is desirable to construct a typical network of a random network model deterministically. Depending on the model, this task may be ill-defined or impossible. Yet, this task is well-defined and can be solved for the class of maximum entropy random graph models [1]. Here, we form definitions of *network typicality* Fig. 1a, and develop derandomization schemes for deterministic construction of such typical networks in various network models. A network is called *typical* in the ensemble if it matches the expected values of the sufficient statistics of the model.

While these methods are applicable in general to any exponential random graph models (ERGMs) and their probabilistic mixtures known as hidden-variable network models (HVNMs) [2], our primary focus is on the degree-corrected latent space models, commonly referred to as the random hyperbolic graph (RHG) model [3] which reproduces sparsity, heterogeneity, clustering, and self-similarity observed in many real-world networks [4]. Ordinary RHGs are built on two layers of randomness: first, each node i is assigned two random hidden (latent) variables θ_i and κ_i sampled from the Uniform and Pareto distributions, respectively; second, edges form independently with probability $p_{ij} = f(x_{ij})$, where f is the Fermi-Dirac distribution function, and with x_{ij} quantifying the hyperbolic distance between nodes i and j. We develop heuristics that deterministically emulate the random hidden variable assignments and link placements of the RHG. The hidden variable and edge derandomization methods together result in deterministic graphs that match the expected values of sufficient statistics of the model, which are the average degree (or equivalently the number of edges, $m = \sum_{i<j} A_{ij}$) Fig. 1b and energy of the graph, $\varepsilon = \sum_{i<j} A_{ij} x_{ij}$ Fig. 1c and hence are *typical* in RHG.

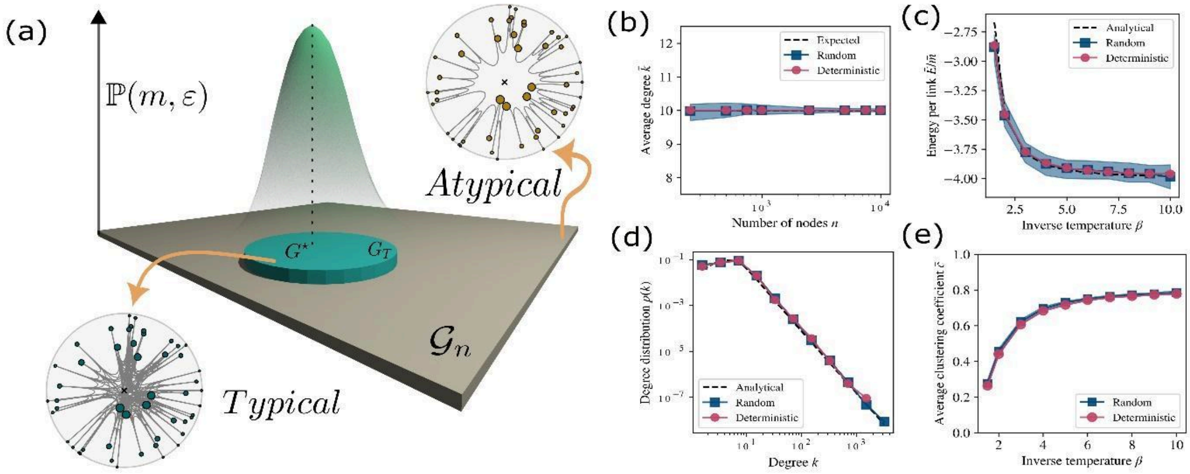

Figure 1: **(a) Network typicality-** Schematic illustration of the concentration of the joint distribution of sufficient statistics (number of edges and energy of graph), $\mathbb{P}(m, \varepsilon)$ on the *typical set*, $G_T = \{G \in G_n :$ $|m(G) - \overline{m}| < \delta$ and $|\varepsilon(G) - \overline{\varepsilon}| < \delta'\}$ in RHG [3] for some $\delta, \delta' > 0$. Since one of the sufficient statistics in RHG is a real-valued function, there exists a unique graph, $G^\star \in G_T$, which is *most typical* in the ensemble, G_n. Two random hyperbolic graph realizations are also shown; one belonging to the typical set as dictated by the closeness of the sufficient statistics values of the graph with that of the model average and another an atypical configuration. **(b)** and **(c) Deterministic typical networks-** Plots comparing the sufficient statistics values of random and deterministic RHGs of size $n = 10^4$, $\overline{\kappa} = 10$, $\gamma = 2.7$, and $\beta = 2.5$. Comparison of **(d)** the degree distribution and **(e)** average local clustering.

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Using causal network to uncover three types of armed conflict

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Social processes often unfold not in isolation but as sequential chains of interrelated events. These chains often propagate through networks that serve as substrates for the transmission of the social process. Extracting these networks from data can reveal pathways of transmission and deepen our

understanding of the underlying processes. Armed conflict is one such social process. In this study, we utilize a dataset comprising of conflict events in Africa from 1997 to 2020 to construct a weighted and directional network between geographical regions, depicted in Figure 1A. This network is built by calculating transfer entropy, a measure of statistical causality [1], between pairs of neighboring regions. Our methodology [2] is multiscale, allowing for the construction of this "causal network" at various spatio-temporal scales. Using this network, we connect temporally adjacent conflict events occurring in spatially connected regions via the causal network into chains of related events, as illustrated in Figure 1B. Furthermore, by integrating additional datasets comprising factors often associated with armed conflict—such as climate, geography, economics, infrastructure, demography, and population—we employ an unsupervised clustering method to uncover three distinct types of conflict based on these factors. Type 1 conflicts primarily propagate in regions with high population, well-developed infrastructure, and flat, riparian geography. Type 2 conflicts are diverse, frequently occurring around towns and small cities, often confined within national borders. Type 3 conflicts are typically observed in low-population areas with poor infrastructure and economic conditions and tend to remain small. Hence, our statistical approach facilitates the construction of a purely data-driven causal network through which conflicts spread across Africa. This network not only reveals chains of related conflict events but also, when combined with relevant conflict factors, helps uncover three distinct systematic types of conflicts and their socio-economic and geographic characteristics. Finally, our methodology provides a novel framework for exploring other similar diffusive social processes.

Keywords: Armed Conflicts; Causal Network; Transfer Entropy; Multiscale;

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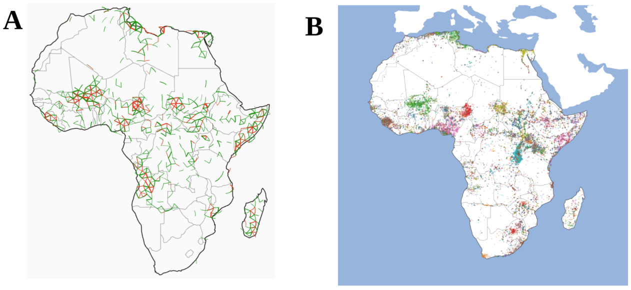

$$\mathrm{TE}_{X\to Y} = \sum_{y_t, y_{t-1}, x_{t-1}} P(y_t, y_{t-1}, x_{t-1}) \log_2 \frac{P(y_t|y_{t-1}, x_{t-1})}{P(y_t|y_{t-1})}$$

A) The causal network at a spatial scale of approximately 130 kilometers and a temporal scale of 32 days, representing statistical causal relationships between geographic regions as calculated using transfer entropy (defined below the figure). Green links are unidirectional and red links are bidirectional. B) Chains of related conflict events identified using the causal network, where each point represents a conflict event. The different colors correspond to distinct chains of related conflict events.

Functional brain network reorganization during task learning

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Understanding the brain's efficiency in adaptation and learning is an open problem in neuroscience [1]. One challenge is understanding how neural mechanisms underlying the brain's adaptive learning evolve in changing environments, and how such meta-learning generalize to new tasks. Here, we address these questions in an animal model that allows experimental access to both behavioral trajectories over the course of learning, and the underlying neuronal dynamics.

The dataset was collected in a systems neuroscience lab, with a custom methodology to record thousands of neurons in mice (Fig. 1A). Mice were trained on a go/no-go task, shuffling the cue-outcome relationships after an initial learning period [2]. The temporal dynamics of thousands of visual cortical neurons in the postrhinal cortex (POR) were recorded using chronic two-photon microscopy (Fig. 1B) as the mice responded behaviorally to the visual cues. Each of the visual cues was associated with an outcome (rewarded; punished; neutral), which were shuffled after the mice learned the task (Fig. 1C). During the initial learning phase, behavioral performances showed evidence of learning in the animals, followed by a drop in performances at the point of cue-shuffling. After the cue-outcome shuffle, performances increase slightly faster than during the initial learning period (Fig. 1D).

To capture the network dynamics underlying the behavioural performances during learning and relearning, we decomposed, using tensor composition analysis (TCA) [3], the activity of neurons into 9 tensor components (TCs) over the learning phases with evolving cue contexts. Each TC exhibits coherent patterns of activation corresponding to different functional behaviours. The TCs' time-series of neuronal activity patterns can then be used to study the patterns of integration and segregation of information during the various phases of learning (Fig. 1E), by computing their functional connectivity (FC) [4]. Doing so, we were able to track the evolution of the collective dynamics of the neural population and identified (i) a phase-transition-like behavior near the cue-shuffle, as well as (ii) identify stable learned representations and differences between initial learning and relearning phases.

Relearning showed distinct TC dynamics compared to initial learning, though learned states were similar before and after the cue-outcome shuffle. Initially, we observed high density in negative edge weights, which sparsify while the connected components merged during initial learning (phases 1-4). At shuffle, negative edge weight density increased and connected components re-emerged, though all TCs remained weakly connected. During relearning, we observe sparsification and the integration of more TCs in the connected component (Fig. 1E). The density and efficiency of these networks reflect these observations (Fig. 1F). Compared to the null configuration model (CM), efficiencies were higher and, importantly, the magnitude of change larger than expected just given the change in degree sequence. These preliminary findings highlight the reconfiguration during learning and the distinct dynamics during relearning, emphasizing the efficiency of adaptability and generalization.

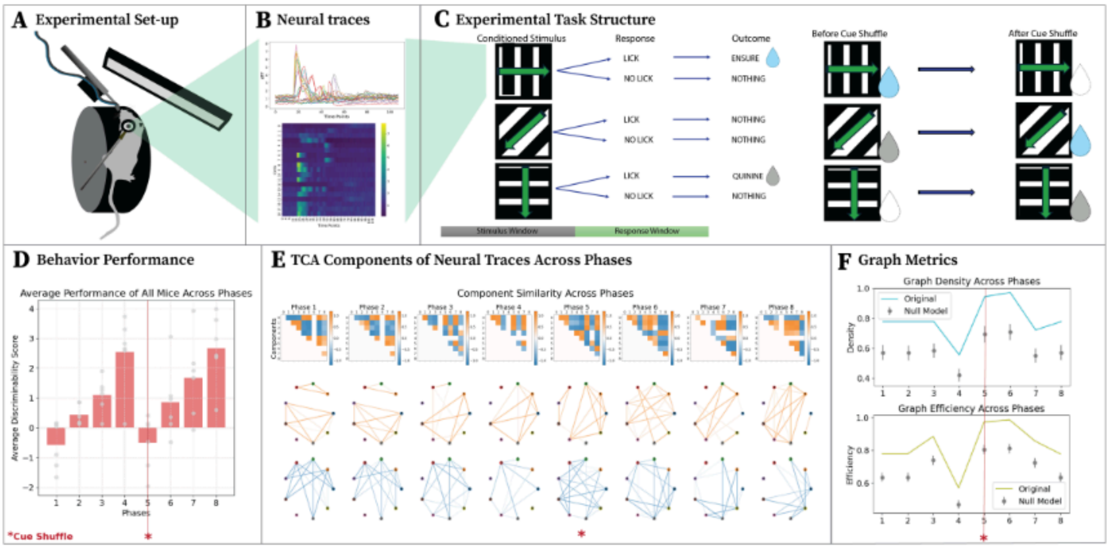

Figure 1: A) Head-fixed mouse with a lickspout delivering quinine and ensure for visual discrimination task. B) Example calcium neural traces with corresponding heatmap. C) Go/NoGo task structure showing orientation gratings and associated outcomes. Cue-shuffle defined as outcomes changing for each visual stimulus. D) Average discriminability score across all mice. E) Phase networks created from Pearson correlation matrices of TCs. F) Network density and efficiency across phases shown alongside null CM.

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Are Network Science Software Communities a Tangled Web?

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Understanding the nature of users of a particular software package is crucial for developers to maintain and expand the software further. This study investigates the software ecosystem and userbase of complex network analysis packages, with a particular focus on the ‘igraph’ library.

Using data from Wheelodex, a module dependency network derived from the Python Package Index (PyPI), we identified ‘bottlenecks’—modules dependent on ‘igraph’ that also have other modules relying on both ‘igraph’ and themselves. This analysis revealed twenty-one such bottlenecks, including popular modules like leidenalg, louvain, scanpy, and graphtools. To explore the scholarly impact and user communities of ‘igraph’, we utilized OpenAlex, an open-source database of scholarly papers. A dataset generated from a full-text query for ‘igraph’ yielded approximately 9000 results. OpenAlex data is only partially complete and accurate compared to other commercial knowledge bases.

Despite data completeness challenges inherent in OpenAlex, we employed unsupervised clustering algorithms and mutual information to identify communities within the citation network. To overcome sparse connectivity issues, we constructed a bibliographic coupling network based on shared citations between papers. The number of shared citations is defined as coupling strength added as an edge attribute. Community detection within this network employed a modularitybased Leiden algorithm adapted for edge-weighted graphs. Additionally, we extended this methodology to the module dependency network as well.

We investigate the alignment of communities derived from the network structure with the disciplinary boundaries as defined by OpenAlex (see figure 1). Notably, ‘igraph’ exhibits significant adoption in biological fields such as Molecular Biology, Ecology, and Evolution, contrasting with the widespread use of NetworkX despite its fewer hits than igraph in the OpenAlex database.

Future work will enhance community detection by incorporating abstract and keyword metadata as a proxy for ground truth classification and identifying meaningful community representatives. We also plan to extend our analysis to other significant network science packages. This study lays the groundwork for a deeper understanding of the interactions among network science software users and their respective communities.

Keywords: Software ecosystem; Dependency graph; Bibliometrics; Community detection; igraph;

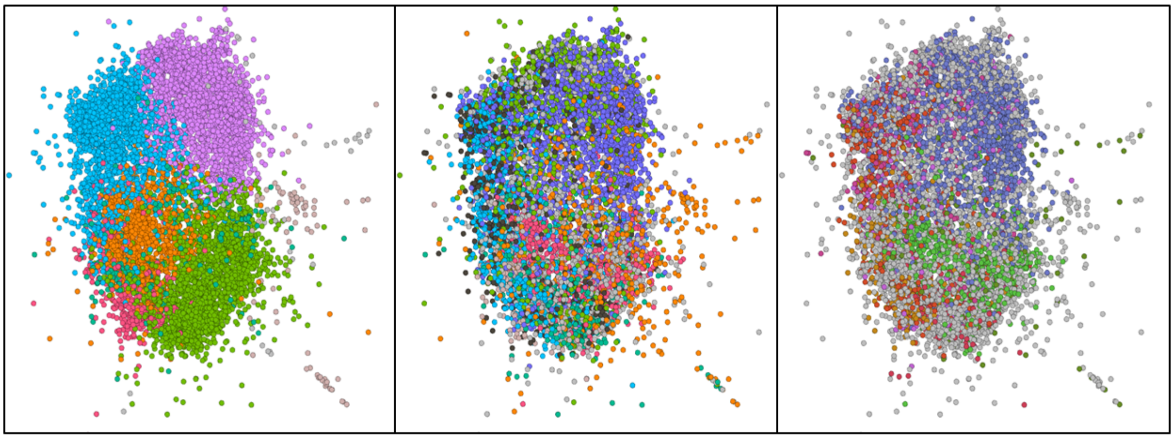

Figure 1: **Visualization of a Bibliographic Coupling network across different attributes for papers mentioning igraph**. In the first map, nodes are colored according to their membership as derived from the Leiden algorithm. The second map assigns colors based on the primary academic fields as defined by OpenAlex. The third map assigns colors based on the secondary or deeper academic fields as defined by OpenAlex.

A Network analysis of Intermedia Agenda-setting in the News discourse about the Mpox epidemic

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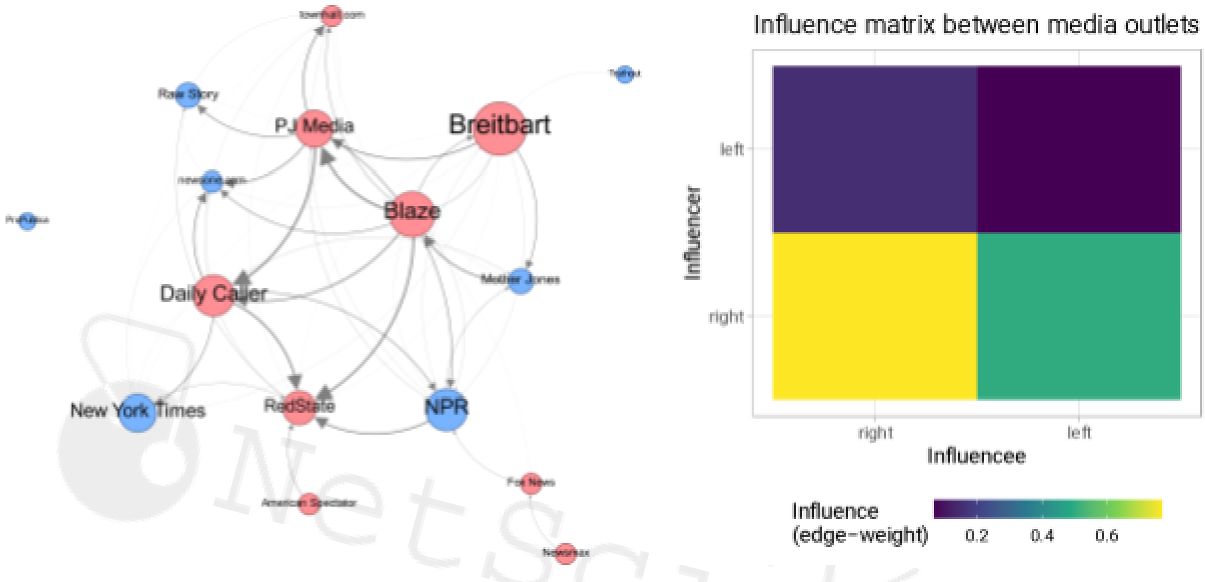
Keywords: Intermedia influence; Social network analysis; Bayesian structure learning; Health communication.

News media can shape public perceptions of political reality and subsequent attitudes towards important health issues (1,2). Crucially, Intermedia Agenda-Setting (IAS) theory posits that news discourses are characterized by outlets that influence each other's coverage by co-orienting journalists towards a specific agenda (3). Prior work (3,4) has shown the merit of representing IAS as a network influence problem, by defining the news outlets as nodes and intermedia influence as directed edges. Given how partisan leanings of news outlets drive their reporting (5), we ask: how does outlet partisanship interact with IAS in intermedia influence networks? Are outlets primarily influenced by other co-partisan, or counter-partisan outlets?

In this paper, we studied IAS in the context of the news discourse during the Mpox epidemic of 2022 in the United States. As Mpox disproportionately (94% of case counts) affected men who have sex with men (MSMs) (6), we focused on the controversial and competitive framings surrounding homosexuality and sexual transmission as factors driving the epidemic. While right-leaning news articles overwhelmingly stigmatized MSMs and preached abstinence, left-leaning articles offered competing frames, highlighting the need for sex-positive and queer affirmative approaches.

We obtained 594 articles published between 1st May and 31st October 2022 by 16 national news outlets from media cloud (7), and annotated them using applied thematic analysis (8), identifying competitive news frames surrounding sexuality and Mpox. Then, we derived time series for 16 news outlets over 6 months, signifying the proportion of published articles every day that featured these framings. In contrast to prior studies that used granger causality to infer relationships (3,4), we used a methodological pipeline combining Bayesian structure learning (9) with transfer entropy (10), dropping the assumption of pairwise independence between edges.

Thus, we inferred a weighted and directed network of intermedia agenda-setting relations (Figure 1A). In contrast to previous findings where mainstream left-leaning outlets such as the New York Times were primary agenda-setters, our analysis underscored low credibility, right-leaning outlets such as Breitbart and Blaze as central influencers. Interestingly, left-leaning outlets exhibited negligible partisan-aligned ties (Figure 1B), borrowing agendas primarily from right-leaning outlets. Importantly, we found that this counter-intuitive result was not true for Mpox-related agendas without competitive framings (such as critiques about vaccine disparities), suggesting that counter-partisan agenda-setting was driven by the controversial and competitive narratives surrounding sexuality. Our study provides important insights as to how social network analysis can be leveraged to understand the reactive intermedia influence patterns underlying health controversies.



(a) **(b)**

Figure 1: Intermedia influence network (left) and normalized mixing matrix (right)
(a) Network of influence between 16 news outlets plotted using Force Atlas layout. Edge weight and opacity denotes strength of influence, node size is scaled by out-degree and node color denotes partisan leaning of the outlet (red and blue are right and left-leaning respectively). Right-leaning outlets are central actors.
(b) Total influence of an average influencer (Y-axis) on influencees (X-axis). On average, right leaning outlets influence each other the most. Notably, left leaning outlets are influenced the most by right-leaning outlets, as opposed to other left-leaning outlets.

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Identification of spurious edges in ChIP-seq derived gene regulatory networks

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Gene regulatory networks (GRNs) have been extensively studied to understand gene expression and cell state dynamics in biological systems. GRNs can be represented as bipartite networks between transcription factors and their target genes (**Figure A**). These networks can be inferred using sequencing technologies such as **Ch**romatin **I**mmuno**P**recipitation **seq**uencing (ChIP-seq) that capture the binding of transcription factors to target gene sequences. However, previous studies indicate that edges identified from ChIP-seq data can contain non-specific — i.e., spurious — interactions that do not lead to transcriptional regulation of the target gene [1,2].

Removal of these spurious edges is crucial for sparsification of complex GRNs and to improve the accuracy of predictive models for transcription and gene expression. Identification of these edges is contingent on the development of appropriate pre-processing pipelines. Critical to such a pipeline are parameters such as signal-to-noise ratio used for edge detection, the reference genome version used for alignment and the interaction distance around the transcription start site used for defining these interactions.

Here, we report a systematic study of the sensitivity of called edges to the choice of pre-processing parameters. Our analysis enables us to develop a two-mechanism statistical model to determine appropriate interaction distance thresholds that minimize spurious binding and remove inessential edges from GRNs (**Figure A**). Additionally, we validate our model using 75 ChIP-seq datasets [3] to show that spurious edges identified by the model display significantly lower pairwise correlation for RNA expression (**Figure B**) and are less likely to be RNA polymerase-bound than true edges. Overall, our model proposes switching from uniform pre-processing parameters for all datasets to a dataset-specific classification threshold that reduces spurious edges and infers GRNs that closely reproduce experimental data.

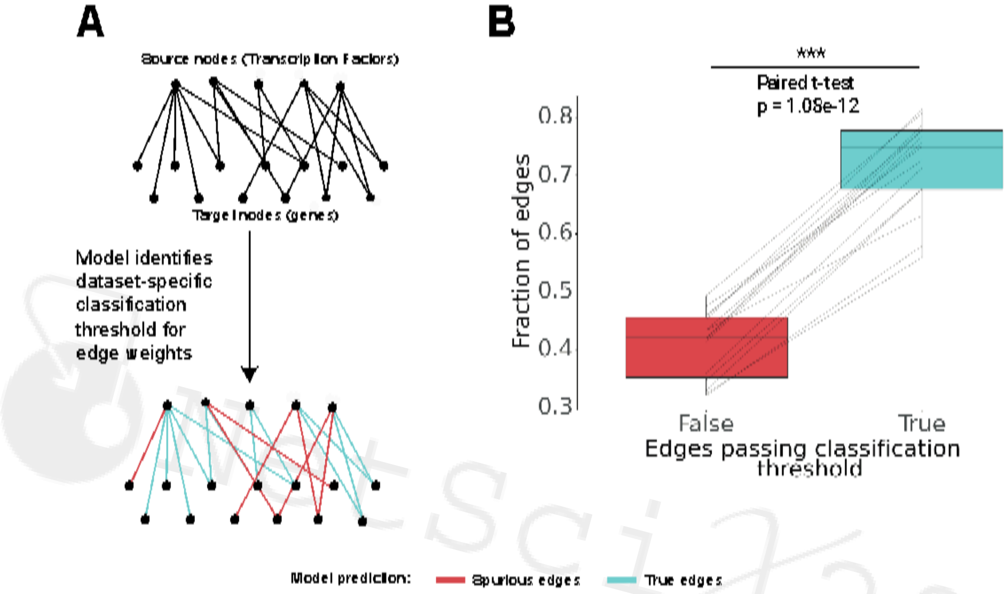

Figure: Two-mechanism statistical model accurately identifies spurious edges.

A. Model identifies interaction distance threshold (FDR = 0.05) to classify edges as true and spurious. Each edge is assigned a weight based on relative distance from the target gene's transcription start site. Edges that are below the source node-specific threshold are classified as true while the rest are assigned as spurious.

B. True edges identified by the model have a significantly higher fraction of edges displaying strong correlation (| Spearman correlation coefficient | > 0.4 and p-value < 0.05) between the source and target transcription levels measured using RNA-seq data for K562 cell line .Thus, edges identified as spurious by the model are less likely to be involved in transcriptional regulation as compared to true edges.

Keywords: gene regulatory networks; network inference; systems biology

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Modelling Epidemic Spread and the Effectiveness of Malaysian Movement Control Regimes in Selangor via Social Networks

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Given the prevalence of disease outbreaks over the years, it is inevitable that future epidemics could occur. In light of the recent COVID-19 pandemic that claimed the lives of many, it is more critical now than ever for authorities to effectively manage epidemic spread to reduce casualties. Despite the advancement of mathematical epidemiology, effective epidemic management remains a challenge globally due to diverse factors making it impractical to generalise a single public health policy universally. Being the most populous state in Malaysia, Selangor has been particularly impacted by the recent pandemic. This study implements social network analyses to quantify the robustness of control regimes in mitigating disease transmission and safeguarding public health. The main aim of this study is to evaluate the effectiveness of Movement Control Orders (MCOs) implemented by the Malaysian government in curbing epidemic spread within Selangor. To capture the crucial dynamical characteristics based on different interventions, network epidemiology modelling techniques are paired with the SEIR mechanism, real-world data validation and compliance quantification. Different network models are generated based on an underlying social contact network of Selangor to simulate each MCO. The Barabási-Albert (BA) scale-free network, Small-World network with varying rewiring probabilities based on compliance, Erdős–Rényi random graph with a cap on mass gatherings and regular lattice model are used to represent normal movements without restrictions, the Movement Control Order (MCO), Conditional Movement Control Order (CMCO) and Enhanced Movement Control Order (EMCO) respectively. Furthermore, by extending epidemic models to various social network topologies, the study aims to elucidate how different social structures influence disease transmission patterns, thereby informing evidence-based public health policies and strategies. Inherently, the reduction in infection spread attributable to the MCOs can be calculated, helping deduce the percentage of compliance needed to curb epidemic spread in Selangor. Based on the models built, this study outlines actionable recommendations for policymakers and stakeholders to enhance epidemic control efforts in Selangor and thus strengthen their preparedness for any future outbreaks. Essentially, this study is able to emphasise the role of network topology in understanding and controlling infectious disease outbreaks.

Keywords: Social network; Epidemic spread; Malaysia; Control regimes

Unraveling The Legal Dynamics: A Network Analysis of Legal Status Transitions Among Migrants and Refugees in Austria

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In today's world, international migrants collectively represent the fourth-largest population globally, and approximately 1% of global GDP is transmitted as international remittances [2, 1]. By the end of 2022, nearly 110 million people had been displaced due to violence, a figure that has doubled in less than a decade [4]. While migration models often focus on the driving forces behind arrivals [3], the legal journeys of migrants and refugees—from entry to exit—remain largely unexplored.

This study employs network analysis to investigate the intricate landscape of legal status among migrants and refugees in Austria, where migrants make up around 20% of the population [3]. We analyze transitions within the Austrian legal system and the dynamics between various legal statuses. Utilizing comprehensive legal administrative data from Austria, which includes all migrant statuses in the country, we construct a network of 11 possible legal statuses. This network maps out the frequency of transitions between statuses (Figure 1). We model these transitions over a one-year period, with edges representing the probability of a change in legal status. By examining transitions across different nationalities, we assess both short-term transitions and the long-term distribution of statuses for migrants and refugees in Austria. Our findings reveal that refugees experience a higher degree of variability in legal status transitions compared to other migrants. With up to 110 potential legal status changes, this highlights the complexities of their integration into Austria. Germans exhibit the lowest variability in legal status transitions, with only eight possible transitions, reflecting a more stable legal trajectory. In contrast, Afghans show significant variability with up to 35 possible transitions, Syrians with 24, Indians with 17, and Ukrainians with 14.

Additionally, our analysis of long-term exit probabilities reveals distinct patterns for each nationality. Syrians exhibit a high likelihood of achieving "Entitled to Asylum", with approximately 91% eventually securing this status. Ukrainians primarily attain the status of "Displaced Person" (55%), but a notable 35% leave Austria. Germans predominantly attain "Residence" status (67%), while 21% leave Austria. Indians have the highest probability of leaving Austria 42%, with 40% obtaining "Residence" and 12% remaining as "Foreigners" without residency. This analysis allows us to estimate the time required for individuals from different nationalities to attain stable statuses, such as "Residence". Understanding these legal dynamics is crucial for developing more effective policies and support mechanisms. By mapping the legal landscape and long-term exit probabilities, our study highlights the complex challenges faced by migrants and refugees, providing valuable insights for enhancing integration strategies and policy development.

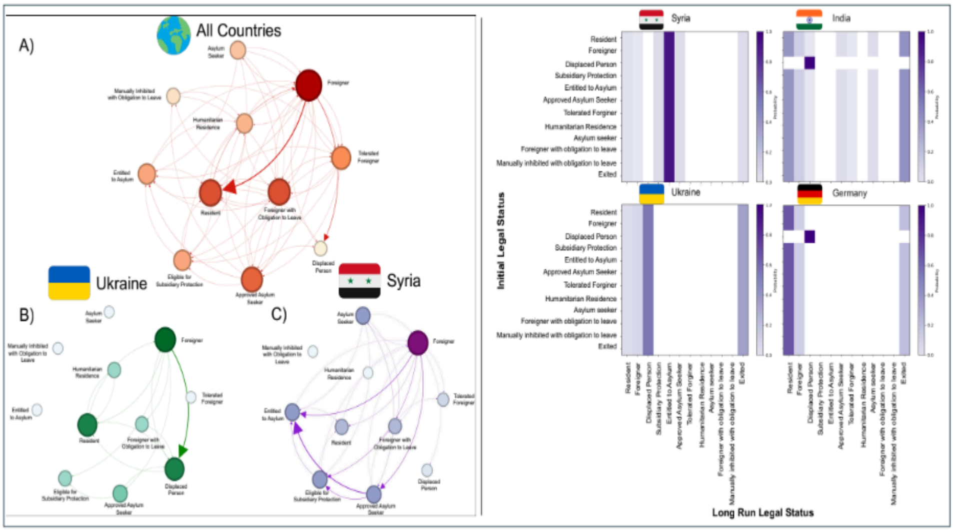

Figure 1: Legal Status Network of Migrants in Austria. (Left) The structure of the network Nodes corresponds to legal statuses, their size corresponds to their degree, and the edge between them is the

probability of having that change in status for migrants (A) from all countries, (B) Ukraine and (C) Syria. (Right) The steady-state distribution of the Markov Transition probability of migrants from Syria, India, Ukraine and Germany.

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Dynamic stability of complex network dynamics

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As we know that the stable functionality of networked systems is a hallmark of their natural ability to coordinate between their multiple interacting components. Yet, strikingly, real-world networks seem random and highly irregular, apparently lacking any design for stability. What then are the naturally emerging organizing principles of complex system stability? Encoded within the system's stability matrix, the Jacobian, the answer is obscured by the scale and diversity of the relevant systems, their broad parameter space, and their nonlinear interaction mechanisms. Emergent patterns in the structure of the Jacobian are also rooted in the interplay between the network structure and the system's intrinsic nonlinear dynamics (Fig. 1 (A)). These patterns help us analytically identify the few relevant control parameters that determine a system's dynamic stability. With the help of the stability classifier parameter (Fig 1 (B), we can predict a system’s stability, exposing three broad dynamic classes namely asymptotically stable, asymptotically unstable and sensitive stable. In the asymptotically unstable class, diversity, indeed, leads to instability (May’s paradox). However, in asymptotically stable class is the class in which most real systems reside, where diversity is not only possible, but, in fact, becomes inevitable. In sensitive stable class, stability abides within a bounded range of the system's parameters. Our theory uncovers the naturally emerging rules of complex system stability, helping us reconcile the May’s paradox that has eluded us for decades.

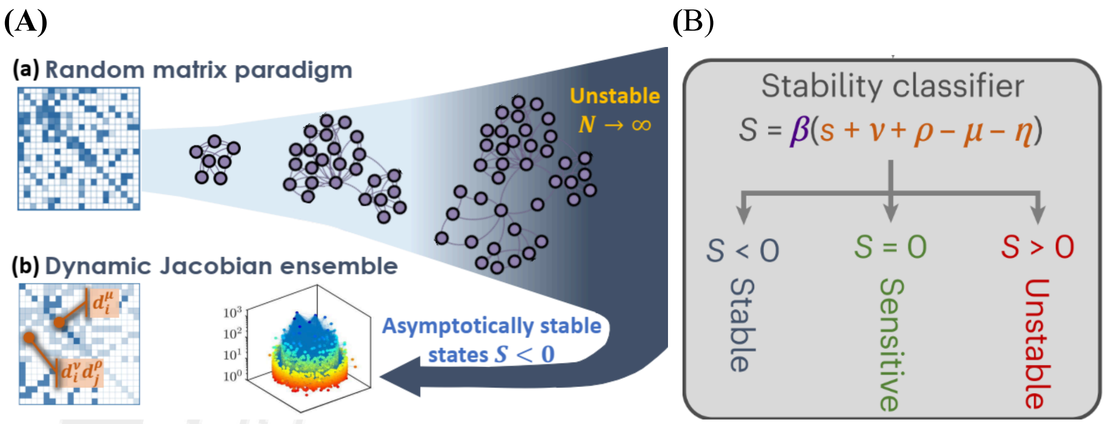

Fig 1: Will a large complex system be stable? Answered using the dynamic Jacobian Ensemble (A) and Stability classifier (B) which depends on network structure and dynamics through the exponents.

Keywords: Complex systems; Networks, Dynamic Jacobian Ensemble, Stability.

Reference: Chandrakala Meena, Chittaranjan Hens, Suman Acharyya, Simi Haber, Stefano Boccaletti and Baruch Barzel, "Emergent stability in complex network dynamics", NATURE Physics, 19, 1033–1042, 2023.

Assessing the Impact of Transportation Infrastructure on Urban Accessibility Equity: A Network-Entropy-Based Approach

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Motivation

Modern transportation infrastructure has drastically reduced travel time between cities. However, city accessibility remains uneven, with some cities benefiting from rapid connections and others remaining relatively isolated. Promoting balanced urban systems is crucial to unlocking the economic potential of peripheral regions and addressing regional disparities [4]. Thus, it is essential to determine whether changes in transportation infrastructure make city systems more equitable or exacerbate existing accessibility imbalances. We propose a network-theoretical approach to assess equity in city accessibility and the impact of transportation infrastructure changes.

Method

We construct a family of disc graphs $\{G_t\}_t$, for a varying travel time threshold t, where nodes represent cities. In these graphs, two cities are connected if their travel time is less than or equal to t. We calculate the first-degree based entropy for each

disc graph, defined as the Shannon entropy $H(G_t)$ of its degree sequence $\{d_j\}_{j=1}^{n}$:

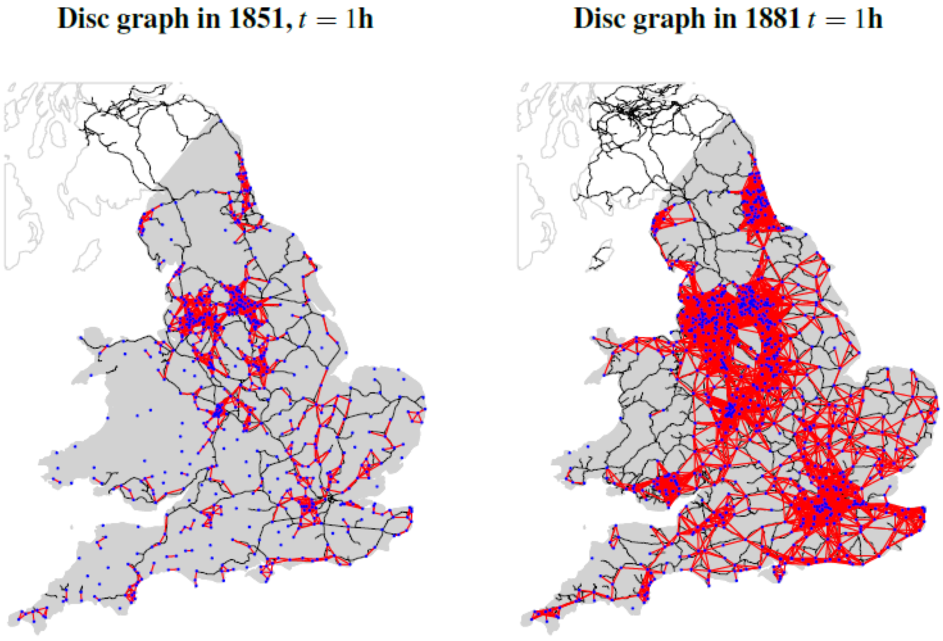
$$H\left(G_t\right) = -\sum_{j}^{n} \frac{d_j}{2m_t} \log \frac{d_j}{2m_t} \ ,$$

where m_t is the number of links. Higher entropy values indicate a more uniform distribution of connections, suggesting a more balanced network [3].

To facilitate comparison across different travel time thresholds and evolving city networks, we normalize $H(G_t)$ using the extremal values for given order n and order n and size m computed in [1, 2, 8], resulting in indices $I_n(G_t)$ and $I_{n,m}(G_t)$, which range from 0 to 1.

Case study

We apply this method to assess the change in accessibility balance for English and Welsh cities from 1851 and 1881, a period marked by rapid urbanisation and railway expansion. Travel times are computed using historical railway shapefiles [6, 10, 5, 7], and a method detailed in [9].



Disc graph in 1851, $t = 1$h

Disc graph in 1881 $t = 1$h

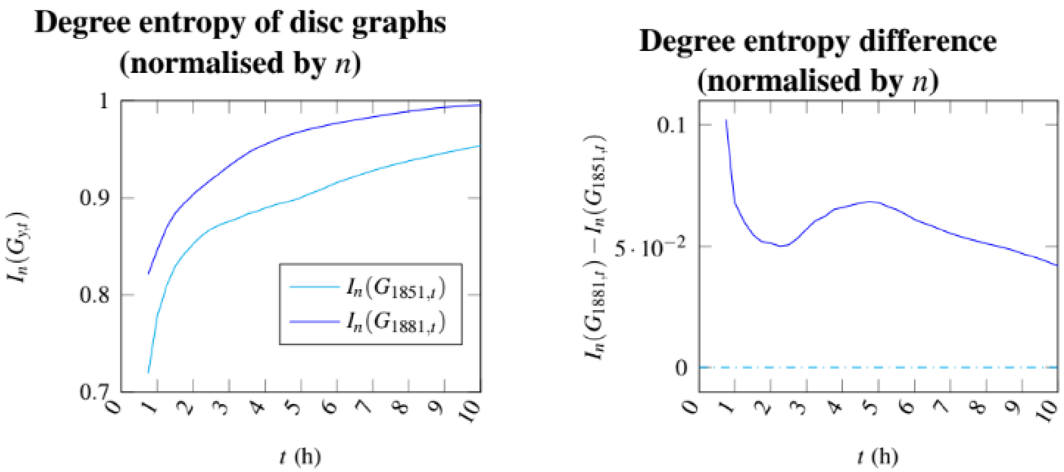
(a) For a travel time threshold of 1h, most links are in the major urban clusters or follow the sparse railway lines. Several towns remain disconnected.

(b) Faster trains and a more capillary railway network expand the link set. Most towns are part of the same giant component, though a few towns remain isolated.

Figure 1: Disc graphs of English and Welsh towns in 1851 and 1881, for a travel time threshold of t = 1h. Towns are represented as blue dots, railway lines are in black, and the network links are in red. Clusters emerge around London in the South, in the Midlands in the centre, and around the Pennines and the Tyne Valley in the North.

Fig. 1 shows the dramatic increase in connections within a 1-hour travel time and improved overall connectivity from 1851 to 1881, driven by an expanded railway network and faster trains. The first degree-based entropy analysis (Fig. 2) indicates that the 1881 network is generally more balanced than in 1851 particularly when considering the order-normalised entropy I_n. For most travel time thresholds t, $I_{n,m}(G_{1881,t})$ exceeds $I_{n,m}(G_{1851,t})$, reflecting a more balanced network, even accounting for differences in network size.

However, normalized entropy values are lower compared to disc graphs based on geographic distance, suggesting that railways improved connectivity around select towns, thereby increasing overall imbalances in accessibility.

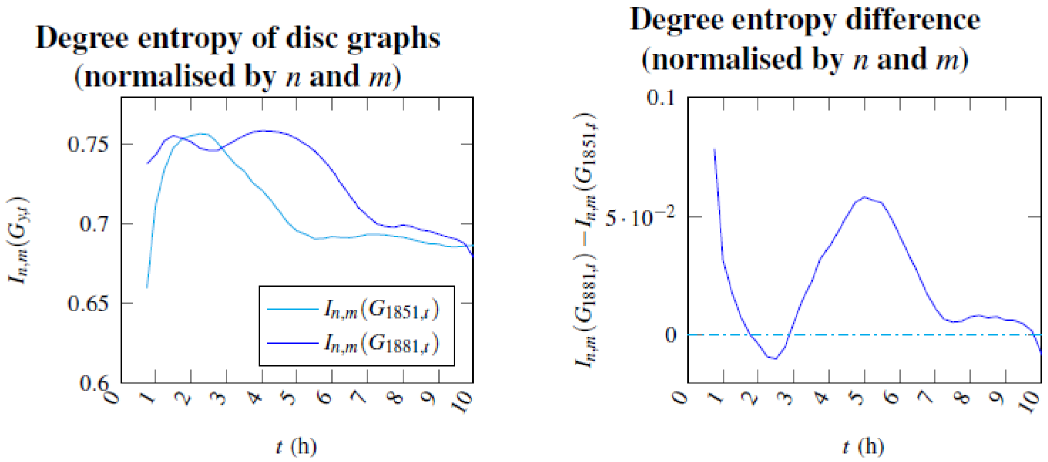


Degree entropy of disc graphs (normalised by n)

Degree entropy difference (normalised by n)

(a) In both 1851 and 1881, the entropy grows monotonically, as the graph size increases. $I_n(G_{1851,t})$ grows fast until $t \approx$ 2h15min, for which most towns are connected in a giant component, whilst for larger thresholds, the increase is more moderate.

(b) $I_n(G_{1881,t}) > I_n(G_{1851,t})$ for all travel time thresholds, with a local maximum at $t =$ 4h45min. In 1881 this travel time was enough to reach London and the Tyne estuary from the main Pennines/Midlands clusters, which means that the clusters were more balanced and integrated.



Degree entropy of disc graphs (normalised by n and m)

Degree entropy difference (normalised by n and m)

(c) $I_{n,m}(G_{1851,t})$ peaks at $t \approx$ 2h15min, but the presence of the railway accentuates imbalances for larger t. $I_{n,m}(G_{1881,t})$ peaks twice, when most towns are part of the same component ($t \approx$ 1h30min) and when the clusters become better integrated ($t \approx$ 4h45min), but for larger values of t, the system is less balanced.

(d) The system is more balanced in 1881 than in 1851 for small travel time, but less so for $t \approx$ 2h15min, when $I_{n,m}(G_{1851,t})$ reaches its peak. When $4 \leq t \leq$ 10h, most towns become densely interconnected in 1881, which is not yet the case for 1851, making the network more balanced than in 1851.

Figure 2: Normalised degree entropy of the disc graphs in 1851 and 1881, for travel time 45min $\leq t \leq$ 10h. Note that for $t >$ 10h, $I_{n,m}(G_{1881,t})$ would not be indicative of the centralisation of the system due to the excessive sensitivity of the measure for large sized graphs.

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Mitigating Epidemic Spread using Digital Contact Tracing

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Digital contact tracing is vital in mitigating the spread of infectious diseases, particularly in managing large-scale outbreaks. However, designing an efficient multilevel digital contact tracing framework for a country remains a significant challenge due to the complexity of analyzing vast amounts of temporal contact data. In response, we have developed a sophisticated multilevel digital contact tracing framework that dynamically constructs contact graphs from proximity data, effectively capturing the nuances of social interactions over time. A key innovation of our framework is the introduction of a binary circular contact queue as the edge label of the contact graph. This queue efficiently stores temporal social interactions within the incubation period, enabling the algorithm to accurately identify both direct and indirect (multilevel) contacts for any given set of infected individuals. Furthermore, the framework's ability to trace infection pathways ensures a comprehensive understanding of potential transmission chains. We have implemented and rigorously tested our framework using both synthetic and real-world datasets. Our analysis demonstrates that, even with COVID-19 close

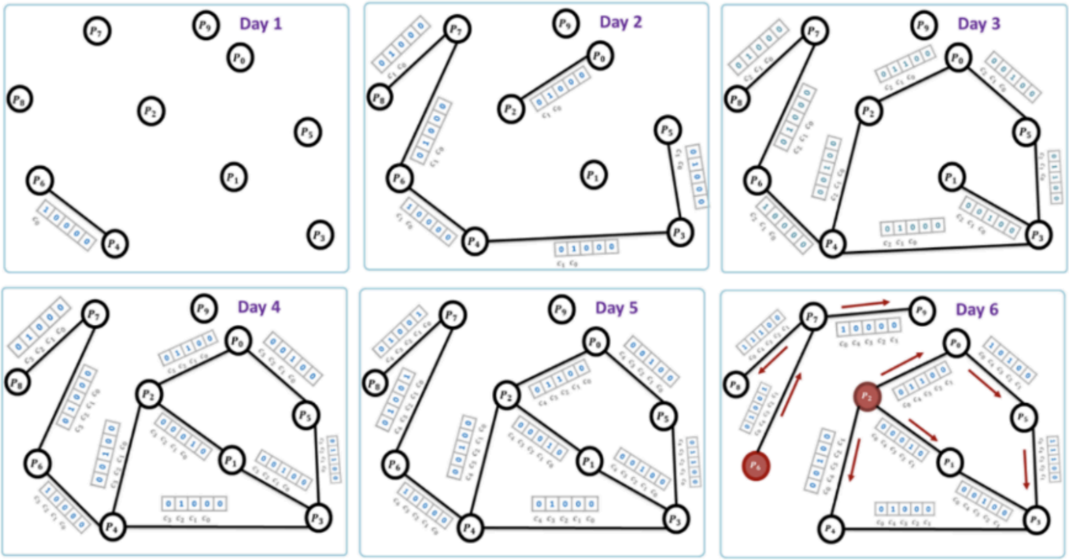

Figure 1: Graphical representation of the multilevel digital contact tracing framework.

contact parameters, the framework is both space- and time-efficient in constructing infection pathways. Notably, the adaptability of our framework allows it to be applied to a wide range of epidemics by simply adjusting the algorithm's parameters. This flexibility makes it a valuable tool in the ongoing effort to contain infectious diseases.

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Measuring multidimensional polarization in social media populations across countries in comparable political dimensions

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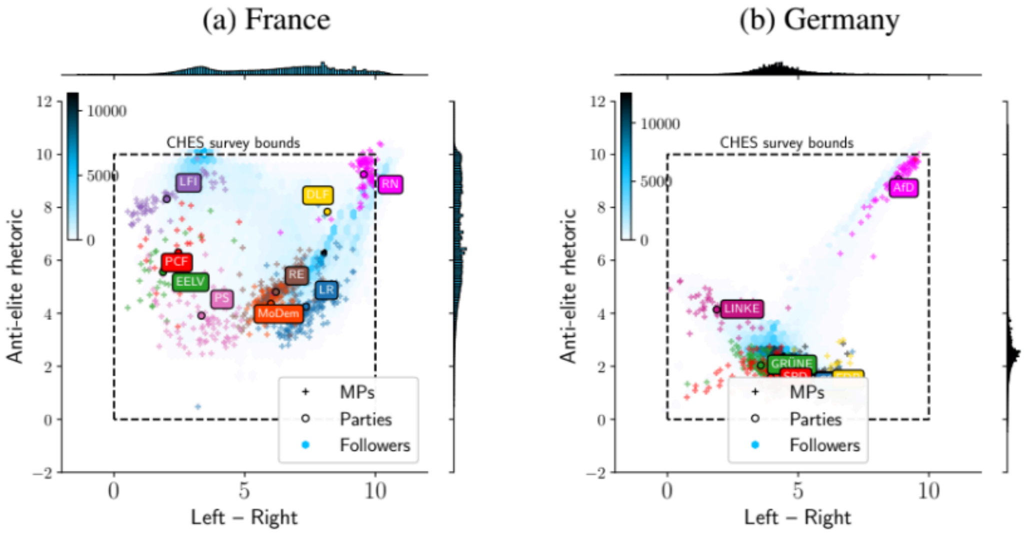
Polarization in society has become a relevant object of scientific study but, despite decades of results, gaps persist in providing a sufficient understanding of this phenomenon, as well as results that would lead to actionable policy (e.g., in social media and algorithm design). One of these gaps is in the measurement of polarization: Is polarization increasing? In which populations is polarization higher? This gap is often structured along three challenges: 1) dimensionality of the underlying political space, 2) observability, and 3) comparability. 1) The problem of dimensionality spawns from the fact that recent results have shown that polarization is a multidimensional phenomenon that cannot be reduced to a single Left-Right or Liberal-Conservative dimension. Different national settings, for instance, require that polarization be measured on several independent issue dimensions (e.g., dimensions of attitudes towards immigration or environmental protection). This dimensional heterogeneity across settings raises the problem of the selection of the relevant issue dimensions on each study. 2) Measuring polarization is also limited by the unobservability of opinions in a population. Tradition-ally, representative samples among which to administer self-positioning political surveys have been leveraged in measurements, which limits temporal resolution, and, because of associated costs, cross-national comparative studies. Survey-based approaches also hinder the possibility of linking individuals with other data traces of interests: e.g., what they see, like, or share in social media. Indirect approaches for measuring stances from social media trace data, on the other hand, introduce different biases when compared with country-wide populations (e.g., age, gender, and education biases). 3) Additionally, opinion or stance estimation on several issues from social media data is difficult to compare across national settings, limiting much needed comparative studies. This is due the language diversity present across national settings, but also because of the lack of reference frames of measurement for opinion scales.

In our work, we address all three challenges using network data from social media across several national settings to provide a comparative multidimensional measurement of polarization. At the core of our method, we leverage homophilic generative network models to infer latent opinions shaping friendship networks. We use X/Twitter data from several countries. Relying on network data (who follows whom networks, and not text data), we are able overcome the challenges imposed by language diversity across national settings by avoiding text-dependent inference. Next, we map inferred latent opinions onto positions on issue scales/dimensions taken from expert surveys providing political party positions on comparable scales across all national settings. The use of expert surveys positioning markers such as political parties in issue dimensions that are common to several countries provide an opinion reference frame dimensions onto which to project the positions of individuals across countries. The result is a multidimensional political issue space comparable across countries on which users are embedded. Finally, using a model trained to infer age and gender, as well as census data, we post-stratify online populations to measure polarization of opinion distribution across different political issues, providing a quantitative multidimensional estimation of political polarization in the world.


(a) France

(b) Germany

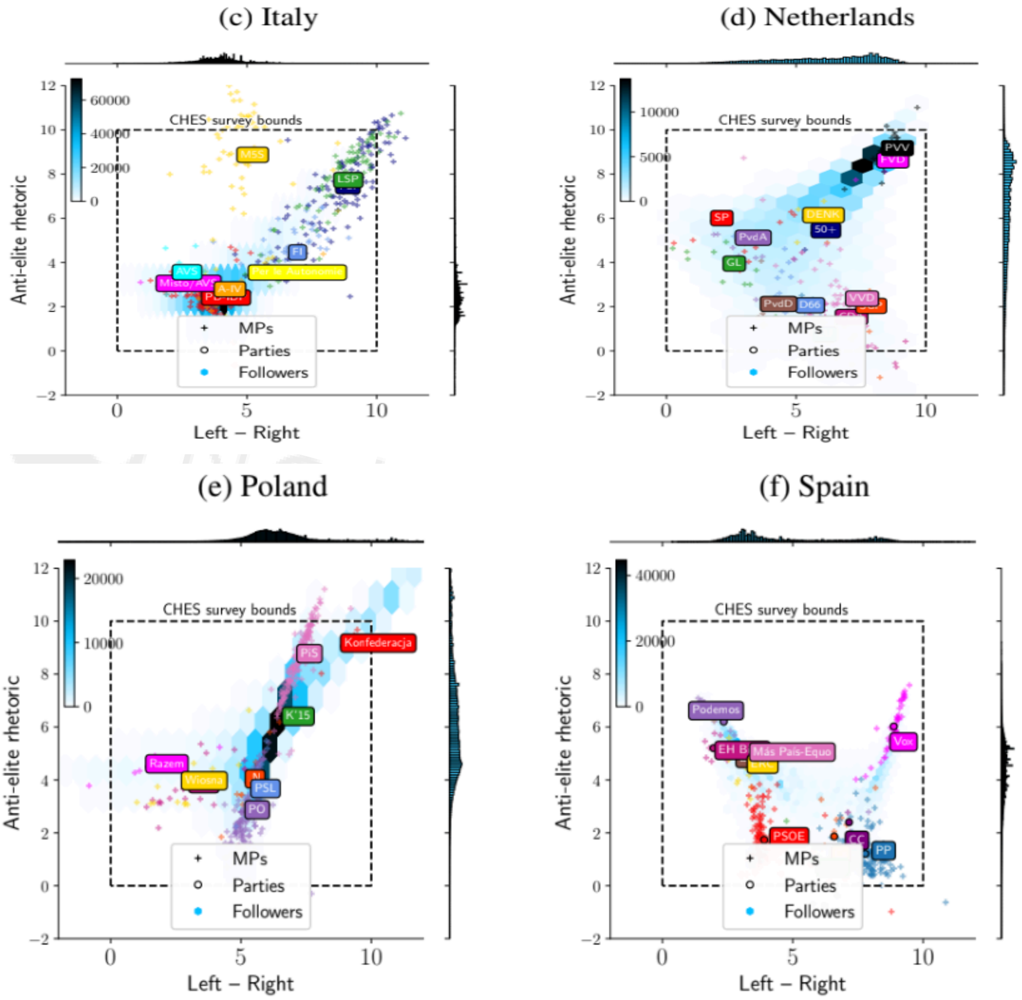


Figure 1: Large Twitter populations in six European countries, selected from neighbors or elected MPs in the follower graph, and embedded in multidimensional po-litical opinion spaces dimensions (dimensions Left-Right and Anti-elite shown in figure) calibrated using as reference space scales of the Chapel Hill Expert Survey (CHES) for parties.

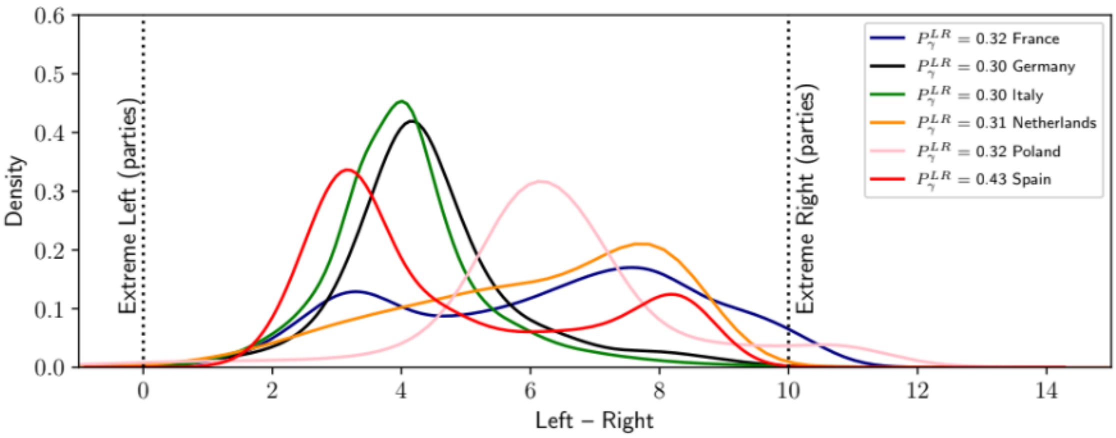


Figure 2: Distribution of our large X/Twitter populations per country along the comparable Left-Right dimension, with polarization metrics P_γ^{LR} computed using the Duclos-Esteban-Ray polarization measure. The political Twitter sphere of Spain is quantitatively the most polarized among the countries in our study.

The interplay of structural balance and frustration governs the emergent dynamics of biological networks

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Structural balance is a well-studied principle in signed social networks, regulating the dynamics and evolution of social interactions. A signed network is considered structurally balanced if all triads (subnetworks of three mutually connected nodes) have an even number of negative signs (0 or 2). Such balanced networks can be divided into two disjoint sets/teams of nodes, with positive interactions occurring only within the same team and negative interactions occurring between nodes of opposite teams. Real networks are often partially balanced, containing some frustrated triads or inconsistent interactions within and across the teams[1].

Recently, we discovered the presence of these disjoint ”teams” of nodes in signed, directed biological networks called gene regulatory networks (GRNs) [2]. Mutually inhibiting teams are found in multiple contexts of binary cell-fate decision systems, where cells can switch between two phenotypes, each characterized by a unique protein expression pattern. However, these networks are only partially balanced, with varying degrees of frustration and edge density (5-30%). The implications of these frustrated edges and varying densities are not well understood. In the current work, we analyze the effects of varying density and frustration in partially balanced GRNs. We generate artificial networks using the stochastic block model with varying degrees of density and frustration. We then simulate these networks along with biological networks using a continuous, ordinary differential equation-based formalism and a discrete, threshold-based Boolean formalism and analyze the configurations and stability of the emergent steady states and their dependence on density and frustration. We found that most of the state space converges to two phenotypes supported by the two teams (referred to as ”terminal” phenotypes) at lower frustration levels. These terminal states remain stable upon extensive external perturbations, demonstrating the robust impact of structural balance in signed, directed networks. The presence of frustration allows for the emergence of weakly stable ”hybrid” states with partial expression of nodes from either team, which play important roles in various biological contexts.

We further show that the average stability of the terminal phenotypes varies sigmoidally with both density and frustration, while the stability variance has a Gaussian nature. Biological networks are found in the region of the sigmoid with high variance, aligning with the hypothesis of near criticality of living systems. Overall, our results provide a detailed characterization of the effects of density and frustration on partially balanced signed, directed networks. Since any network can be viewed as a partially balanced network of two teams, our characterization can help empirically predict the stability of emergent phenotypes in any signed, directed network, aiding in the development of a general theory of stability for such networks.

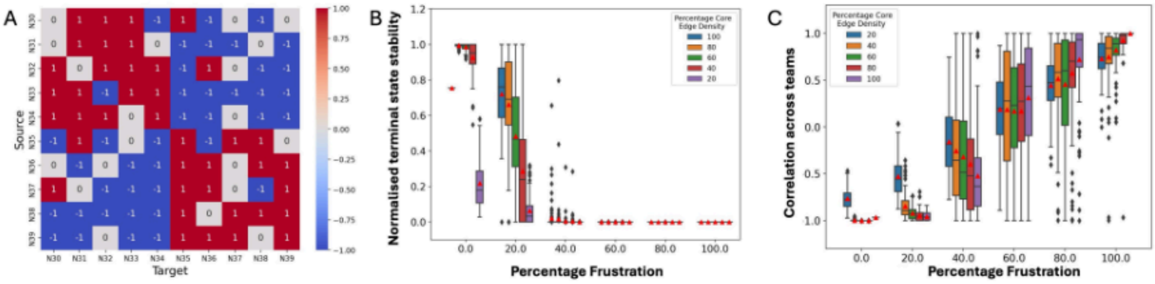

Figure 1: A. Example of an artificial network generated using SBM model with 80% density and 20% impurity B. Stability of terminal steady states as a function of frustration (x-axis) and density (fill). C. Correlation between the expression of the two teams as a function of frustration and density

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The dynamics of higher-order novelties

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Understanding how novelties emerge in science and technology is key for fostering innovation. Recent studies have shown that human-generated discovery processes, e.g. creating new ideas, cultural artworks, inventions, share common patterns in how new elements emerge and are exploited. Among these patterns, the Heaps' law—–a power-law relation between the number of novel elements and the length of a sequence—–can quantify, for example, the use of new words in a text or the discovery pace of new artists in a music playlist. With the growing availability of data on human behavior and consumption habits, researchers have proposed various models to explain these dynamics. These models, ranging from urn-based extractions to random walks on complex networks, are built on the idea that discoveries occur among items that are 'one step away" (or *adjacent possible*) from what is already known. However, an overlooked aspect is that novelties can also arise from the combination of existing material. This phenomenon is widely observed across various domains, including biology, economics, and science. For instance, successful scientific publications are often novel combinations of prior results.

In this work [1], we extend the notion of novelty to groups of *n* consecutive elements that appear for the first time in a sequence. Specifically, we consider not only the first occurrence of a single element but also pairs, triplets, and so on. To characterize these occurrences, we introduce the *n*th-order Heaps' law, which quantifies the first appearance of *n*-tuples in a sequence. Through extensive analysis of empirical data sets, we reveal that processes with the same rate of discovery and clustering properties can exhibit different higher-order Heaps' exponents, indicating distinct ways of exploring a similar set of elements (see Fig. 1(a-c)). We also analyze a recently proposed family of urn-based models and random walks, finding that these models fail to capture the higher-order characteristics observed in empirical data.

To address this limitation, we extend the concept of the adjacent possible to include novelties that emerge as new associations between existing elements. We envision innovation as a process of exploring a growing complex network, where each node represents a concept or an item, and edges symbolize the connections between them. This network expands over time, either by adding new nodes, creating new links, or reinforcing existing ones. We propose to model this exploration process using an edge-reinforced random walker with triggering (ERRWT), which balances the reinforcement of traversed edges with the triggering of new adjacent possible nodes and links whenever a node or link is explored for the first time. By effectively balancing the exploitation of existing knowledge and the exploration of new elements and associations, the ERRWT can reproduce different 1st- and 2nd-order Heaps' exponents (see Fig. 1(d)).

By capturing the observed properties of higher-order Heaps' laws, our work sheds light on the patterns and mechanisms underlying the emergence of novelties. In particular, it highlights the critical role of the exploration process in shaping the growth of the space of possibilities.

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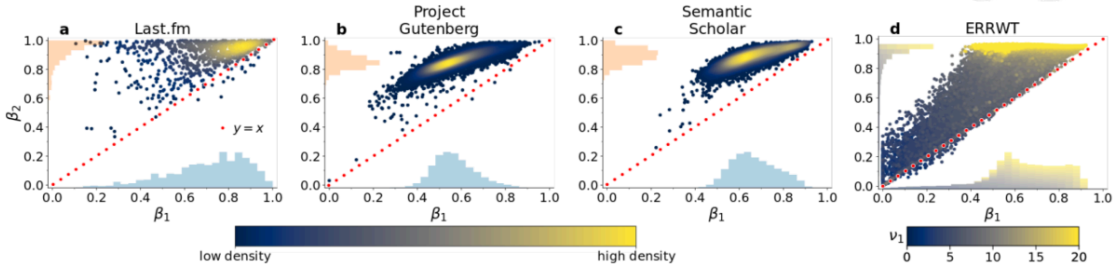

Figure 1: Scatter plots between the (standard) Heaps' exponents β_1 and the 2nd-order ones β_2. Each point refers to a different sequence, made of (a) songs listened by a user of Last.fm, (b) words in a book from Project Gutenberg, (c) words in titles of top-journals available in Semantic Scholar, and (d) nodes visited by the Edge-Reinforced Random Walk with Triggering model. Notice how the ERRWT can reproduce different pairs (β_1, β_2) varying the parameters.

Finite size effect in Kuramoto oscillators with higher order interactions

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Finite-size systems of Kuramoto model display intricate dynamics, especially in the presence of multi-stability where both coherent and incoherent states coexist. We investigate such a scenario in globally coupled populations of Kuramoto phase oscillators with higher-order interactions and observe that fluctuations inherent to finite-size systems drive the transition to the synchronized state before the critical point in the thermodynamic limit. Using numerical methods, we plot the first exit time distribution of the magnitude of complex order parameter and obtain numerical transition probabilities across various system sizes. Further, we extend this study to a two-population oscillator system, and, using the velocity field of the associated order parameters, show the emergence of a new fixed point corresponding to a partially synchronized state arising due to the finite-size effect, which is absent in the thermodynamics limit.

Polarization and issue alignment on Twitter

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In the public debate on the role of social media, they are frequently cited as bot the cause and the arena of a growing political polarization. In order to provide better empirical evidence for such claims we investigated polarization on Twitter by analyzing both the interaction structure as well as the content of trending topic (which we call trends in the following) of the German Twitter sphere over two years (March 2021 until July 2023). Our dataset contains 2964 trends with more than 20M German tweets and ca. 842k interacting users.

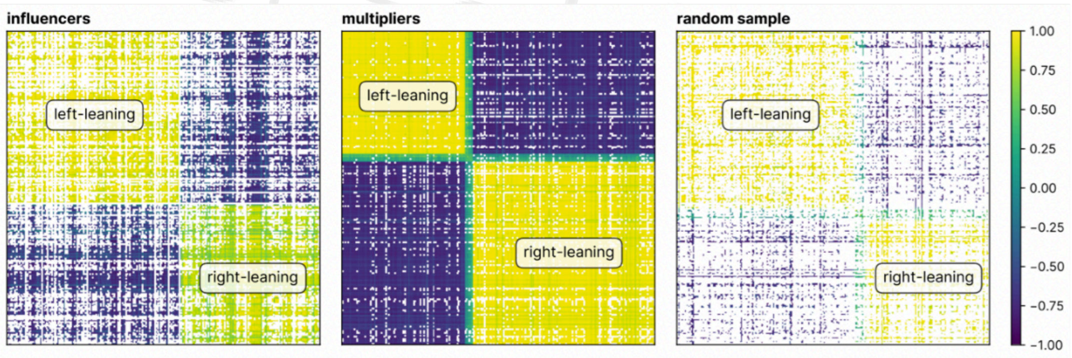
In order to extract the issues discussed in the corpus, we compute a BERTopic model (Grootendorst 2022) on the single tweets and hand-label the trends based on their most frequent topics. The most prominent issues are related to Covid, German politics, the war in Ukraine, sports and climate change. With this issue assignment at hand, we measure the polarization of each trend, assuming that a trend can either be polarized or not: there can be either two opposing opinion camps or one single consensual camp. We operationalize this assumption by computing clusters in the retweet network of each trend. Each node is a user, and a directed link is drawn from i to j if i retweets j. Assuming that retweets are endorsements, we interpret densely connected clusters in the retweet network as opinion groups in the underlying debate (Conover et al. 2011). Conceptually, we treat the retweet network as an opinion poll. For each polarized issue, a user can either take the stance -1 or 1 or they can abstain from responding. We determine whether a trend is polarized by inferring a stochastic block model using a minimum description length procedure while constraining the number of blocks to $N_{blocks} \in \{1,2\}$. If the 1-block model has a smaller description length, then we assume the trend not to be polarized. Otherwise, we extract the opinion groups of the trend network using the 2-block model. The resulting opinion clusters for each trend allow us to compute both a user alignment and a trend alignment. We assume that two users are more aligned the more often they find themselves in the same opinion cluster, as encoded in the score

$S(i,j) = \frac{1}{m}\sum_{k-1}^{m} s_k(i,j)$ with

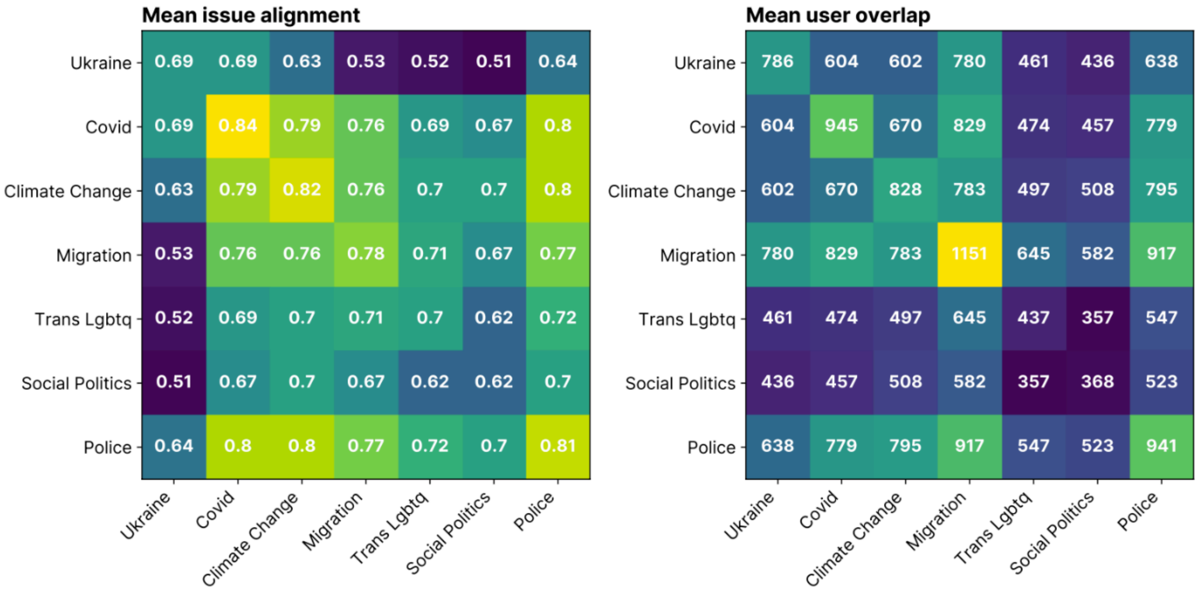
$$s_k(i,j) = \begin{cases} +\,1 \; if\ they\ are\ in\ the\ same\ cluster \\ -\,1 \; if\ they\ are\ in\ different\ clusters \end{cases} \quad (1)$$

We compute issue alignment by comparing the clusterings of trends from different issues. If different issues sort users into similar opinion clusters, we assume the issues to be aligned. We measure this formally using the Adjusted Rand Score between two partitions and average these scores over all trend networks between two issues.

The results are shown in Figure 1. We show a consistent polarization into left vs right-leaning users for influencers (most retweeted), multipliers (most retweeting) and a random sample of users. As for the issue alignment, we observe that Covid, climate change, police and migration-related issues are the most aligned. In the next step, we aim to examine the origins of the observed alignment and the roles of different types of users in shaping the perception of a polarized online issue landscape.



A. USER ALIGNMENT



B. ISSUE ALIGNMENT

Mean issue alignment

	Ukraine	Covid	Climate Change	Migration	Trans Lgbtq	Social Politics	Police
Ukraine	0.69	0.69	0.63	0.53	0.52	0.51	0.64
Covid	0.69	0.84	0.79	0.76	0.69	0.67	0.8
Climate Change	0.63	0.79	0.82	0.76	0.7	0.7	0.8
Migration	0.53	0.76	0.76	0.78	0.71	0.67	0.77
Trans Lgbtq	0.52	0.69	0.7	0.71	0.7	0.62	0.72
Social Politics	0.51	0.67	0.7	0.67	0.62	0.62	0.7
Police	0.64	0.8	0.8	0.77	0.72	0.7	0.81

Mean user overlap

	Ukraine	Covid	Climate Change	Migration	Trans Lgbtq	Social Politics	Police
Ukraine	786	604	602	780	461	436	638
Covid	604	945	670	829	474	457	779
Climate Change	602	670	828	783	497	508	795
Migration	780	829	783	1151	645	582	917
Trans Lgbtq	461	474	497	645	437	357	547
Social Politics	436	457	508	582	357	368	523
Police	638	779	795	917	547	523	941

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Self-supervised modularity maximization on graph embeddings for clustering

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Recent studies showed that basic graph embedding methods may be able to encode community structure optimally [1,3] into a vector space. Yet, existing clustering methods may not accurately identify these clusters due to the mismatch between their (implicit) objectives and the nature of the community structure. Here, we introduce a self-supervised clustering algorithm based on contrastive learning to address this gap. Our method does not require prior knowledge about the number of communities and does not exhibit biases towards large and homogeneous communities. The method learns representations from Node2Vec, uses the self-supervision task to learn a decision boundary in the embedding space and applies a modified Louvain method to obtain community partitions while overcoming said shortcomings.

Our method circumvents the problem of specifying the number of communities by only co=nsidering whether each pair of node vectors belongs to the same community or not ($\delta(g_i, g_j) = 0/1$) where the probability of that happening is captured using the logistic regression parameters w_1 and b_0 as $P(g_i = g_j) = \frac{1}{1+exp(-w_1 \vec{u}_i^{T} \vec{u}_j + b_0)}$. We essentially reframe the traditional clustering problem as multiple binary classification problems. We then maximise the likelihood as: $L\left(g_1, ..., g_N, w_1, b_0\right) = \sum_{i,j}\left[\delta(g_i, g_j)\, log\, P(g_i = g_j) + (1 - \delta(g_i, g_j))\, log\,(1 - P(g_i = g_j))\right]$. The key logistic regression parameters are obtained by designing a contrastive learning self-supervision task that makes the reasonable ansatz that if embeddings can capture nodes that are similar to each other in the form of vectors that are close to each other, then a node and its closest neighbours in the embedding space likely belong to the same community. We get a decision boundary from this which we use to apply modularity maximization to get the final community partition. This results in performance comparable to other methods (Fig. 1b). Moreover, our method demonstrates the recovery of heterogeneously sized communities while being agnostic to the frequency distribution (Fig. 1c). Our approach exhibits robustness in clustering by being agnostic to the choice of embedding methods and parameters, addressing the instability observed in traditional methods (Fig. 1d).

While embedding networks and clustering vectors to identify communities, the notions of similarity employed in these two steps are not inherently aligned. This discrepancy may impact the optimality of the resulting clusters, yet the consequences of such a choice remain unexplored in existing literature. In our case, Node2Vec employs dot product similarity for embedding, and K-Means clustering uses

Euclidean distance. Modifying centroid-based clustering methods like K-Means with alternative distance metrics compromises the algorithm's convergence guarantees. However, Alt-Means, integrates the concept of similarity within the binary classifier framework (the logistic regression Eqn.), allows for adapting different distance metrics by modifying the distance between the two embedding vectors from dot similarity ($\vec{u}_i^{T} \vec{u}_j$) to another metric like Euclidean distance, for instance ($\| \vec{u}_i - \vec{u}_j \|$). This flexibility enables us to systematically investigate the more general and important question of whether consistent notions of similarity are required for optimal clustering results.

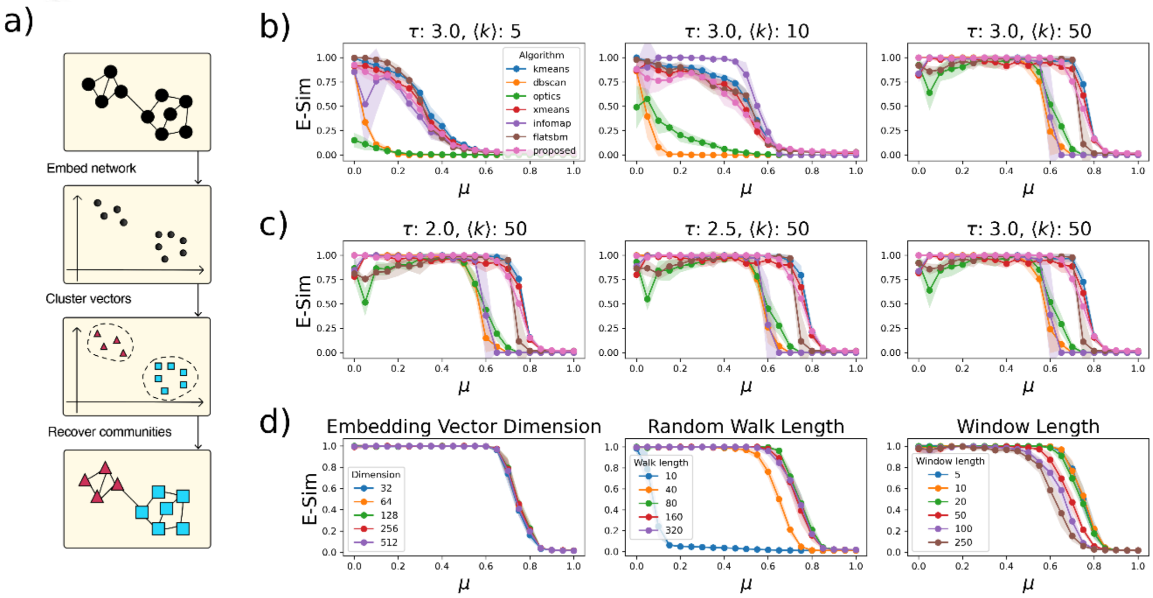

Figure 1: Proposed method performs well across network density, degree heterogeneity and is robust. a) Workflow of the method, b) The element centric similarity (corrected for randomness) plotted against mixing parameter (μ) of 1,000 node LFR networks with increasing network density across panels (from left to right), c) Performance against increasing heterogeneity of degree distribution (from left to right), d) Impact of changing embedding parameters—dimension, random walk length, and window length on performance.

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Contributed Posters

Estimating epidemic threshold under individual vaccination behavior and adaptive social connections: A game-theoretic complex network model

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In the contemporary interconnected world, the dynamics of infectious diseases are intricately intertwined with information dissemination. Acknowledging the pivotal role of public awareness, individual vaccination choices seem to be an imperative factor in the collective efforts against emerging health threats. This study delves into characterizing disease transmission dynamics under evolving social connections, information sharing, and individual vaccination decisions. We present an integrated behaviour-prevalence model over an adaptive multiplex network to deal with the important problem. The network comprises two layers: the physical layer (layer-II) focuses on disease transmission under vaccination, and the virtual layer (layer-I) is adaptive and deals with information dissemination resulting in dynamics of vaccination choice in a socially influenced environment. The intricate complex network model investigates synergistic interactions between information dissemination resulting in dynamics of vaccination choice in a socially influenced environment. The intricate complex network model

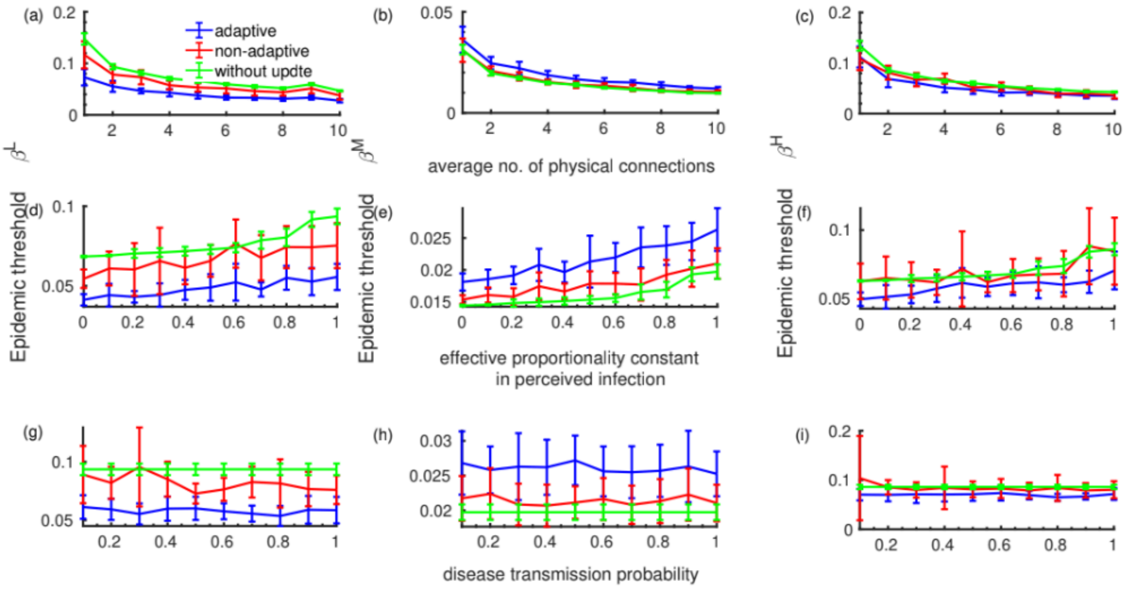

Figure 1: Plots of epidemic thresholds β^L, β^M and β^H respectively for (a-b-c) different values of average physical connection in the Layer-II, (d -e-f) different proportions of the isolated non-vaccinated neighbors (ζ), (g-h-i) different values of disease transmission rate (β). As indicated, each plots considers three different scenarios; (i) adaptive property of the virtual network (i.e. removing the old connection and introducing a new connection is conducted in Layer-I) (ii) non-adaptive property in the network i.e. virtual network is static during the epidemic season. (iii) without update i.e. none of the individuals in the virtual network updated their perceived vaccine risk during the entire time period of disease transmission. Error bars display the standard deviations for 50 simulations.

investigates synergistic interactions between individual choices, societal pressure, and disease dynamics. Utilizing the Microscopic Markov Chain Method (MMCM), we derive an analytical expression of the epidemic threshold. Numerical simulations highlight the dual nature of the epidemic threshold concerning varying levels of perceived vaccine risk in infected states. The adaptive nature of social contacts contributes to the enhancement of epidemic threshold compared to non-adaptive scenarios. We demonstrate that physical network proximity corresponds to a lower epidemic threshold, while it increases with the proportion of individuals that have a perceived risk of infection (figure 1). The power-law exponent significantly influences escalating infections in the network population. Moreover, the vaccine uptake increases with the proportion of non-vaccinated neighbors and the number of individuals with higher perceived infection within the community. Our results have insights for public health officials in developing vaccination programs, in face of evolution of social connections, information dissemination, and vaccination choice in the digital era.

Complex networks and bunching of extreme events

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Extreme events such as earthquakes, floods, and power blackouts, are ubiquitous in nature, and are characterized by their rarity and significant deviations from the average behavior. These deviations often manifest from the tail of a probability distribution. The extreme events frequently display a localized bunching or bursting phenomena where they occur multiple times within a short duration. In this study, we explore similar bunching events on complex networks using a transport model of random walks. An extreme event on a node is defined as an event where the number of walkers on a node exceeds a certain threshold. We study a modular network with two clusters (one large and one small), where nodes within each cluster are densely connected, and the two clusters are sparsely connected which we take as a single bridge across the two clusters. Our study reveals a temporally inhomogeneous sequence or bunching of extreme events in the smaller cluster. The inter event time distribution shows a power law behavior, suggesting correlations in the extreme events in the smaller cluster. The larger cluster does not show bunching of extreme events and the inter event time distribution shows an exponential behavior. We further study other measures such as the burstiness parameter, memory coefficient, and autocorrelation, confirming the bunching phenomena. Our study shows that the network structure can play an important role in the bunching of extreme events. We also note that the correlations emerge naturally in our system, unlike many other theoretical studies where they are assumed to be present.

Rumor Diffusion Model on Social Networks with Experts Strategy & Crawley Martin Functional Response

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Information flows around the world are no longer the same since the advent of social media. In today's connected world, ideas, news, and even rumours may travel at a speed never seen before, reaching millions of people in a matter of seconds. Rumours are one of the most well-known methods of information dissemination because of their power to influence public opinion, social dynamics, and decision-making processes. Comprehending the mechanisms underlying the dissemination of rumours on social media platforms is essential, as it enables the identification of the components that expedite their rapid propagation and the formulation of mitigation strategies against their deleterious consequences. In this work, we investigate the intricate dynamics of rumour spreading on social media. We provide a dynamical model of the ordinary differential equation that is both thorough and adjusted to take information diffusion into consideration, thus capturing the intricate dynamics involved in rumor propagation. This essay explores the importance of expert roles and emphasizes how they can provide a solid framework for developing strategies that successfully stop rumours from spreading on social media. By learning more about the complex mechanisms at work, policymakers, social media companies, and academics may work together to build targeted interventions, educational remedies, and a more resilient online environment.

Keywords: Epidemic model; Crowley-Martin functional response; Pattern formation; Social networks.

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A network biology approach to elucidate mechanisms of disease progression by utilizing compiled databases specific to human health

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Data related to human health and therapy are scattered across literature, which when compiled can serve as a great resource for analyzing and uncovering mechanisms of disease progression. One such data is the differentially expressed biomolecules upon ultraviolet (UV) radiation exposure. UV is the leading cause of skin cancer and is part of the physical component of the human exposome. A large body of published research has been conducted to uncover the mechanisms underlying the adverse outcomes of UV radiation exposure on living beings. We have created a structured database named UVREK (**U**ltra**V**iolet **R**adiation **E**xpression **K**nowledgebase), containing manually curated data on biomolecules induced by UV radiation exposure from published literature. UVREK has compiled information on 985 genes, 470 proteins, 54 metabolites and 77 miRNAs along with their metadata. We utilized the human gene set to construct a protein-protein interaction (PPI) network wherein RPS23 (ribosomal protein S23), RPS9 (ribosomal protein S9), RPS28 (ribosomal protein S28), TP53 (tumor protein p53), RPS5 (ribosomal protein S5), UBC (ubiquitin C), RPS20 (ribosomal protein S20), CTNNB1 (catenin beta 1), RPS25 (ribosomal protein S25), and RPSA (ribosomal protein SA) are hub proteins. These proteins are either related to translation or have a role in UV damage response pathways, making them potential candidates for developing diagnostic procedures and drug targeting. Moreover, we also performed analysis of a separate PPI network for genes that are differentially expressed in human skin-specific cell lines. Thereafter, gene ontology and pathways enrichment analysis were performed on the gene set of UVREK database, which showed the importance of transcription related processes in UV related response, and enrichment of pathways involved in cancer and aging. While significantly contributing towards characterizing the physical component of the human exposome, we expect the compiled data in UVREK will serve as a valuable resource for development of better UV protection mechanisms such as UV sensors and sunscreens. Noteworthy, UVREK is the only resource to date, compiling varied types of biomolecular responses to UV radiation with corresponding metadata. UVREK is openly accessible at: https://cb.imsc.res.in/uvrek/.

Keywords: Database; network biology; ultraviolet radiation; cancer.

Reference:

S.P. Baskaran[#], J. Ravichandran[#], P. Shree, V. Thengumthottathil, B.S. Karthikeyan[*], A. Samal[*], UVREK: Development and analysis of an expression profile knowledgebase of biomolecules induced by ultraviolet radiation exposure, bioRxiv 2024.03.31.587452.
[*]Corresponding Author(s), [#] Equal Contribution.

Bakry–Émery–Ricci curvature: an alternative network geometry measure in the expanding toolbox of graph Ricci curvatures

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The characterization of complex networks with tools originating in geometry, for instance through the statistics of so-called Ricci curvatures, is a well-established tool of network science. Various types of such Ricci curvatures capture different aspects of network geometry. In our work, we investigate Bakry Émery–Ricci curvature, a notion of discrete Ricci curvature that has been studied much in geometry, but so far has not been applied to networks. We explore standard classes of artificial networks as well as selected empirical ones to what the statistics of that curvature are similar to or different from that of other curvatures, how it is correlated to other important network measures, and what it tells us about the underlying network. We observe that most vertices typically have negative curvature. Furthermore, the curvature distributions are different for different types of model networks. We observe a high positive correlation between Bakry–Émery–Ricci and both Forman–Ricci and Ollivier–Ricci curvature, and in particular with the augmented version of Forman–Ricci curvature while comparing them for both model and real-world networks. We investigate the correlation of Bakry–Émery–Ricci curvature with degree, clustering coefficient, and vertex centrality measures. Also, we investigate the importance of vertices with highly negative curvature values to maintain communication in the network. Additionally, for Forman Ricci, Augmented Forman–Ricci, and Ollivier–Ricci curvature, we compare the robustness of the networks by comparing the sum of the incident edges and the minimum of the incident edges as vertex measures and find that the sum identifies vertices that are important for maintaining the connectivity of the network. The computational time for Bakry–Émery–Ricci curvature is shorter than that required for Ollivier–Ricci curvature but higher than for Augmented Forman–Ricci curvature. We therefore conclude that for empirical network analysis, the latter is the tool of choice.

Keywords: Discrete Ricci curvature; Scalar curvature; Complex network; Robustness.

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ViCEKb: Creation and network-based analysis of a curated knowledgebase on vitiligo-triggering chemicals to link exposome and health

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The concept of exposome has been proposed to understand and evaluate the life course of environmental exposures of an individual, and how such exposures impact their health. Environmental chemicals are a key component of the human exposome and exposure to these chemicals is a major contributor to global disease burden. Hence, there is immense interest in characterizing this chemical component of the human exposome and employing network biology approaches to link such chemical exposure to diseases. Vitiligo is one such complex human disease wherein the environmental factors, in conjunction with the underlying genetic predispositions, trigger the autoimmune destruction of melanocytes, ultimately leading to depigmented patches on the skin. Apart from being susceptible to other autoimmune disorders, the affected patients may face social stigmatization leading to a decreased quality in life. While genetic factors have been extensively studied, the knowledge on environmental triggers remains sparse and less understood. Towards this, we present the first comprehensive resource on vitiligo triggering chemicals namely, Vitiligo-linked Chemical Exposome Knowledgebase (ViCEKb), which is openly accessible for research at https://cb.imsc.res.in/vicekb. ViCEKb involved an extensive and systematic manual effort in curation of 113 unique chemical triggers of vitiligo from published literature and categorized them based on their evidence and source of exposure. ViCEKb catalogues various chemical information, including a wide range of metrics necessary for different toxicological evaluations. A network-based analysis of the ViCEKb chemical space highlighted its diversity and uniqueness in comparison to skin specific chemical regulatory lists. In addition, a transcriptomics-based analysis of ViCEKb chemical perturbations in skin cell samples highlighted the commonality in their linked biological processes. Furthermore, a network-based exploration of toxicity pathways using the Adverse Outcome Pathway (AOP) framework can provide deeper insights into the mechanisms of toxicity induced by ViCEKb chemicals, thereby enhancing our understanding of such chemical-induced effects. In sum, this study is the first to characterize potential chemical triggers of vitiligo, deepening our understanding of the environmental factors involved. It also highlights the potential for network-based analyses to assist future chemical regulations.

Keywords: Knowledgebase ; Chemical exposome; Network biology; Toxicogenomics.

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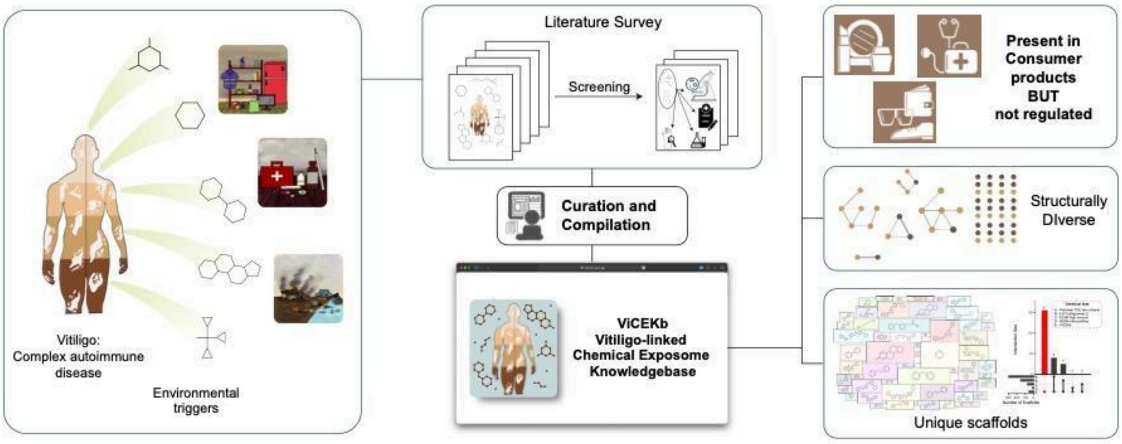
Relevant figure:



Network toxicology approach for investigation of environmental contaminants-induced toxicological effects on human and ecosystem health

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The exposome encompasses the entirety of an individual's lifetime exposures, starting from conception. The chemical exposome constitutes a significant portion of the exposome and is composed of chemicals such as petroleum hydrocarbons and heavy metals that can potentially have detrimental impacts on humans as well as ecosystem health. Anthropogenic activities serve as a primary source of chemical contaminants released into the environment that subsequently come into contact with humans and other organisms. Thus, it is essential to study the chemical exposome and its components to understand the risks associated with the chemicals and develop effective regulations. Here, we leveraged different network-based frameworks to explore and understand the adverse effects associated with chemical contaminant exposure in humans and ecological species as part of the broader exposome. To this end, we systematically curated a list of contaminants from sources such as fuel oils by relying on published reports, integrated biological endpoint data from toxicological databases, and constructed a stressor-centric adverse outcome pathway (AOP) network linking various contaminants with high quality and complete AOPs within AOP-Wiki, the primary repository for globally developed AOPs. Moreover, we analyzed the AOP network for certain contaminants using different network measures and studied the toxicity pathways underlying adverse effects in humans and other organisms. Further, to understand the ecotoxicity of these contaminants, we relied on stressor-species network constructions, based on reported toxicity concentrations and bioconcentration factors data, and found that crustaceans are documented to be affected by contaminants like petroleum hydrocarbons. Finally, we utilized aquatic toxicity data within ECOTOX, one of the largest knowledge bases on environmental chemical toxicity data for ecological species developed by the United States Environmental Protection Agency (US EPA), to perform ecological risk assessment using species sensitivity distributions for contaminants prioritized by US EPA and derived their corresponding hazard concentrations (HC05) that are hazardous to 5% of species in the aquatic ecosystem. Overall, the obtained inferences highlight the importance of using network-based approaches and risk assessment methods to effectively understand toxicities induced by contaminants constituting the chemical exposome.

Keywords: Network toxicology; Adverse outcome pathway network; Stressor-species network; Ecological risk assessment

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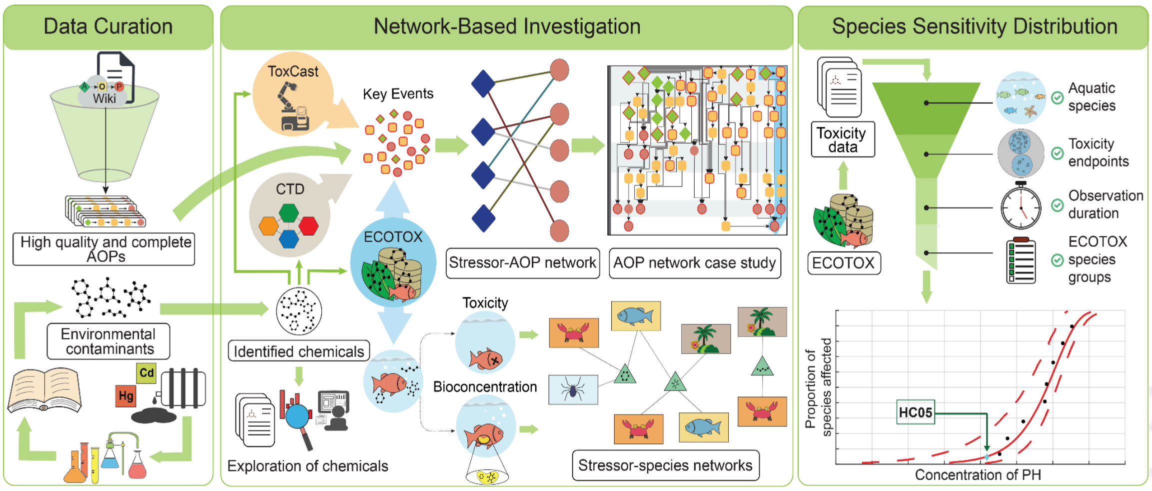

Effects of structural properties of neural networks on machine-learning performance

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In recent times, neural-network-based machine learning techniques such as deep learning or graph neural networks have earned significant attention. One important recent study based on relational graph representation (defining neural networks as a message exchange function over graphs) called “graph2nn” [1] aims to understand the relationship between the graph structure of the neural network and its predictive performance, based on elementary types of model networks. In this work, we extend it to an even more general network structure, i.e, the static model [2] and study the effect on the predictive performance of a 5-layer multilayer perceptron (MLP). We found out that the network performance demonstrates a smooth U-shape correlation with degree exponent and increases proportionaly with edge number. Additionally, there exists a sweet spot of relational graphs, which leads to neural networks with significantly improved predictive performance. In the ongoing work, we are using more nontrivial and realistic networks, such as mesoscale structures with communities on diverse datasets, which will allow us to comprehensively understand the neural dynamics for optimal network performance [3].

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Streamlined approach to mitigation of cascading failure in complex networks

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Cascading failures pose a significant threat to the stability of complex systems, often leading to widespread collapse across various infrastructures and financial networks. This study presents a robust and practical methodology aimed at reducing the risk of such failures within complex networks, with a particular focus on the importance of local network topology. Central to our approach is an advanced algorithm designed to identify a critical subset of nodes within the network, with this subset being notably substantial relative to the network's overall size. To refine this algorithm, we incorporate a graph coloring heuristic to precisely target the most crucial nodes, thereby minimizing the subset size while maximizing its strategic impact. By securing these key nodes, the network's resilience to cascading failures is significantly enhanced. Our method for identifying critical nodes, supported by experimental results, demonstrates superior performance compared to conventional techniques. We validate the effectiveness of our approach through comparative analysis with existing strategies and assess its performance across various network configurations and failure scenarios. Empirical validation is achieved by applying our method to real-world networks, affirming its effectiveness as a strategic tool for improving network robustness.

Keywords: Mitigation, Cascading Failure, Complex Network, Graph Theory.

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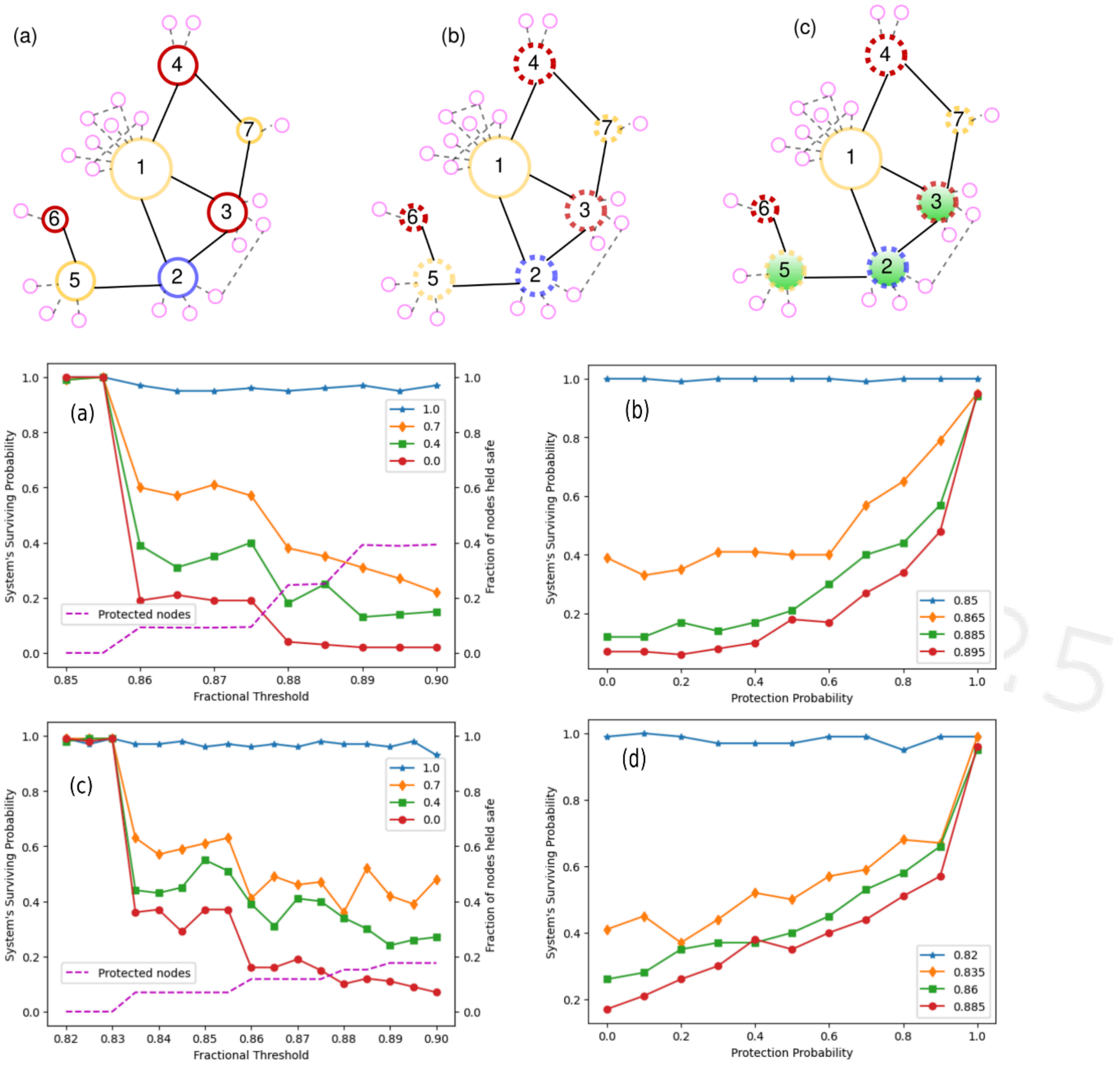

Figure 1: Top fig (a-c): Visualization of the mitigation scheme.

Bottom fig(a-d): Mitigation of cascading failure on standard ER and Scalefree networks. (a) The plot shows the surviving probability vs Fractional threshold for ER network ($N = 20000$ and $\langle k \rangle = 8$) with four protection probabilities - Blue, orange, green and red representing probabilities 1.0, 0.7, 0.4, and 0.0, respectively.

Disparity-driven heterogeneous nucleation in finite-size adaptive networks

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Phase transitions are crucial in shaping the collective dynamics of a broad spectrum of natural systems across disciplines. Here, we report two distinct heterogeneous nucleation facilitating single step and multistep phase transitions to global synchronization in a finite-size adaptive network due to the trade off between time scale adaptation and coupling strength disparities. Specifically, small intracluster nucleations coalesce either at the population interface or within the populations resulting in the two distinct phase transitions depending on the degree of the disparities. We find that the coupling strength disparity largely controls the nature of phase transition in the phase diagram irrespective of the adaptation disparity. We provide a mesoscopic description for the cluster dynamics using the collective coordinates approach that brilliantly captures the multicluster dynamics among the populations leading to distinct phase transitions. Further, we also deduce the upper bound for the coupling strength for the existence of two intraclusters explicitly in terms of adaptation and coupling strength disparities. These insights may have implications across domains ranging from neurological disorders to segregation dynamics in social networks.

Keywords: Adaptive networks, Multi time-scale dynamics, Synchronization.

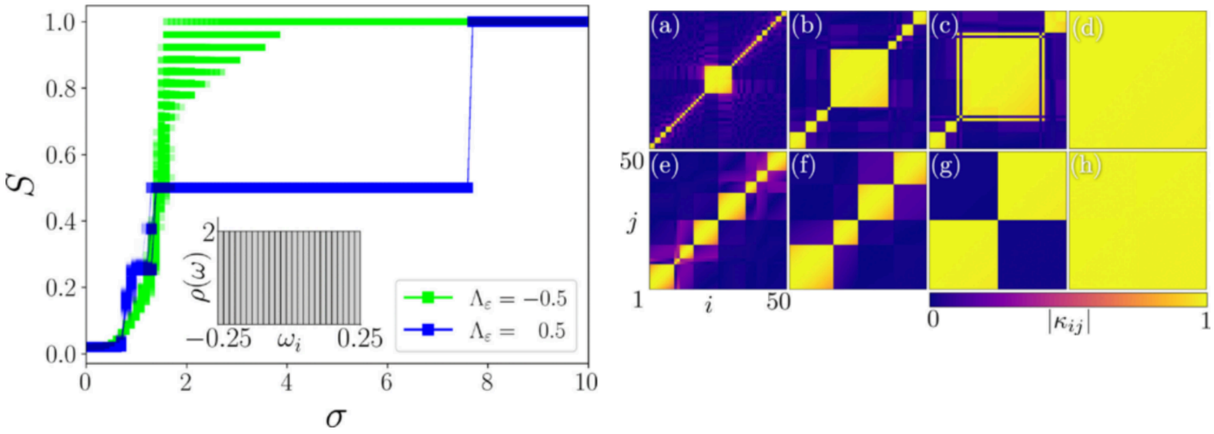

Figure 1: Synchronization transition of the system of adaptively coupled phase oscillators for 500 realizations. The system undergoes a distinct synchronization pathway(multi-step/single-step) depending on the adaptation rate disparity (Λ_ε).

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Effects of repulsive coupling in non-locally coupled ring of phase oscillators

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We study the effect of repulsive coupling in non-locally coupled ring of phase oscillators with phase lag. The system exhibits a variety of states ranging from global synchrony, splay states to clustered chimeras with in-phase and anti-phase clusters. Interestingly, we observe that repulsive coupling can flip the phases of the clusters from in-phase to anti-phase in multi-clustered chimeras. The stability of synchronised solutions and the robustness of the results are also investigated.

The Ripple Effect of Retraction on an Author's Collaboration Network

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Scientific community is hinged upon trust and the growth of the retraction database raises a severe concern to the scientific community. Although scientific collaborations increase research productivity by using an individual's knowledge and research skill set; however, a wrong collaboration can create distrust among peers. The present study aims to (i) analyze the impact of scientific misconduct on collaboration networks computed from the author's entire career. (ii) Whether scientific misconduct reduces collaboration of misconducting authors as opposed to those who never faced allegations of scientific misconduct. From Web of Science database, we extracted and analyzed 24209 unique authors from 5972 retracted papers from 1990 to 2020. In the collaboration network, the authors tagged as "Got Retraction" if they received at least one retraction in their career else "Never Retracted". For each year, we computed the average degree and average clustering coefficient of all retracted and non-retracted authors. We further computed the difference between the last and current retraction for each author. Interestingly, we observe that the average degree of authors with at least one retraction keeps increasing with the publication year and is significantly higher than authors with no retractions. A similar trend is observed through local clustering coefficient too. We observe that the network structure of authors involved in retractions does not change significantly over the years compared to that of the "innocent coauthors". Our results suggest that stigmatization rarely affects the collaboration network of stigmatized authors. Our findings have implications for institutions adopting stringent measures and fostering ethical practices in research.

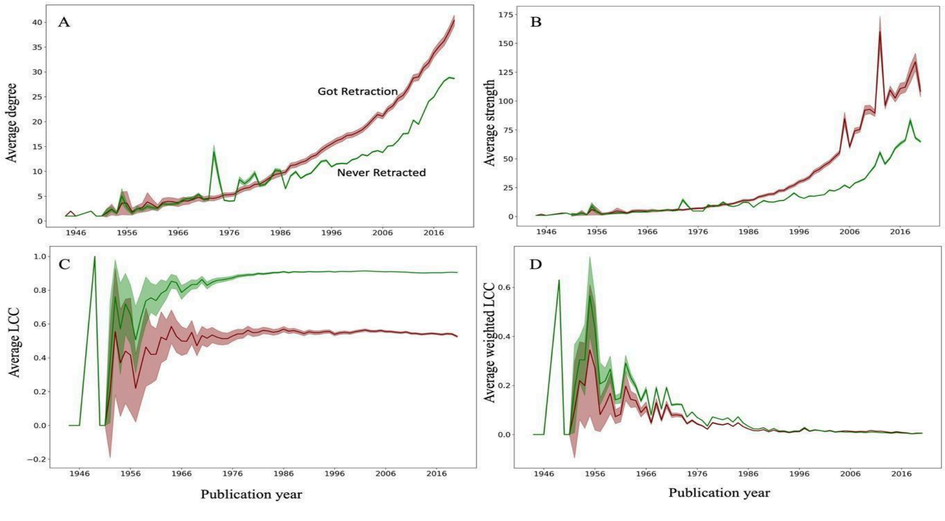

Figure 4. Average (A) degree, (B) strength, (C) local clustering coefficient (LCC), and (D) weighted LCC of "Got Retraction" (Maroon color) and "Never Retracted" (Green color) authors with publication year.

Keywords: Scientific misconduct, Author's career, Scientific collaboration, and Collaboration network

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Global synchrony in presence of higher order interactions

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Higher-order interactions in addition to pairwise interactions, are found in many systems like neurological, biological, ecological, sociological etc. Here we present an analytical framework to achieve perfect synchronization under the paradigm of the Sakaguchi-Kuramoto (SK) model in presence of higher-order interactions. We analytically derive a frequency set to achieve perfect synchrony at some desired coupling strength in complex networked systems. We numerically verify the proposed theory considering scale-free (SF), random (ER), and small world (SW) networks. We observe that the analytically derived frequency set provides stable perfect synchronization in the network at desired coupling strengths along with achieving a high level of synchronization around it compared to the other choices of frequency sets. We also check the stability of the perfect synchronization states by deriving a low dimensional model. By introducing a Gaussian noise around the derived frequency set we observed that the perfect synchronization states are robust against small deviations of the derived frequency set[1].

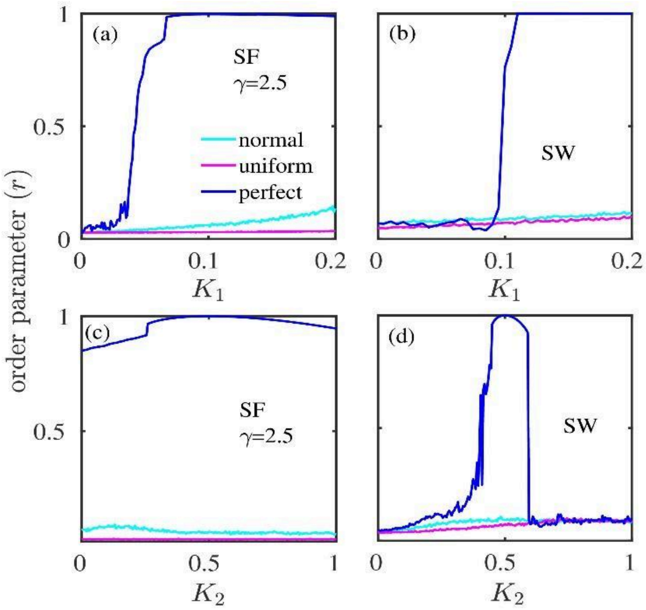

Figure 1: (a)-(b) r vs pairwise coupling strength K1. (c)-(d) *r* vs triangular coupling K2. The networks achieve perfect synchronization at the targeted coupling K1 = 0.1, K2 = 0.5 only for derived perfect frequency sets.

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Dynamical stability of complex systems

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Despite being an extremely complex system, nature remains remarkably stable, often returning to its equilibrium state effortlessly after experiencing a small perturbation. To assess the stability of such a complex system with many interacting elements, a common approach is to calculate the largest eigenvalue of the system's *Jacobian* matrix.

May [1] introduced the idea of modeling complex ecological communities using random matrices. Current interest focuses on how stability changes when the Jacobian matrix elements are influenced by network structure, such as degree.

Recently, Meena *et al*[2] explored a natural emergent rule for stability, assuming the underlying network is a star graph. We are now relaxing this assumption and investigating the suitable range of variables within the stable zone using an alternative approach. The matrix *J* is obtained by sampling from the given distribution. $[J]_{ii} = -Cd_{nn}^{\eta} d_i^{\mu}$, $[J]_{ij} = -Dd_i^{\nu} d_j^{\rho} A_{ij}$,and we analytically derive that the largest eigenvalue is

$$\lambda_{max} = (n-1)\mu_0 s - \mu_d \qquad (1)$$

where $\mu_d = \langle C d_{nn} d^{\mu} \rangle$ and $\mu_o = \langle D d^{\nu} d^{\rho} \rangle$. The above formula is applicable for a given range of C and beyond this range the largest eigenvalue predicted by $\lambda^{*}_{max} =- C[d^{\mu}_{max/min}]$, where $d^{\mu}_{max/min}$ is the maximum or minimum degree of the network. We have utilized this approach to examine the stability of numerous non-linear systems.

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Investigation of plastic additives-induced toxicities by leveraging network-centric approach

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Network science offers powerful tools for understanding complex relationships between chemical contaminants and their adverse effects on humans and ecosystems. Plastic additives, an important class of chemical contaminants which are intentionally added to plastics to achieve specific functionality, can leach into the environment and pose considerable risks to ecological and human health. However, limited knowledge about their presence throughout the plastic life cycle hinders their effective regulation, thereby posing risks to product safety. We leveraged network-centric approaches to analyze plastic additives-induced toxicities. First, we systematically curated 6470 plastic additives from chemicals documented to be found in plastics in a detailed published report. We then integrated heterogeneous toxicogenomics and biological endpoint data from various toxicological databases and identified associations between 1287 plastic additives, and 322 complete and high-quality adverse outcome pathways (AOPs) within AOP-Wiki. Based on these plastic additive-AOP associations, we constructed a plastic additives-AOP network, wherein the plastic additives are categorized into 10 priority use sectors and AOPs are linked to 27 disease categories. We visualized the plastic additives-AOP network for each of the 1287 plastic additives and made them available via a dedicated website: https://cb.imsc.res.in/saopadditives/. Finally, we demonstrated the utility of the constructed plastic additives-AOP network by identifying highly relevant AOPs associated with three well-known pollutants and thereafter, constructed various networks of these AOPs to explore the associated toxicity pathways in humans and aquatic species. Overall, the construction and analysis of different AOP networks highlighted the risks associated with plastic additives, thereby contributing towards a toxic-free circular economy for plastics.

Keywords: Stressor-AOP network; Toxicogenomics; Network analysis

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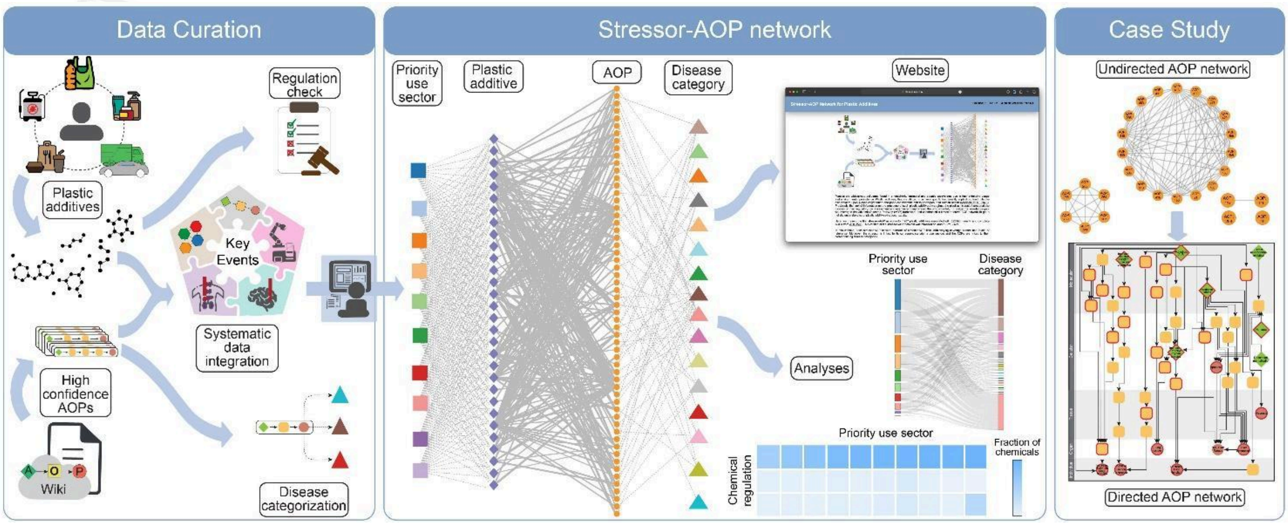
Relevant figure:



Continuous Time Quantum Walks on Complex Network Topologies

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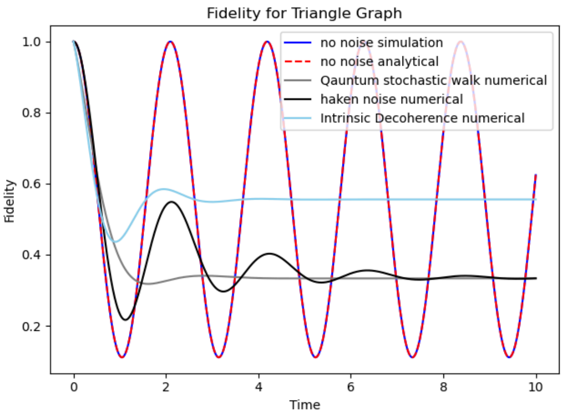
We study the stability of continuous time quantum walks (CTQWs) on complex network topologies like scale-free, Erdos-renyi and small world networks. Quantum walks are quantum analog for classical random walks. Our work focuses on analyzing metrics such as fidelity of initial and evolved states, inverse participation ratio and von neumann entropy. We also study the density matrix visualization to get a better



understanding of populations in each node and quantum coherences. We present a comprehensive study of how different network topologies influence the behavior of CTQWs through simulation results. Our findings reveal the variations in quantum walk dynamics across different network topologies and provide insights into the impact of network topologies on stability of quantum walks. Through detailed simulations and comparisons, we aim to get a better understanding of the stability of quantum networks, which can impact both theoretical research and practical applications in quantum computing and network analysis.

Keywords: Fidelity; Inverse Participation Ratio; Von Neumann Entropy; Coherence

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Tropical climate classification based on the Intertropical Convergence Zone dynamics from a complex networks perspective

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By utilizing network analysis, our study offers a novel approach to classifying tropical climate based on the spatio-temporal dynamics of the Intertropical Convergence Zone (ITCZ). The ITCZ is a narrow tropical belt of high convection driven by the differential solar heating and convergence of moisture-laden trade winds from the Northern and Southern hemispheres. As the moisture-laden winds convect to higher altitudes, condensation leads to the formation of deep clouds, resulting in high cloudiness and precipitation. We use outgoing longwave radiation (OLR), which is a good proxy for cloudiness, to quantify the ITCZ dynamics and we construct functional networks where geographical locations are nodes that are connected if the dynamics of the ITCZ at these locations are correlated.

Even though the ITCZ is a planetary scale phenomenon, the cloudiness and precipitation exhibit high variability across the ITCZ because they are sensitive to the local geophysical and meteorological conditions. Furthermore, the extent of migration of the ITCZ and its structure are not uniform across the tropics. Therefore, classifying tropics based on the spatio-temporal dynamics of the ITCZ is a challenging yet necessary task as it deepens our understanding of the underlying physics and patterns of teleconnections. To classify the tropics, we perform community detection on the OLR network using Louvain’s method, which is a modularity-optimizing algorithm. Communities refer to a group of nodes that are densely connected, while connections between nodes of different communities are sparse. Community detection on the network reveals seven dominant communities corresponding to distinct ITCZ dynamics (Fig. 1), primarily driven by seasonal cycle, local topography, air-land interactions, and air-sea interactions.

The two largest communities in the network represent regions affected by the ITCZ during the summers in the northern (1) and southern hemispheres (2). These communities have dense connections, which is indicative of coherent ITCZ dynamics. The central and eastern equatorial Pacific and equatorial Atlantic oceans (5) emerges as separate community since these regions are affected by equatorial upwelling that suppresses convection along the equator and pushes the ITCZ northward. The Indian Ocean community (7) is found to have relatively sparse connectivity revealing that the ITCZ dynamics is incoherent and inhomogeneous over this region. Through our analysis, we provide a simple and concise representation of the complex spatio-temporal dynamics of the ITCZ. In the talk, we will also discuss the interdecadal variability in the topology and community structure of the OLR network, along with the associated physical mechanisms.

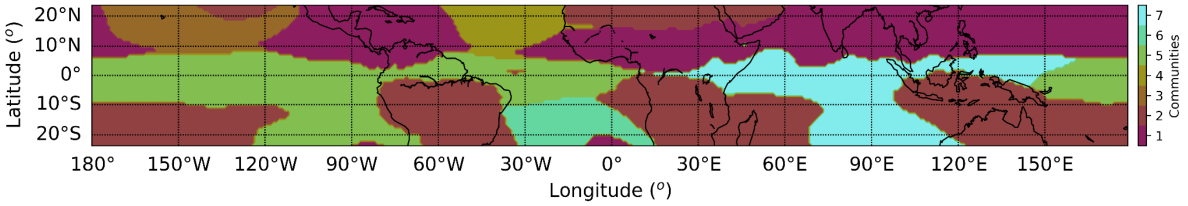

Figure 1. Community structure of the OLR network.

Keywords: Functional networks; Tropical climate dynamics; Community detection; Climate classification.

Study of Higher-Order Interactions in Unweighted, Undirected Networks Using Persistent Homology

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Persistent homology has been studied to understand the structural properties and topology of weighted networks. It can uncover hidden layers of information about the higher-order structures formed by non-pairwise interactions in a network. In this study, we constructed the weighted adjacency matrix by using the concept of adjacency strength of simplices in a clique complex derived from an unweighted, undirected network. This weighted adjacency matrix is thus used to calculate the global measure, which is called generalised betweenness centrality, which further helps us in calculating the persistent homology on the given simplicial complex by constructing a filtration on it. Moreover, a local measure called maximal generalised degree centrality has also been established for better understanding of the network topology of the studied simplicial complex. Two different filtration schemes for constructing the sequence of simplicial complexes have been given with the help of both global and local measures, and by using these measures, the topology of higher-order structures of the studied network due to the interactions of their vertices has been compared. Further, the illustration of established definitions has been given using a real-life network by calculating Betti numbers up to dimension three, given in Figure 1.

Keywords: Persistent homology, Weighted adjacency matrix, Simplicial complex.
MSC: 05C82, 55U10, 55U05

Asynchronyous dynamics of ecological systems induced by higher order interactions

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Phase-synchronized population dynamics of various species cohabiting in a complex ecosystem elevate its risk of extinction due to environmental stochasticity and simultaneous low-density fluctuations. Therefore, the extinction risk of an ecosystem can be quantified by the phase synchrony of their populations. Generally, in models describing population dynamics of ecosystems, both trophic and non-trophic interspecies interactions are classified as two-species interactions. This approach contradicts the fact that when several species live in close proxim- ity, more than a pair have to interact simultaneously with each other and influence each other's population dynamics. To address this, higher-order interactions need to be incorporated in the models describing the population dynamics of an ecosystem, and their effect on the phase synchronization of populations needs to be investigated. In this study, we model a species-rich ecosystem as a multi-node complex ecological network and examine the phase dynamics of the total species population. Each node of this network represents a constituent species modeled as a Sakugachi-Kuramoto phase oscillator coupled non-linearly to the other nodes (species) through first-order and higher-order inter-species interactions. The interactions we consider are non-trophic and commensalist/mutualist (i.e., positive:+,+) and antagonistic (i.e., negative: -,-). Along with the higher-order interactions, we consider inherent phase asymmetry among the nodes to account for habitat heterogeneity. We investigate the effects of both higher-order coupling and asymmetry on the phase synchronization of the ecological network as a whole. Our findings demonstrate that higher-order interactions above a threshold amplitude result in the ecosystem's transition from synchronous to asynchronous dynamics. Further, we find that an increase in the size and diversity of the ecosystem leads to an increased threshold of higher order coupling required to reach asynchronous dynamics, though eventually, it happens. We also demonstrate that the asynchrony in dynamics induced by higher-order interactions is further promoted by high asymmetry among the individual nodes. We further demonstrate that a high degree of negative inter-species interactions also induce asynchrony in the system. Notably, the network size also influences the threshold value of higher-order coupling required to induce asynchrony. Since the asynchrony of an ecosystem implies stability, the continued existence of ecosystems can be explained by our work. Fig. 1 represents asynchrony induced by higher-order and negative coupling.

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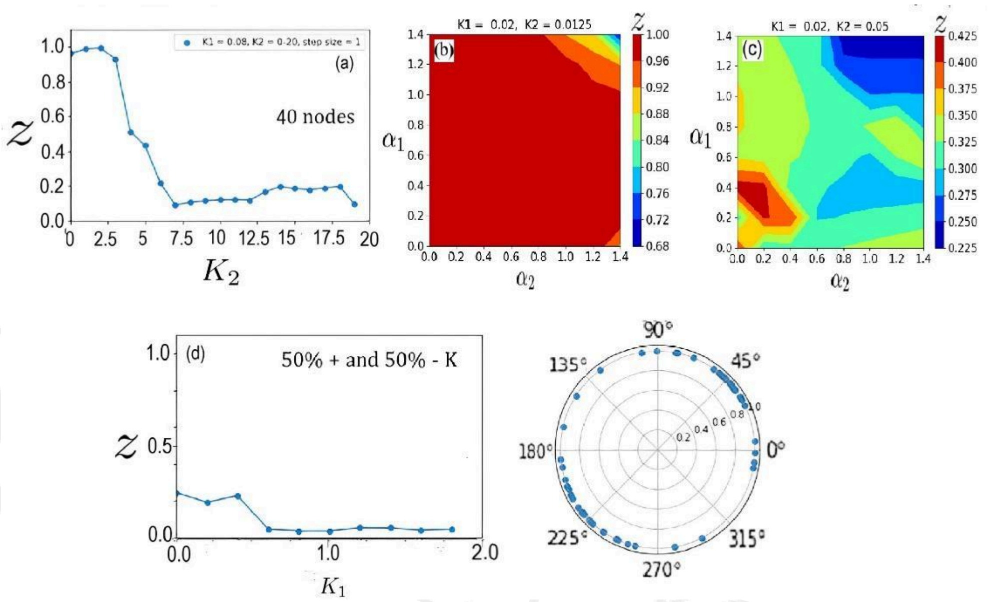

Figure 1: (a) Order parameter vs second order coupling magnitude (b) and (c) Order parameter vs first and second order phase lag in presence of higher-order coupling (d) Order parameter vs absolute coupling strength, when 50 % couplings are negative / repulsive.

A Modified SIR Model for Simulating Competitive Information Diffusion in Real-World Social Network

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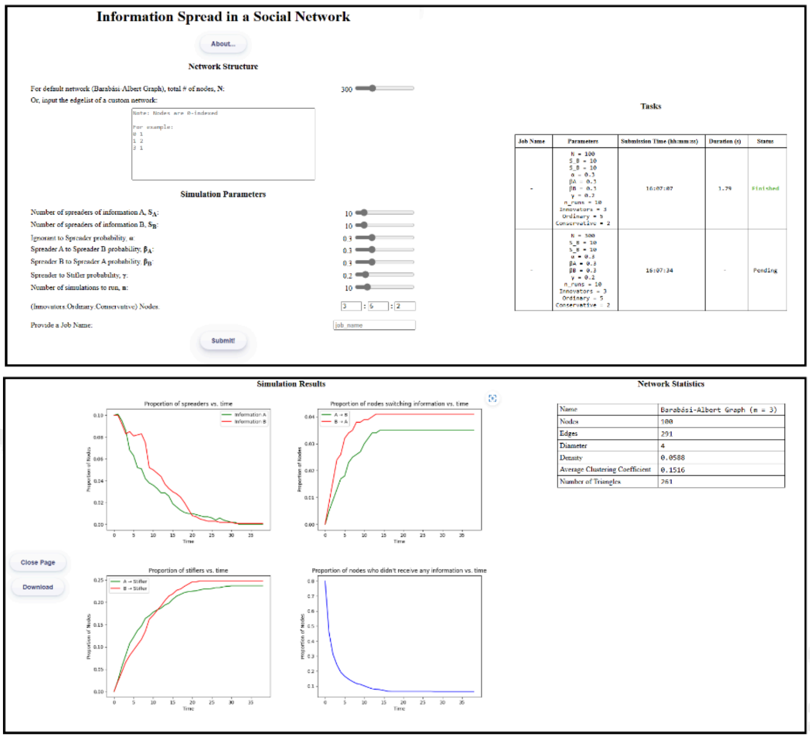
The widespread use of social networks for information dissemination requires a deeper understanding of how competitive information spreads within these complex structures. The traditional Susceptible-Infected-Recovered (SIR) model, while valuable for modeling the spread of single pieces of information, models developed for competing information diffusion need to capture the dynamics of human behavior, such as biases, decaying freshness, etc. We address this gap by introducing modifications to the SIR model, incorporating factors such as an individual's polarity towards specific information, the level of trust between people, and the decaying freshness of information in the network. We then employ the enhanced model to simulate the diffusion of competitive information across diverse real-world social networks. The results provide insights into the distinct diffusion patterns observed in different networks and the influence of network structure and individual characteristics on information spread. We developed a web-based interface (Figure 1) to simulate the model on user-uploaded graphs. The application simulates the spread of information based on the user-defined parameters' values and generates a comprehensive visual report. We have also created a provision for simultaneously submitting multiple simulation jobs. Using the developed simulation platform, we reported experimental results on several synthetic and real-world networks.

Keywords: SIR Model; Information Propagation; Simulation; Social Network Analysis.



Information Spread in a Social Network

Network Structure

For default network (Barabási-Albert Graph), total # of nodes, N: 300

Or, input the edgelist of a custom network:

```
Note: Nodes are 0-indexed

For example:
0 1
1 2
3 1
```

Simulation Parameters

Number of spreaders of information A, S_A: 10

Number of spreaders of information B, S_B: 10

Ignorant to Spreader probability, α: 0.3

Spreader A to Spreader B probability, β_A: 0.3

Spreader B to Spreader A probability, β_B: 0.3

Spreader to Stifler probability, γ: 0.2

Number of simulations to run, n: 10

(Innovators:Ordinary:Conservative) Nodes. 3 : 5 : 2

Provide a Job Name: job_name

Tasks

Job Name	Parameters	Submission Time (hh:mm:ss)	Duration (s)	Status
-	N = 100 S_B = 10 S_B = 10 α = 0.3 βA = 0.3 βB = 0.3 γ = 0.2 n_runs = 10 Innovators = 3 Ordinary = 5 Conservative = 2	16:07:07	1.79	Finished
-	N = 300 S_B = 10 S_B = 10 α = 0.3 βA = 0.3 βB = 0.3 γ = 0.2 n_runs = 10 Innovators = 3 Ordinary = 5 Conservative = 2	16:07:34	-	Pending

Simulation Results

Network Statistics

Name	Barabási-Albert Graph (m = 3)
Nodes	100
Edges	291
Diameter	4
Density	0.0588
Average Clustering Coefficient	0.1516
Number of Triangles	261

Figure 1. UX of Simulation Application and Result Page

Communities in Streaming Graphs: Small Space Data Structure, Benchmark Data Generation, and Linear Algorithm

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Identifying and preserving community structures in streaming graphs presents significant challenges. However, numerous applications, such as event detection and community spread, demand the rapid and efficient identification of these com- munities within constrained spatial and temporal limits. In this study, we introduce a novel data structure, **ComSketch**, which comprises a forest and a sparse triangular matrix to contain macro-level communities derived from social streams. This structure allows for constant-time community retrieval upon query. Additionally, we propose a linear streaming community detection algorithm that merges communities based on the edge density within (inner) a community and with (outside) other communities. This algorithm achieves community detection in linear time, $\mathcal{O}(|E|)$, and requires minimal space, $\mathcal{O}(|V| + |C|^2)$, where $|E|$, $|V|$, and $|C|$ represent the number of edges, nodes, and communities respectively, considering that $|C| << |V|$ or $|E|$. The workflow of our algorithm is depicted in Figure 1. Mergers occur only when the edge density increases. Experimental evaluations on large real-world networks demonstrate that our algorithm surpasses other state-of-the-art streaming and static community detection algorithms in terms of quality metrics such as NMI, F1-score, and WCC. Furthermore, we develop a streaming network generator, Temporal Community Benchmark Dataset (TCBD), which contains both true community labels and temporal information of edges.

These synthetic networks serve to validate the effectiveness of our proposed algorithm. Details can be found in preprint[1].

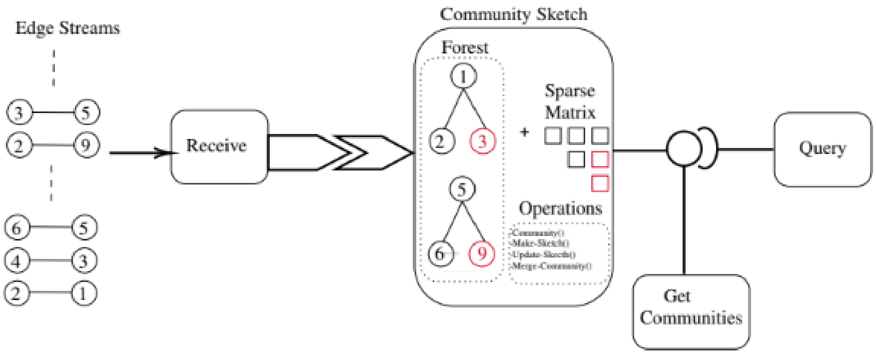

Figure 1: Workflow of the proposed algorithm.

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Fitness fluctuations in the Bak-Sneppen model

Abha Singh

We study the one-dimensional Bak-Sneppen model for the evolution of species in an ecosystem. Of particular interest are the temporal fluctuations in the fitness variables. We numerically compute the power spectral density and apply the finite- size scaling method to get data collapse. A clear signature of $1/f^{\alpha}$ noise with $\alpha \approx 1.2$ (long-time correlations) emerges for both local and global (or average) fitness noises. The limiting value 0 or 2 for the spectral exponent corresponds to the no interaction or random neighbors version model, respectively. The local power spectra are spatially uncorrelated and also show an additional scaling ~ $1/L$ in the frequency regime $L^{-\lambda} \ll f \ll 1/2$, where L is the linear extent of the system.

Keywords: Self-organized criticality (SOC), Power law, Extremal dynamics.

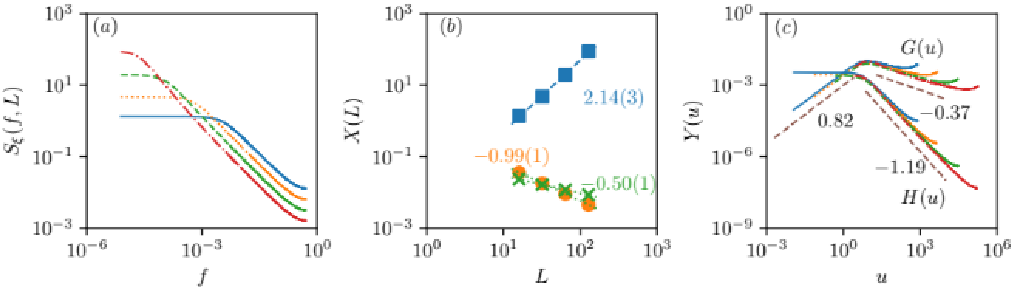

Figure 1: The power spectra properties for the local fitness fluctuations.

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Emergence of order through multilayer interactions in a turbulent reacting flow

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Turbulent thermo-fluids are complex systems involving interactions between acoustic, flame and fluid subsystems [1]. These systems exhibit the emergence of order in the form of high-amplitude limit cycle oscillations in the acoustic pressure (p'), periodic patterns of large coherent flow structures and large spatial pockets of coherent heat release rate fluctuations [2]. Such ordered dynamics is catastrophic to practical combustors in rocket and gas-turbine engines, and is referred to as thermoacoustic instability [3]. We use multilayer networks [4] to unravel the pattern of inter-subsystem interactions during the emergence of order. The interactions between different subsystems manifest as spatial and temporal patterns that characterize the dynamical state of the system. These patterns influence the interactions and the dynamics ensuing in the systems. Such interplay between the web of inter-subsystem interactions and the emergent patterns are essentially higher-order interactions [5]. Using multilayer networks we encode the spatial web of inter-subsystem interactions during chaotic, intermittent and ordered dynamics in a turbulent thermo-fluid. We show that such interactions become localized at certain flow conditions leading to self-organized feedback and the emergence of ordered dynamics [6].

Experiments are performed in a turbulent reacting flow confined to a duct with a bluff-body flame stabilizing mechanism. The flame and flow dynamics are captured simultaneously during experiments. Heat released rate fluctuations ($\dot{q}'$) due to combustion are captured using chemiluminescence imaging and the vorticity field is obtained through Particle Image Velocimetry (PIV) performed on flow seeded with TiO_2 particles. We construct a multilayer network where two layers encode the vorticity (ω) and acoustically driven heat release rate dynamics ($p'\dot{q}'$, also called thermoacoustic power). The spatial locations in the flow field are nodes of each layer and inter-layer links are established based on short-window cross-variable correlations.

During the state of intermittency prior to the emergence of order, we discover the presence of hubs in a spatial pocket upstream of the bluff-body in each layer (Fig. 1(a,b)). Further, we show that the inter-layer link distribution is disassortative Fig. 1(c). However, high-density connections exist between the spatial pockets formed by a group of hub nodes in both layers (Fig. 1(d)). This peculiar interlayer link distribution reveals the unique flow-flame-acoustic interactions during the state of intermittency. Disassortativity implies that interactions in the vorticity dynamics (and thermoacoustic power generation) in the hub locations influence the thermoacoustic power generation (and vorticity) in regions with low-degree nodes. Further, high-density links between the pockets of hubs imply localized and intense inter-subsystem interactions in these spatial pockets found upstream of the bluff-body.

Thus, the existence of localised feedback between vorticity and thermoacoustic power generation also influences the dynamic downstream of the bluff body. When these localized interactions become sustained, order emerges in the form of thermoacoustic instability. Our framework reveals the crucial locations that can be perturbed to disrupt the feedback between subsystems and suppress the emergence of order [6].

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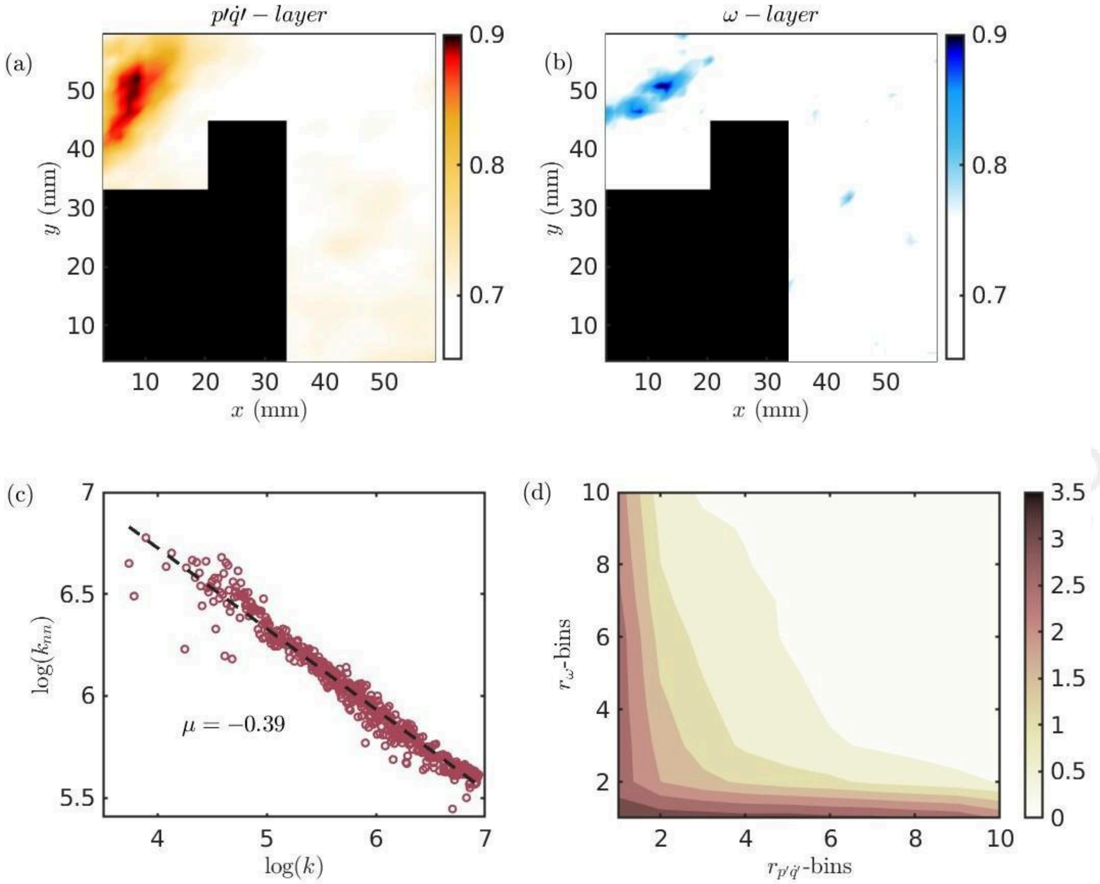

Fig. 1. Spatial distribution of node strength in the (a)$p'\dot{q}'$ and (b) ω layers of the multilayer network during the state of intermittency that precedes the emergence of order. (c) Variation of the interlayer degree correlation function (k_{nn}) with the interlayer degree of nodes exhibiting a disassortative link distribution. (d) Link-rank distribution obtained by plotting the density of links between groups of nodes ranked according to their degree.

Epidemic Modelling on Contiguous District Networks in Peninsular Malaysia

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In this study, we model the 90 contiguous districts of Peninsular Malaysia as an undirected network to simulate the spread of infectious diseases using the Susceptible-Infectious-Recovered (SIR) framework. Each district is represented as a node in the network, with edges connecting nodes based on geographical contiguity—either through shared land borders or geographic proximity across water bodies. The network is unweighted and relies on static geographical data, excluding the effects of dynamic factors such as traffic or population density. Our SIR simulation aims to understand how infectious diseases spread across different regions based solely on their geographical connections. This basic unweighted network model highlights the influence of geographical contiguity on disease transmission, without being affected by other factors.

Keywords: SIR; District Network; Network Science; Malaysia

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Mapping Learning Dynamics: A Study of Friendship and Peer Tutor Networks using SNA and TDA in Malaysian Higher Education

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The COVID-19 pandemic has fundamentally transformed higher education, shifting from a traditional face-to-face approach to online learning environments. This transition has significantly impacted students' engagement, both socially and academically. This study utilizes social network analysis (SNA) to analyze and compare friendship and peer tutor networks among undergraduate students in Malaysia during the COVID-19 pandemic. By constructing directed and weighted networks, we investigate how these networks may influence the learning community, especially in their impact on the dissemination of information. Through the results of weighted indegree and betweenness centrality, we provide several strategies for cultivating a better learning community. The results reveal that popular and important peer tutors who may act as superspreaders of knowledge in the learning community are not always excellent students, raising the possibility of false information spreading. In addition, we incorporate persistence homology (PH), a technique from topological data analysis (TDA), to predict student performance by extracting topological features such as Betti numbers and persistence entropy from k-hop ego networks. These TDA features, reflecting the shape and structure of student interaction networks, are used as input for machine learning models to classify students into high and low achievers. The results show that TDA features can classify students into high and low achievers, demonstrating the potential of this approach in educational data analysis. Thus, this study emphasizes the significance of monitoring influential students to promote a healthy and effective online learning environment. By combining SNA and PH, this research offers valuable insights into student engagement, providing

educators with strategies to improve learning communities and address challenges related to online learning environments.

Keywords: Social network analysis; topological data analysis; persistence homology; educational data analysis.

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Dynamical analysis of a parameter-aware reservoir computer

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Reservoir computing is a useful framework for predicting critical transitions of a dynamical system if the bifurcation parameter is also provided as an input. Fundamentally, RC functions as a discrete map system. Our study illustrates how applying dynamical system concepts improves the understanding of the prediction capabilities of the RC framework. Our numerical analysis demonstrates how the trained reservoir map successfully generates the dynamics of a continuous system. To learn the correct dynamical behavior around the Hopf bifurcation, the map undergoes the Neimark-Sacker bifurcation such that the critical point of the map is in immediate proximity to that of the original dynamical system. It also correctly captures the intricate behaviour in the phase space like torus formation by the successive crossing of two conjugate eigenvalue pairs. Our findings provide insight into the functioning of machine learning algorithms for predicting critical transitions. The method used for the analysis of parameter-aware RC algorithm can be extended to other RC architectures like the single node reservoir, next-generation reservoir computing to understand their learning mechanism.

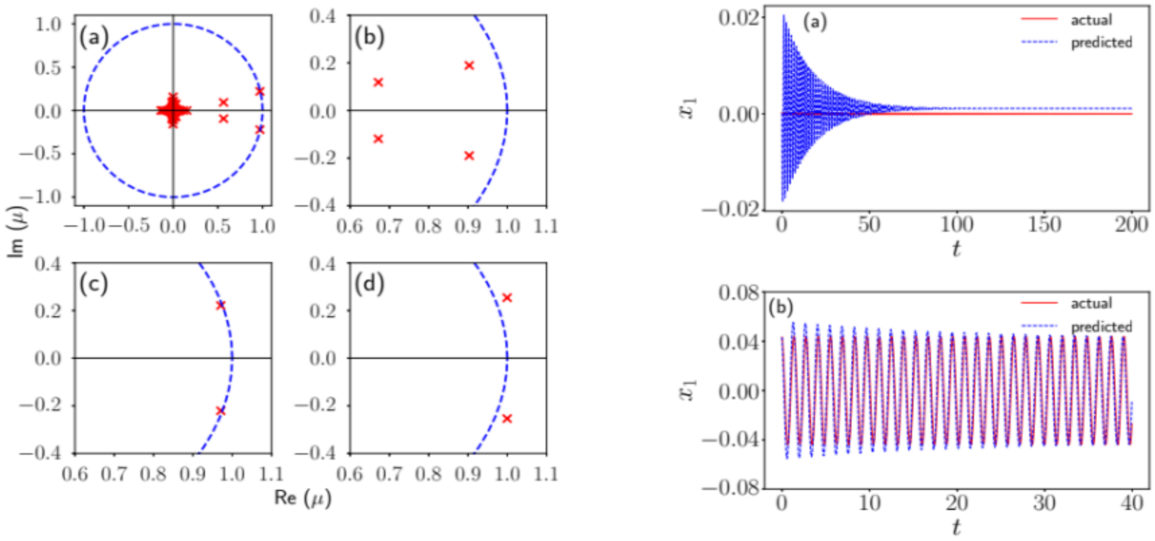

Figure 1: Eigenvalue analysis for a system of coupled Stuart-Landau oscillators. Left figure shows the Neimark-Sacker bifurcation. Figure on the right shows the comparison between the actual and the predicted time-series after successful training.

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Synchronization transitions in adaptive Kuramoto-Sakaguchi oscillators with higher-order interactions

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Coupled oscillators models help us in understanding origin of synchronization phenomenon preva- lent in both natural and artificial systems. Here, we study coupled Kuramoto oscillators model having phase lag and adaptation in higher-order interactions.

$$\dot{\theta}_i = \omega_i + \frac{K_1}{N}\sum_{j=1}^{N} \sin sin\,(\theta_j - \theta_i) + \frac{K_2}{N^2} r_1^{\nu} \sum_{j=1}^{N}\sum_{k=1}^{N} \sin sin\left(2\theta_j - \theta_k - \theta_i - \beta\right).$$

We find that the type of transition to synchronization changes from first-order to second-order through tiered synchronization depending on the adaptation parameters. Phase lag enables this transition at a lower exponent of the adaptation parameters. Moreover, an interplay between the adaptation and phase lag parameters eliminates tiered synchronization, facilitating a direct transition from first to second-order. In the thermodynamic limit, the Ott-Antonsen approach accurately describes all stationary and (un)stable states, with analytical results matching those obtained from numerical simulations for finite system sizes.

Moreover, beyond the critical value of phase lag, the phase transition shifts from first-order (sub- critical pitchfork) to second-order (supercritical pitchfork). Also, inclusion of adaptation in higher- order interaction facilitates the occurrence of tiered synchronization depending upon the exponent of adaptation.

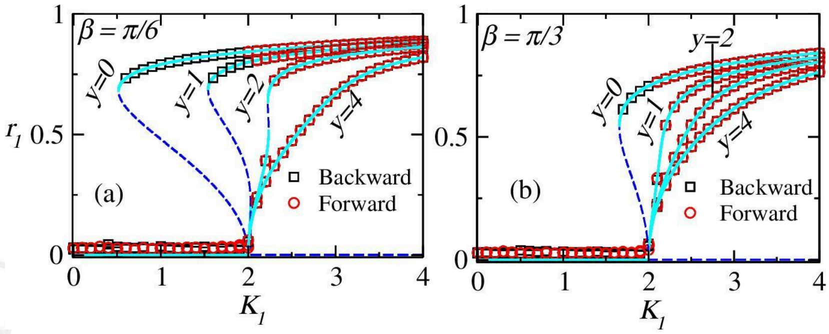

Figure 1: r_1 vs K_1 for different value of y. (a) $\beta = \pi/6$, (b) $\beta = \pi/3$, with $K_2 = 8$.

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Stochastic Kuramoto oscillators with inertia and higher-order interactions

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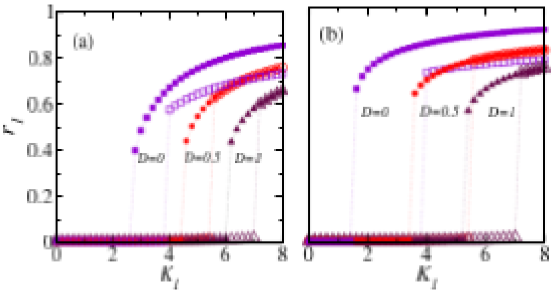
The impact of noise in coupled oscillators with pairwise interactions has been extensively ex- plored. We study second-order Kuramoto model with higher-order interactions and Gaussian white noise. The study investigates noise-induced transitions in the model. Further, investigate that an in- crease in noise strength shifts the forward (backward) critical point associated with an abrupt jump from an incoherent to a coherent state (and vice versa) toward higher coupling values (Fig. 1). Additionally, in an overdamped system, we analytically predict all (un)stable states using the OttAntonsen approach. Also, even in the presence of higher-order interactions, note a shift from first-order to second-order phase transitions as noise strength increases (Fig. 2).

Model: We consider a stochastic Kuramoto model with 2−simplex interactions and inertia. The equation of motion of N globally coupled oscillators is given as,

$$m\ddot{\theta}_i = -\theta_i + \Omega_i + \frac{K_1}{N}\sum_{j=1}^{N} \sin sin\,(\theta_j - \theta_i) + \frac{K_2}{N^2}\sum_{j=1}^{N}\sum_{k=1}^{N} \sin sin\left(2\theta_j - \theta_k - \theta_i - \beta\right) + \xi_i(t).$$

Results



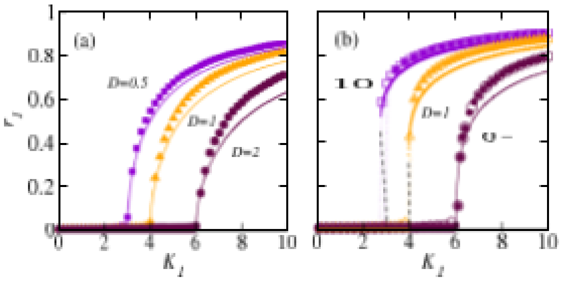


Figure 1: First-order phase transition, an increase in D, shifts forward(backward) transition points towards higher value.

Figure 2: For an overdamped system as D increases, second order transition happens even in the presence of higher-order interactions.

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Classification of brain networks of Caenorhabditis elegans into different life stages using supervised machine learning

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The developmental trajectory of neural networks is key to understanding brain function and evolution. In this study, we investigate the brain network of *Caenorhabditis elegans* across its life stages, aiming to unravel the changes in network structure that accompany development. The raw data for the structural brain networks of *C. elegans* at various developmental stages were obtained from Witvliet et al. (2021)[1]. By analysing eight distinct brain networks, each representing a different stage of *C. elegans'* life cycle, we sought to identify and quantify the alterations in network features that reflect the organism's neural maturation.

We began by mapping and plotting various network parameters, such as node degree, clustering coefficient, and network centralities, to capture the evolving topological characteristics at each developmental stage. Our analysis revealed distinct patterns of change, highlighting the progressive complexity and reorganization within the neuronal network as the organism advances through its life stages.

To test the predictive power of these network features, we applied a machine learning approach using a random forest classifier. For data augmentation, we used random walk sampling without replacement thus, generating multiple subgraphs corresponding to each life stage. Our objective was to determine whether the developmental stage of *C. elegans* could be accurately predicted from the computed network features. The model achieved robust classification performance, demonstrating that network features such as weighted degrees, clustering coefficient and closeness centrality can be reliably used to distinguish the brain networks belonging to the different life stages of the organism.

This study provides new insights into the developmental dynamics of the *C. elegans* brain network, showcasing the utility of network features as indicators of neural maturation. Furthermore, our approach illustrates the potential of combining network analysis with machine learning to predict developmental stages, offering a valuable tool for studying neural development in other organisms with well-defined connectomes.

Keywords: *C. elegans*; Brain Network; Brain Development; Random Forest.

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Detection of Core-Periphery Structure in Networks Using Ant Colony Optimization

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Network science has increasingly focused on unraveling the core-periphery structure, a key mesoscale structure in networks. In this work, we develop a model to identify core-periphery structure using Ant Colony Optimization (ACO). Drawing inspiration from the foraging behavior of ants, our method employs artificial pheromone trails to iteratively build and refine solutions, thereby eliminating the need for arbitrary partitions found in previous approaches. We rigorously test our method on diverse real-world datasets, including historical, literary, linguistic, sports, and animal social networks, and benchmark its performance against leading core-periphery detection techniques. Our findings demonstrate that the ACO-based approach provides exceptional flexibility and precision, significantly improving the accuracy of core-periphery detection compared to existing methods.

Keywords: Core-periphery structure, Ant colony optimization(ACO), Social Networks.

Network	Proposed	Rossa	Rombach	MINRES
Word Adjacencies	69.55	70.64	71.09	73.95
Books about US politics	66.89	65.83	70.27	70.44

Table 1: Frobenius norm of the difference between the ideal core-periphery model and the normalized permuted adjacency matrices of ($\| \delta_{\text{ideal}} - \delta_0 \|_F$) for different core score estimation algorithms on various networks.

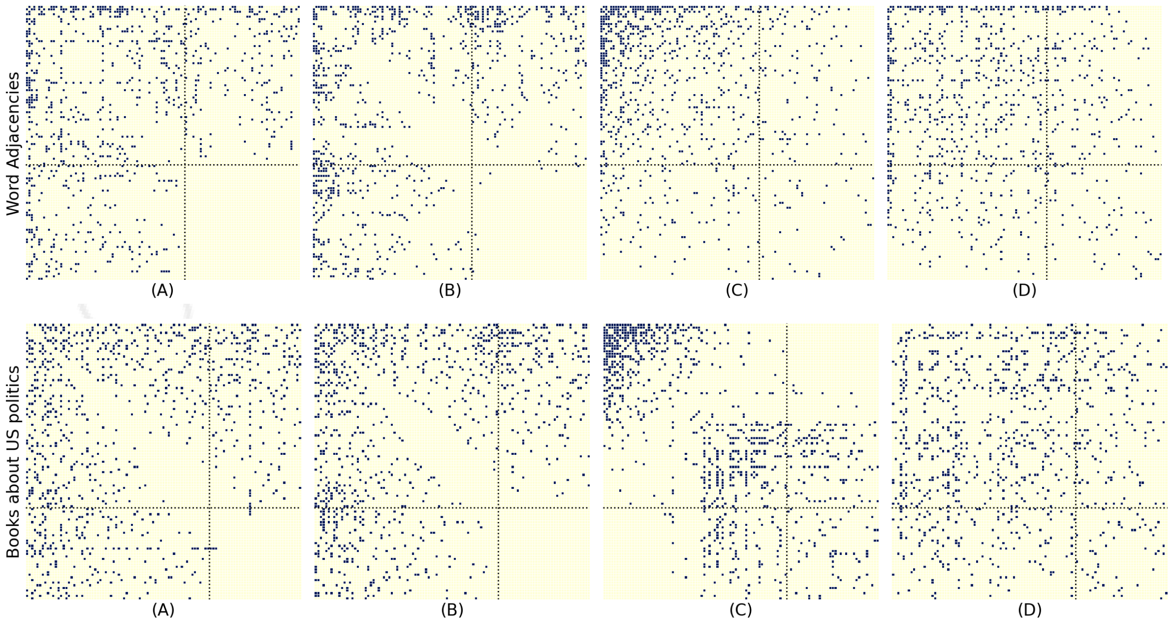

Figure 1: Groundtruth adjacency matrices for the networks, specifically the ”Word Adjacencies” and the ”Books about US Politics” matrix. The adjacency matrices are ordered in decreasing order of core scores obtained using (A) our proposed method, (B) the Rossa method, (C) the Rombach method, and (D) the MINRES method.

Global synchronization in generalized multilayer higher-order networks

Palash Kumar Pal

Networks with higher-order interactions are increasingly recognized for their capacity to introduce novel dynamics into various processes, including synchronization. While previous studies on synchronization in multilayer networks often focused on specific models, such as the Kuramoto model, or restricted higher-order interactions to individual layers, we introduce a comprehensive framework for investigating global synchronization in multilayer networks that incorporate higher-order interactions. Our framework accounts for interactions beyond pairwise connections, both within and across layers, and demonstrates the existence of a stable global synchronous state. This state is characterized by a condition analogous to the master stability function, contingent on the choice of coupling functions. Our theoretical results are supported by simulations with Hindmarsh-Rose neuronal and Rössler oscillators, which illustrate how higher-order interactions, both within and across layers, facilitate synchronization. These findings underscore the advantages of multilayer interactions over single-layer scenarios, offering new insights into the dynamics of complex systems.

A Generalized Network Model for Complex Graph-Data

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We propose a generalized network model, namely, Heterogeneous Multi-layered Network (HMN), which can simultaneously be multi-layered and heterogeneous. We proved that the sets of all homogeneous, heterogeneous, and multilayered net- works are subsets of the set of all HMNs, depicting the model's generalizability. It is experimentally found that the HMN model when used with GNNs improves tasks such as link prediction. In addition, we propose a novel parameterized algorithm (with complexity analysis) to generate synthetic HMNs. The networks generated from our proposed algorithm are more consistent in modeling the layerwise de- gree distribution of a real-world Twitter network (represented as HMN) than those generated by existing models. Moreover, we also show that our algorithm is more effective in modeling an air transport multiplex network compared to an algorithm designed specifically for the task. Further, we define different structural measures for HMN. Accordingly, we establish the equivalency of the proposed structural measures of HMNs with that of homogeneous, heterogeneous, and multi-layered networks. An example HMN is shown in Figure 1. In the Figure, black and green colors are used for undirected, and directed edges, respectively. More details can be found in our complete paper in [1].

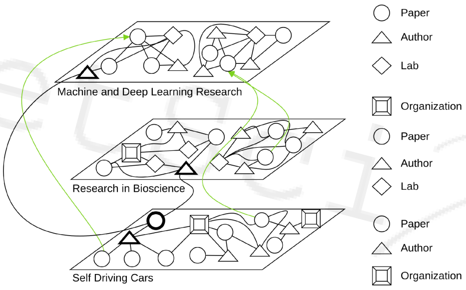

Figure 1: HMN with node and edge types.

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Effect of Phase lag parameter on the Swarmalator dynamics

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Swarmalators are a unique class of systems that integrate both synchroniza- tion and swarming. Synchronization is the process by which individual oscil- lators adjust their internal state to achieve a unified behavior, seen in phenom- ena like metronomes ticking in unison or fireflies flashing together. Swarming refers to the collective movement of individuals within a group, leading to coordinated motion without a central leader, as observed in flocks of birds or schools of fish. Swarmalators are particles that simultaneously exhibit coordinated motion and synchronization of their intrinsic behaviors, like internal phases, resulting in complex pattern formation. This system is accurately modeled by coupled differ- ential equations, yielding five distinct collective states. These states can be observed in various biological and physical systems like Japanese tree frogs, and colloidal suspensions of magnetic particles. The Space-phase order parameter(S), which quantifies the degree of correlation between the internal phase and the spatial angle of swarmalators, is employed to analyze these five collective states. In our study, we investigate the impact of introducing a phase lag factor (α) that signifies the effects of interaction delay in swarmalator systems. Our analysis reveals that the inclusion of this phase lag results in significant changes to the space-phase order of the swarmalators .We observe in S-K plot with increasing α , the system requires less critical coupling strength (K_c) to transition from uncorrelated state (zero S) to correlated state(non zero S). In the two-parameter space where the evolution of collective states can be observed, we found that the regions exhibiting high correlation expand, while the regions of no correlation decrease in size. Additionally, the nature of the transition of the parameter S with varying coupling strength (K) from a non-zero value (correlated state) to zero (uncorrelated state) undergoes a significant transformation as α increases. For a phase lag of zero, the S-K plot, exhibits a continuous transition, characteristic of a second-order transition. However, as the phase lag is increased to $\pi/6$ and $\pi/3$, this transition becomes abrupt or first- order. The introduction of phase lag has been shown to significantly influence the dynamics of the swarmalator system. As phase lag increases, the transition from a high spatial-phase order parameter to zero value shifts from being continuous to abrupt. Moreover, the most striking result observed is that after increasing phase lag, system is driven towards higher values of spatial-phase order, indicating en- hanced correlation between spatial and phase dynamics.

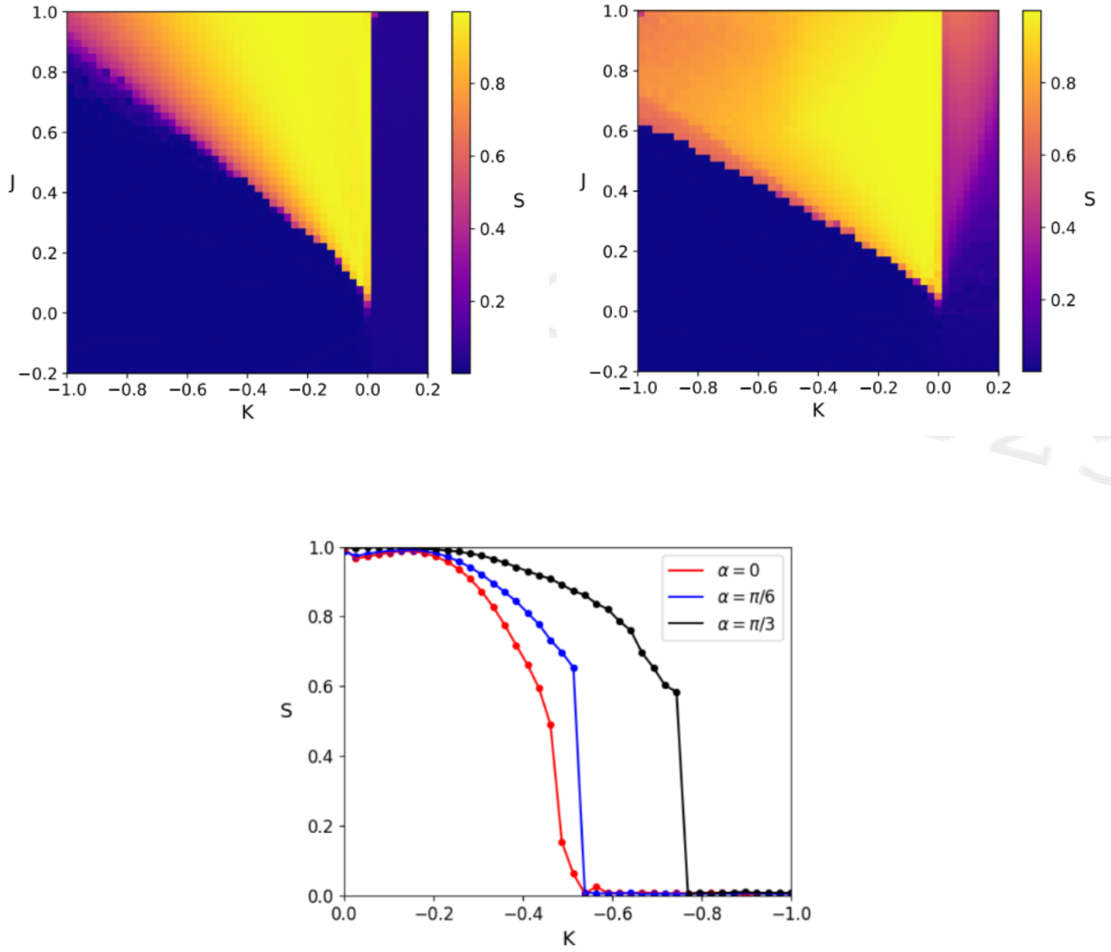

Figure 1: J-K plot with S as the mapping for (a) α=0, and (b) α=π/3, shows that as α increases, the region of high correlation between space and phase increases, while uncorrelated region decrease. Fig 1(c), shows that with increasing α, the transition shifts from a continuous to an abrupt nature

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Spatiotemporal dynamics of deep convective clouds across a wide range of scales using multiresolution analysis

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Climate variability is characterized by a range of oscillatory components spanning intraseasonal, interannual, and decadal timescales. The interactions across multiple scales contribute to the complexity of the climate system, where cross-scale processes can trigger abrupt transitions and extreme events. This study employs a complex network approach to understand the spatio-temporal dynamics of deep convective clouds over the tropics. We use outgoing longwave radiation (OLR) data, a reliable proxy for the presence of deep clouds, over a uniformly gridded tropical region. We construct a functional climate network by estimating the statis- tical similarity between the OLR time series of different scales decomposed using maximal overlap discrete wavelet transform (MODWT). By analyzing the OLR network topology at multiple scales, we unravel the spatiotemporal dynamics of deep convective clouds across a wide range of scales over the tropics, which remains hidden when analyzing the network at a single timescale. This approach highlights teleconnections and aids in classifying tropical climates based on the coherence of cloudiness across different regions and time scales. The climate network at smaller scales exhibits only short-distance connections, as the coherence of cloudiness only occurs for short timescales. When the oscillations smaller than 16 days are suppressed, long-distance connections emerge resulting from the Intertropical convergence zone (ITCZ). The community structure of the OLR network at this scale represents the spatiotemporal dynamics of the ITCZ. At even larger scales, the equatorial Pacific Ocean associated with El-Niño southern oscillations emerges as a coherent region. During the presentation, we will discuss the network topology and the associated physical mechanisms across all the scales considered.

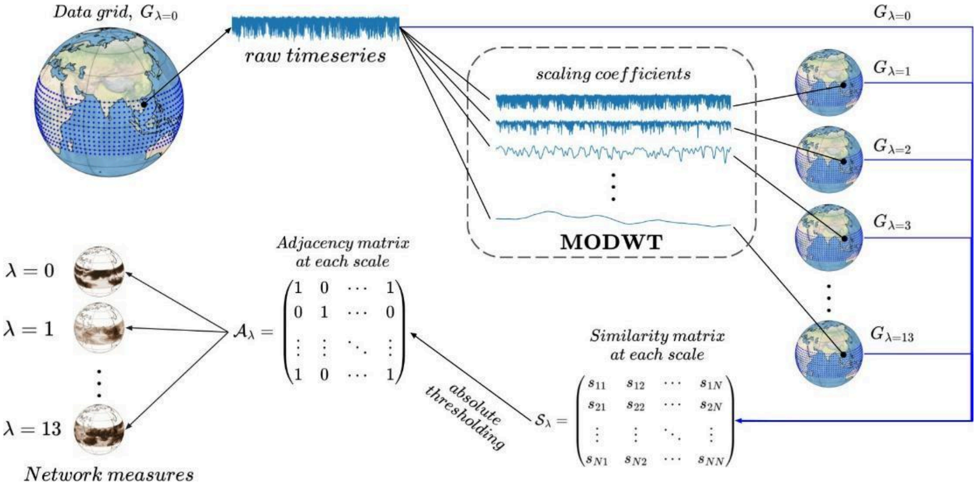

Figure 1: The multiresolution network analysis of OLR in the tropics

Keywords: climate variability, functional climate network, convective cloudiness, multi-resolution analysis.

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Rising inequality signals collapse in a network based model of complex adaptive systems

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Understanding why collapses happen in complex systems around us is significant for forecasting and response planning. In this work, we attempt to understand the origin of crashes in a mathematical model of an evolving complex network. The model [1] describes the dynamics of a directed network of s nodes, represented by the adjacency matrix $A = (A_{i\,j})$, coupled to the populations x_i of the nodes ($i, j = 1 \ldots s$). The network shows the spontaneous growth and collapse of structure and complexity in its time evolution.

Although previous studies have identified proximate reasons for collapses in the model [2, 3, 4], the long term dynamics that leads the network to become fragile is not understood. One of the common theoretical paradigms that study collapses is critical transitions[5], in the present work we show that collapses in this model do not fit this paradigm . We have further computed the Gini coefficient, a measure used by economists to study income inequality, for the distribution of node populations x_i in the model. We find that there is an average rise in inequality among the nodes as the network approaches collapse. We show that the peripheral nodes of the network become richer at the expense of the core thereby increasing the fragility of the network to collapse. Some of the lessons from this model could be relevant for other complex adaptive systems.

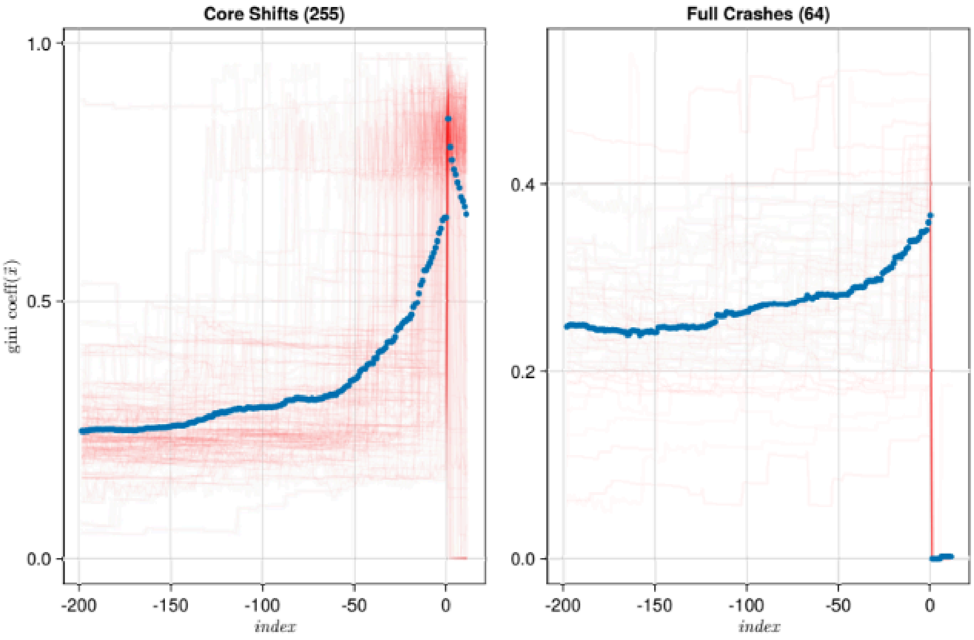

Figure 1: Rising inequality among nodes (Gini coefficient) as a function of time (collapse occurs at 0), averaged over multiple crashes. The two figures correspond to two distinct topological classes of crashes (core shifts and full crashes) in net- works of size $s = 100$.

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A multidimensional systems biology approaches on Mtb-host interactions reveals potential regulators for host metabolic reprogramming

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Tuberculosis (TB) is a pervasive and devastating air-borne disease caused by the organisms belonging to the Mycobacterium tuberculosis (Mtb) complex. To persist and induce pathogenesis, Mtb has developed various strategies to modulate host metabolism, which is pivotal in determining various disease outcomes. But to study this through metabolomics only provides static snapshots, missing dynamics profiles of metabolite trafficking and fluxes, which are essential for understanding metabolic regulation mechanisms. Given the challenges of metabolic profiling, transcriptomic analyses serve as a proxy to uncover metabolic reprogramming and vulnerabilities. This transcriptomic data enables a systematic interrogation of gene expression patterns in biospecimens at tissue and cellular levels. Hinging on this, present study investigates the RNA-seq data of Mtb strain H37Rv infected mice lung tissue to understand host metabolic reprogramming. Preliminary analysis of RNA-seq data revealed that the differentially expressed genes are enrichment in various metabolic processes like lipid, amino acid and nucleotides metabolism. To capture the metabolic-flux profiles of infected and uninfected mice lung, we applied genome-scale metabolic model by integrating the gene expression data. The flux states analysis shows alterations in carbohydrate, amino acid, cholesterol, lipid, vitamin, nucleotide, and energy metabolism in infected mice lung. Our analysis also uncovered 8 up-regulated, and 17 down-regulated genes were responsible for these metabolic reprogramming in infected mice lungs. The same was also confirmed from two separate independent studies. Currently, we are developing network tool to link between the perturbation observed in the host metabolic flux profile capture from transcriptomic data, with various pathogen proteins.

Keywords: Tuberculosis; Genome-scale metabolic model; Host-pathogen interaction network; Host directed therapy

Forecasting User Aggressive Behavior in Online Social Networks

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The widespread use of aggressive behaviour on Twitter raises concerns about potential negative influences on user behavior. Despite previous research exploring aggression and negativity on the platform, the relationship between users' aggressive behavior and that of feeds of followee being exposed to this user, remains underexplored. This study investigates whether exposure to aggressive feeds can lead to an aggressive behavior of an user. We formalize the problem using a heterogeneous network where nodes represent users and tweets, while edges denote following relationships and tweet-posting actions. We detected tweet nodes as aggressive or non-aggressive by developing a transformer-based aggression detection model (macro F1=0.92). User aggression was quantified using a proposed "user aggression intensity" metric based on their overall aggressive activity. Our analysis of 14M tweets from 63K user nodes revealed that aggressive feeds (incoming edges from followed users) can significantly influence users to behave more aggressively on online platforms (P-value < 0.05) (Fig.1a). This effect is also pronounced for event-specific behavior (Fig.1b). Furthermore, the study found that users tend to support and encourage aggressive behavior of their followee users (Fig.1c), which can contribute to the proliferation of aggressive behavior [1].

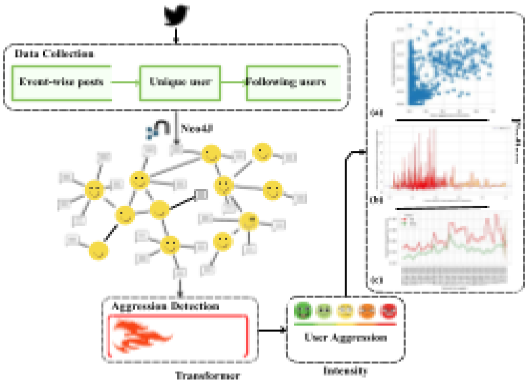

Figure 1: Flow of the methodology used to answer our research questions.

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Collective rotation-flips in directed ring of non-isochronous Stuart-Landau oscillators

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The synchronization of coupled oscillators is critical to understanding how individual systems can spontaneously coordinate their behaviour through interaction. Here, we study the dynamical phenomenon of coupled heterogeneous limit cycle oscillators in a directed ring network, which gives rise to smooth and explosive synchronization. We analyze the rotation flips by computing the effective frequencies of the oscillators and order parameters to characterize the frequency locking and synchronization states. For a small number of oscillators, oscillators change the direction of rotation smoothly inside the synchronization regime. As the network size increases, the system imparts explosive synchronization characterized by abrupt frequency locking associated with rotation flips. Finally, with the help of standard deviation, we found that the increment of the critical coupling for effective frequency locking changes with the increment in the number of oscillators.

Keywords: Rotation-flips; Explosive Synchronization; Ring network

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Extreme events in a coupled chaotic non-identical oscillators

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Unravelling the existence of extreme events in coupled dynamical systems is an important area of scientific research that helps in determining the precursors/mechanism behind such emergence. In this direction, in the present article, we determine the emergence of extreme events in an exemplary chaotic system that is attractively coupled with another non-identical counterpart. The heterogeneity is introduced in the mean frequency of the two oscillators and this heterogeneity makes the system exhibit extreme events. The emergence of extreme events in this system is determined using the peak over threshold method. Furthermore, we confirm these events using statistical measures. At this point, we find that extreme values fit well with the generalized extreme value distribution and the inter event interval fits well with the exponential distribution. Finally, upon examining the mechanism, we find that, heterogeneity in the frequency makes the oscillator oscillate out-phase with each other and occasionally go in phase with each other. This intermittent phase synchronization produces extreme events in the system. We also find that the coupled system also exhibits an on-off intermittency. Owing to this, system's trajectories occasionally get ejected from the invariant manifold and get reinjected back within a short span of time.

Overlapping community detection in bipartite networks

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Networks are essential for modeling complex systems with interacting entities, especially when accounting for dynamic and multifaceted relationships. Overlapping community detection methods better capture the complexities of real-world networks by allowing nodes to belong to multiple communities. Traditional community detection methods assign each node to a single community, which often fails to capture the multifaceted relationships inherent in real-world networks. Overlapping community detection methods address this limitation by allowing nodes to belong to multiple communities, reflecting the complexity of interactions in social networks, biological systems, and other complex networks. Compared to a one-mode network in the real world, a bipartite network is a more complicated network that emphasizes authenticity and application in various fields, such as recommendation systems, ecological networks, and social network analysis. Our comparison of various algorithms across two datasets showed that SLPA, Membership Degree, and COPRA often outperformed other methods in detecting communities in bipartite networks.

Keywords— Node embeddings, Bipartite networks, Network representation learning, Overlapping Community detection

A network is a general data structure that models the symmetric and asymmetrical relationships among discrete objects in the real world [10]. A bipartite network [12] is a unique kind of complicated network with two separate node types and edges connecting nodes of different types. Compared to one-mode networks, bipartite networks have more intricate relationships, topologies, and implicit information[6]. Community detection in bipartite networks is relevant for the recommendation system. For instance, in the recommendation system of commodities and e-commerce users, users are classified based on their attributes, and users with distinct attributes are categorized into distinct communities. The products in the recommendation system are suggested for users based on the connections between users within the communities, then the suggested products will be more relevant to the needs of the users.

Community structure can be separated into overlapping and non-overlapping categories based on the subordinate relationships between nodes. In complex networks, overlapping nodes frequently have significant roles to perform. Identification of overlapping nodes is an important subject of study in complex network analysis because overlapping nodes belong to and connect different overlapping communities and play a crucial role in information flow. Overlapping nodes are those that belong to multiple communities and of- ten act as bridges, facilitating the flow of information or resources between different parts of the network. However, traditional non-overlapping community detection algorithms cannot be directly applied to overlapping community detection, hence various overlapping community detection methods such as Community Detection Algorithms[3], Soft Clustering Techniques [5], and Matrix Factorization[17], etc have been developed to identify overlapped nodes from a network [8]. We begin by categorizing the algorithms into several methods: Clique Percolation Methods [7], Fuzzy Clustering Methods[9], Speaker-Listener Label Propagation Algorithm [13].

1. Clique Percolation Method (CPM) is a community detection algorithm used to identify overlapping communities in complex networks. The method works by finding k-cliques, which are fully connected subgraphs of k nodes, within the network. These k-cliques are then merged if they share (k-1) nodes, allowing for the formation of larger communities. CPM is particularly effective at detecting tightly-knit groups, allowing nodes to belong to multiple communities. This makes it useful in networks where nodes have multiple roles, such as in social or biological networks.

2. Fuzzy Clustering Methods: Fuzzy Clustering Methods apply fuzzy logic principles to allow nodes to belong to multiple communities with varying degrees of membership. Algorithms such as Fuzzy C-Means and Fuzzy K-Means enable flexibility in community membership, which better captures the nuances of overlapping communities. Despite their adaptability, these methods can sometimes lack precision and clarity in the resulting community structures.

3. Speaker-Listener Label Propagation Algorithm (SLPA) is designed to detect overlapping

communities in networks by enabling nodes to hold multiple labels, representing membership in different communities. Initially, each node is assigned a unique label. During iterative propagation, nodes alternately listen to neighbors to collect labels and then speak to share one of their collected labels, chosen based on frequency. This process continues until label distributions stabilize. After convergence, label distributions are analyzed to determine overlapping communities, with nodes belonging to multiple frequent labels. SLPA is flexible, scalable, and adaptable, making it suitable for large networks without needing predefined community numbers. However, its performance can be sensitive to parameters and may require many iterations in dense networks. It is particularly effective in networks with common overlapping structures, such as social, biological, and collaboration networks.

4. Central node [11] Taking the “central node” as the initial community C, it adds the neighbor node with the largest contribution to the community C to this community, and a community will be built when the global contribution reaches the maximum; if there are more nodes with larger contribution to the community, these nodes will be added to these communities. After extracting the community C, the nodes and edges of community C are not deleted from the network, in order to mine the overlapping nodes between communities. Obtained overlapped community nodes from the network

5. COPRA (Community Overlap Propagation Algorithm) [1] method is an algorithm designed to detect overlapping communities in networks. COPRA works by propagating labels through the network in an iterative process. Initially, each node assigns itself a unique label. During each iteration, nodes update their labels based on the labels of their neighbors, allowing them to adopt multiple labels. This process continues until the labels stabilize, indicating the detection of overlapping communities. The key feature of COPRA is its ability to allow nodes to belong to multiple communities simultaneously, reflecting the complex and multifaceted nature of real-world networks

We consider two bipartite networks in our study. They are:

1. *Corporate leadership* [2] is a bipartite network containing person–company leadership information between companies and 20 corporate directors. The data was collected in 1962. Left nodes represent per- sons and right nodes represent companies. An edge between a person and a company shows that the person had a leadership position in that company.
2. *Southern women* [4] : This dataset consists of 32 nodes, out of which 18 represent 18 women and the remaining 14 represent 14 informal social events. It records which women met for which events. To evaluate the quality of obtained overlapping communities, we employ the widely used Modularity [14] and nor- malized mutual information [16] as the accuracy measures. In addition, three quality measures: Precision, Recall, and F-measure [15] are used to assess the quality of the data.

Table 1 : **NMI values on dataset**

lgorithm	NMI	
	Corporate leadership	**Southern Women**
Clique	0.0	0.0
SLPA	1.06	1.0
Central node	0.0	1.0
Fuzzy	0.0	0.0
Corpa	1.0	0.0
Membership degree	1.0	1.0

Table 1 shows the NMI comparison of the simulation results of Clique percolation, SLPA, Central node, Copra, and Membership degree. From the values it could be found that SLPA and Membership degrees have NMI values 1 for both datasets. It indicates that better alignment between the detected communities and the ground truth or reference communities than the other three algorithms. In considering the Southern Women dataset NMI value is 1 for the Central node algorithm also for Corporate leadership NMI value is 1 for Corpa Algorithm.

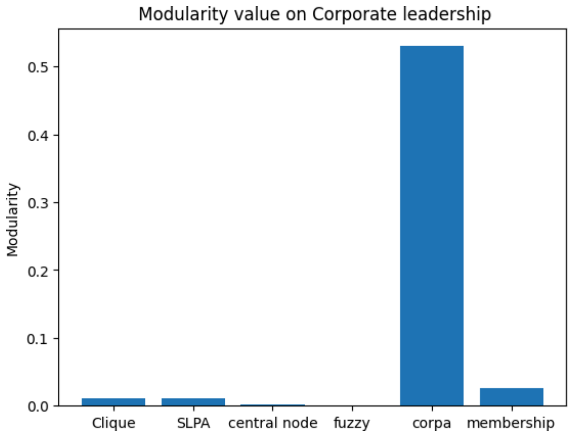

Figure 1: **Modularity value on Corporate leadership**

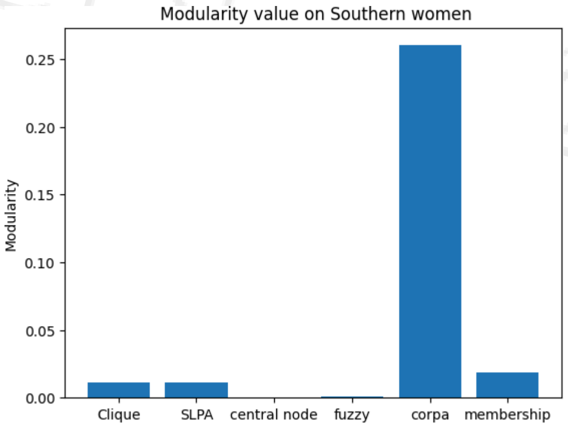

Figure 2: **Modularity value on Southern Women**

Figures 1 and 2 show the Modularity scores of our simulation results of Clique percolation, SLPA, Central node, Copra, and Membership degree. Corpa shows a higher value in the modularity of 0.53 on dataset Corporate leadership and 0.26 on the dataset Southern Women than the other algorithms indicating a strong community structure, while a value close to 0 for the other algorithms suggests a random or weak community structure.

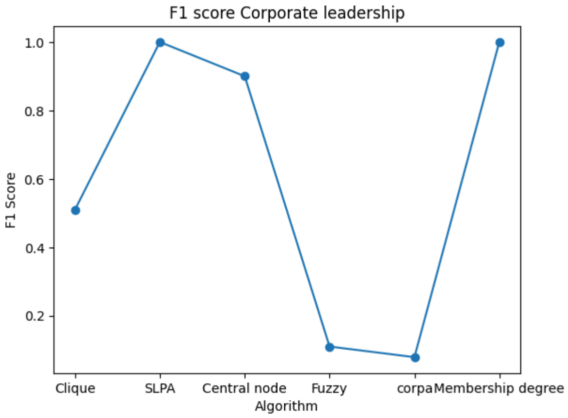

Figure 3: **F1 score on Corporate leadership**

The performance of identifying overlapping nodes, Clique percolation, SLPA, Central node, Copra, and Membership degree algorithms are also compared on the F1 measure. Figure 3 shows the comparison results of the five algorithms on the F1 measure of Corporate leadership. In this, SLPA central node and Membership degree show a high F1 score of 1 indicating high accuracy in community detection, with detected communities closely matching the true communities.

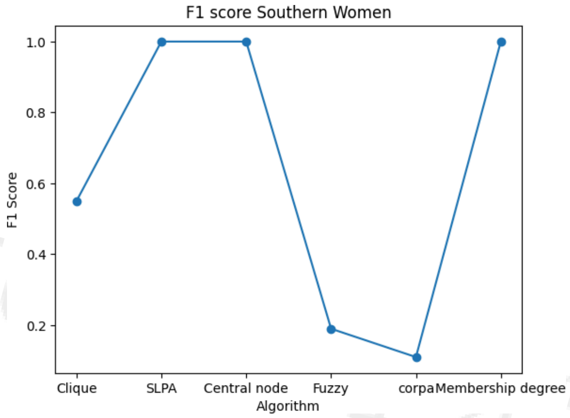

Figure 4: **F1 score on Southern Women**

Figure 4 displays the five algorithms' comparison findings on the F1 measure on the dataset Southern Women. In this, SLPA and Membership degree show a high F1 score of 1 and the central node has a value of 0.5 indicating high accuracy in community detection, with detected communities closely matching the true communities and the central node has a value of 0.5 where the detected communities capture some but not all of the true community structure.

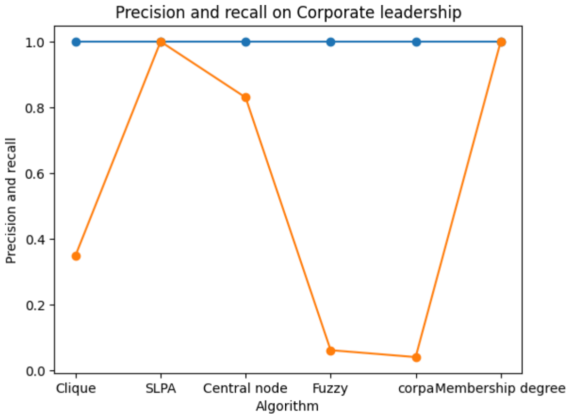

Figure 5: **Precision and recall on Corporate leadership**

Figure 5 displays the five algorithms' comparison findings on the Precision and recall measure on the dataset Corporate Leadership. Higher Precision means a more accurate prediction. The blue Colour line shows the precision value. In this, Clique percolation, SLPA, Central node, Copra, and Membership degree show a high Precision score of 1 indicating that most of the detected memberships are correct. Obtain better value of Recall mainly because they found significant numbers of communities. The red color line shows the recall value. SLPA and Membership degree show a high recall score of 1 means that most of the true memberships have been detected and the central node had a value of 0.5 means many true memberships were missed, with many false negatives.

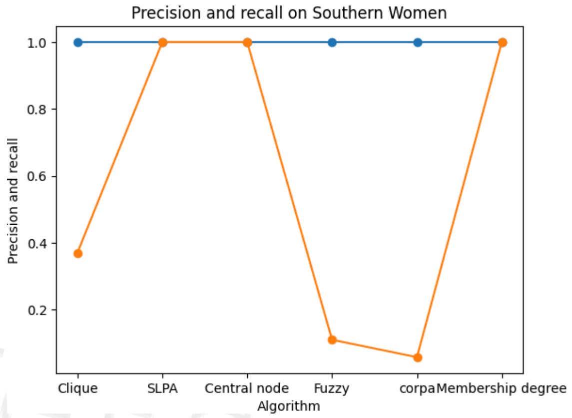

Figure 6: **Precision and recall on Southern Women**

Figure 6 displays the comparison results of the five algorithms on the Precision and recall measure on the dataset Southern Women. In this, Clique percolation, SLPA, Central node, Copra, and Membership degree show a high Precision score of 1 indicating that most of the detected memberships are correct. SLPA, central node, and Membership degree show a high recall score of 1 means that most of the true memberships have been detected and a low value means many true memberships were missed, with many false negatives. A high value of F-measure means that both Precision and Recall are sufficiently high.

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Avalanche event in number theoretic division model

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Self-organized criticality (SOC) is a concept in which a complex dynamical system spontaneously organizes itself into a critical state where *scale-invariant phenomena*, such as power-law distributions, can be observed. Luque *et al.* introduced a number-theoretic division model that exhibits SOC behavior. This model operates on a *scale-free network* with simple dynamics. The objective is to con- struct a primitive set of integers—a set in which no number divides another—from an ordered set of integers (referred to as the pool). A number is added from the pool to the primitive set. Let this number exactly divide and divisible by s numbers, then a *division avalanche* of size s take place and these numbers are returned to the pool. By this, the primitiveness of the primitive set is preserved. The size of these avalanches follows a power-law distribution with an exponent of 2. Additionally, the avalanche size is constrained by a cutoff $s_o \sim M/\ln M$, where M is the size of the pool. Careful analysis reveals the presence of a logarithmic term, $\ln M$, in the distribution of avalanche sizes.

Keywords: Self-organized criticality, Scale-free networks, Power spectral density.

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Exploring Comorbidity Networks in Mild Traumatic Brain Injury Subjects through Graph Theory: A Traumatic Brain Injury Model Systems Study

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Mild traumatic brain injury (mTBI) is a common condition characterized by temporary cognitive impairment following head trauma. Despite its prevalence, mTBI remains poorly understood, and effective prevention and treatment strategies are lacking. One major challenge in addressing mTBI is the complex interplay between various comorbidities that often accompany this condition. Comorbidity refers to the co-occurrence of two or more diseases or health conditions within an individual. In the context of mTBI, comorbidities can significantly impact patient outcomes and treatment efficacy. In our study, we explore the application of network analysis techniques to investigate comorbidity patterns following mild traumatic brain injury. By leveraging data from the Traumatic Brain Injury Model Systems Database (TBIMS 2021), our study aims to uncover the underlying structure and dynamics of disease co-occurrence in mTBI patients.

We employed a graph-theoretical approach, constructing disease comorbidity networks for young and middle-aged adults separately. The resulting network consisted of nodes representing various diseases or health conditions, while edges represented the frequency of co-occurrence between these conditions. To identify vital nodes (comorbidities) that control information flow and transition within the network, we computed three centrality measures: degree centrality, eigenvector centrality, and betweenness centrality. Our analysis revealed a complex comorbidity landscape in mTBI patients, with multiple clusters of interconnected diseases emerging from the network graph. Notably, our results showed that certain comorbidities (e.g., depression, anxiety) exhibited strong associations with other conditions, while others (e.g., chronic pain) displayed weaker connections. Psychiatric comorbidities tend to co-occur after mTBI incidents, in line with such illnesses occurring at a higher rate in TBI subjects compared to the general population. Endorsed by previous literature, we find non-trivial links between seemingly disparate conditions such as rheumatoid arthritis and obsessive compulsive disorder, cardiovascular disease and bipolar disorder, chronic obstructive pulmonary disease and depression and anxiety, to name a few. The findings presented here demonstrate the effectiveness of network analysis in uncovering hidden patterns and relationships within complex systems like mTBI using real-world data. By leveraging graph-theoretical techniques to identify vital nodes and clusters, our study provides a novel perspective on comorbidity dynamics following TBI.

Keywords: Traumatic brain injuries; Graph theory; Comorbidities; Disease comorbidity network.

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Computational Analysis of Transcriptomic data reveals factors associated with prognosis and treatment in Pancreatic Ductal Adenocarcinoma

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Pancreatic ductal adenocarcinoma (PDAC) is a highly lethal cancer with a dismal 5-year survival rate of under 10%, primarily due to late diagnosis, rapid progression, and resistance to treatment. Recent advances in high-throughput sequencing have illuminated the complex molecular landscape of PDAC, revealing significant genetic heterogeneity and dysregulated pathways. Understanding

survival-related genes whose expression or genetic alterations correlate with patient outcomes is crucial for developing predictive biomarkers and novel therapies. These genes affect various cellular processes such as proliferation, apoptosis, metastasis, and immune response. Identifying genes linked to poor or favourable prognosis can improve risk stratification, personalize treatments, and guide the development of targeted therapies. Transcriptomic data, which captures the expression levels of multiple genes across various biological conditions, embodies several layers of complexity, such as high dimensionality, batch effects, non-linear relationships, etc. So, advanced computational techniques help elucidate the complex relationships between genes involved in disease pathways and can classify the disease subtype. This study leverages transcriptomic data from The Cancer Genome Atlas (TCGA) to systematically identify and characterize survival-related genes in PDAC. We employed Cox regression and bootstrapping to correlate gene expression with overall survival (OS), and estimated immune infiltration using MCP-counter and gene set variation analysis (GSVA) to assess pathway activity. Additionally, we explored regulatory mechanisms underlying biomarker expression by identifying transcription factors (TFs) and microRNAs (miRNAs) through large-scale data analysis. Our objective is to develop a robust prognostic gene panel utilizing computational methods based on tumor microenvironment (TME)-relevant genes for PDAC patients. This panel aims to accurately predict overall survival (OS) and disease-free survival (DFS) among PDAC patients, serving as a biomarker for identifying patients who may benefit from targeted therapies.

Keywords: PDAC; Survival related genes; Prognosis; Personalized treatment

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Time-varying network captures emerging phenomena prior to the Kerala floods in 2018 and 2019

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In recent years, the frequency and intensity of extreme rainfall events have increased due to global climate change, often leading to catastrophic devastation such as flooding, landslides, and mudslides. It is essential to understand and unravel the physics behind extreme rainfall events. The southwest coast of the Indian subcontinent experienced intense anomalous rainfall which led to devasting floods in Kerala in the years 2018 and 2019. This study explores these extreme rainfall events from the perspective of complex networks. We construct a time-varying functional climate network where nodes represent geographical locations, and links represent interactions between these locations by estimating the statistical similarity of extreme precipitation events using event synchronization. From the topology of the network, we observe that the extreme rainfall events in 2018 and 2019 are associated with a mesoscale pattern of synchronized rainfall. This pattern originates from the central Indian Ocean and moves eastwards over the Bay of Bengal stopping over the Maritime Continent. Then the pattern moves westward towards the Indian peninsula and accumulates over the southwest coast of India, especially over Kerala which leads to floods. Additionally, we find that the coherent pattern of synchronized extreme rainfall is accompanied by enhanced convective cloudiness and moisture transport. The discovery of coherent emergent phenomena is crucial for the development of precursors for such extreme rainfall.

Keywords: Extreme rainfall events; Kerala floods; Time-varying network, Event synchronization.

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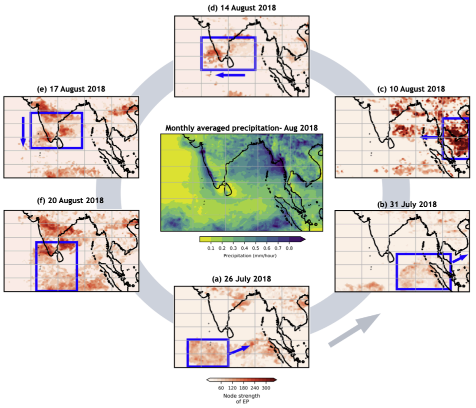

Figure 1 Circulatory movement of synchronized extreme rainfall pattern during 2018.

Genome-scale community modeling for deciphering the metabolic synergisms in termite gut microbiota

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Microbiome research has revolutionized our understanding of the microbial world in different ecosystems, specifically in the insect, animal, and human gut microbiota. Microbial guilds in the wood-feeding insect, like the termite gut microenvironment, help to degrade complex lignocellulosic material through collaborative metabolic activities. The biochemically synergistic microbial consortia produce complementary enzyme cocktails, offering a compelling strategy for effective lignocellulose degradation bioconversion. (Auer et al., 2017; Bredon et al., 2018; Brenner et al., 2008). However, to develop defined microbial communities with efficient lignocellulolytic functionalities, a system-level understanding of the inter-microbial metabolic interaction patterns is required (Faust and Raes, 2012; Seth and Taga, 2014). Therefore, genome-scale community metabolic network reconstruction strategy has been implemented to map the growth and metabolic compatibility among crucial bacterial species isolated from the wood-feeding termite gut microbiota. The community metabolic network analysis revealed the activation of amino acids, SCFAs, and small sugar exchange in the pairwise and multispecies communities. Several flux-based parameters like pairwise metabolic assistance (PMA) and pairwise growth support index (PGSI) were introduced to quantify the growth and biochemical synergisms among these bacterial pairs. The assessment of PMA and PGSI identifies the positively interacting microbial species, showing metabolic mutualisms for executing the complex process of lignocellulose bioconversion. The knowledge of microbial metabolic assistance and interaction patterns derived from the computational work has been tested by developing synergistic co-culture systems with termite gut bacterial isolates. The degree of bacterial enzymatic synergisms in the lignocellulosic substrates showed good coherence with the model-predicted PMA in the bacterial communities. The computational pipelines and flux-based parameters established in this study can be further extended to map the biochemical signature, inter-microbial cross-talk, and critical functional landscape in various microbial ecosystems.

Keywords: Metabolic network; Microbiome; Synergistic co-culture

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A Multi-Level Boolean Formalism

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Metastasis, the cause of more than 90% of cancer mortality, is the mechanism by which cancer cells spread to multiple organs. It involves a transition between Epithelial and Mesenchymal phenotypes (EMT) in cancer cells. Several studies have established the importance of hybrid E/M phenotypes – cells that partially express both Epithelial and Mesenchymal markers – in the emergence of key phenomenon such as stemness, drug resistance and metastasis. Despite their importance, the composition, stability and emergence of such hybrid states is not well understood. Computational models of underlying gene regulatory networks (GRNs) are very helpful in understanding the dynamics of EMT and emergence of hybrid states. Predominantly, these models use either ordinary differential equations (ODEs) or Boolean formalism. While ODEs capture the complexity of biological systems by incorporating kinetic parameters and a continuous state space, several drawbacks including computational expense and limited parametric information render them impractical to model GRNs in many scenarios[1].

Boolean formalism on the other hand takes a much simpler treatment of the GRNs, considering only the network structure that can be established with a higher degree of certainty than the kinetic parameters. Multiple studies have demonstrated the usefulness of Boolean networks in describing various biological systems, including EMT[2]. However, standard Boolean systems allow for only two levels (high, low) of gene expression, while the study of hybrid states requires admittance of partial expression levels as shown by experimental as well as ODE based models of EMT. Therefore, the current work aims to modify Boolean frameworks We take up an existing boolean model that has previously been employed to study EMT GRNs, and modify it by introducing various intermediate expression levels while still adhering to the motivations behind boolean formalisms (low complexity, parameter independence). This “multi-level” formalism gave rise to a significantly larger number of hybrid states than the original Boolean formalism. The most stable hybrid states had partial expression of E and M nodes, in accordance with the experimental data. Furthermore, we find that these hybrid states are more stable to various constraints on the simulation formalism, as compared to the original Boolean formalism. Thus, we propose the multi-level formalism as an alternative to the currently existing Boolean formalisms that can better capture the complexity of biological phenotypes.

Keywords: Gene Regulatory Networks; Boolean Modeling; Epithelial-Mesenchymal Transition

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Study of El Niño Southern Oscillations using recharge-discharge model and machine learning approach

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This work focuses on studying dynamic behaviours obtained from the various climate models that mimic El Nino Southern Oscillation. We start our study by studying a solar-forced recharge-discharge model for ENSO which has been transformed to a van der Pol-Duffing oscillator model with a 11 year forcing.

$$\frac{\mathrm{d}x_1}{\mathrm{d}t} = \dot{x_1} = x_2$$
$$\frac{\mathrm{d}x_2}{\mathrm{d}t} = \dot{x_2} = \mu x_2 - \mu\epsilon x_1^2 x_2 + \gamma x_1 - \beta x_1^3 + F\cos(x_3)$$
$$\frac{\mathrm{d}x_3}{\mathrm{d}t} = \dot{x_3} = w$$

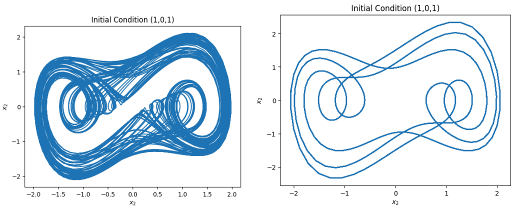

Figure 1: The van der Pol-Duffing equation is given above along with a phase plot showing a chaotic and periodic state respectively

The time series analysis of this model, with forcing, shows more chaotic behaviour as the forcing term is increased, with windows of periodic behaviour in the middle. These transitions from chaotic to periodic and back were observed in a bifurcation plot drawn by varying the amplitude forcing F. Furthermore, we simulated various climate models like simple recharge discharge model, delayed action oscillator model etc. and using the time series of these models we have implemented recurrence quantification analysis. Further, we used recurrence measures as input features for the machine learning (ML) algorithms. ML algorithms help to predict and classify the behaviour of the system. We utilise algorithms like Logistic Regression, Random Forest and Support Vector Machine for classifying the behaviour of the system to periodic, chaotic, hyperchaotic and noisy categories. Using the ML algorithms with good accuracy we classified dynamical states successfully.

Keywords: Machine Learning Classification; El Niño Southern Oscillation (ENSO); Climate Models

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Comparing the dynamics of binary-fate and multi-fate team-based regulatory networks in cellular decision making

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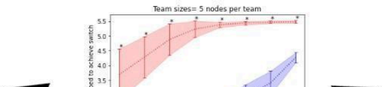
Conserved design principles underlie the gene regulatory networks involved in cell-fate decision-making.
The gene regulatory networks governing binary cell-fate decisions give rise to bimodal and low-dimensional phenotypic spaces **[1]** **[2]**. Such emergent properties can be attributed to the presence of two mutually inhibiting "teams" of genes in the network, with each "team" being comprised of drivers specific to a phenotype; this design behaves analogous to a toggle switch**[1]**. Though most known cell-fate decisions are binary, there are at least a few known scenarios involving three or more possible fates **[3]**. While we find a similar "team" structure in these multi- fate networks, the emergent properties of such non-binary decision systems are not understood.

In this work, we investigate whether it is feasible to construct n-way decision/multifate networks using the principles of teams, and if so, how their stability characteristics fare against those of binary decision networks. We start by identifying the potential network topologies that can give rise to n-way steady states based on the design principle of mutually inhibiting teams. We then characterize the composition and stability of prominent 'cell-fates' emergent from these networks as well as the transition dynamics between these states upon perturbation in various forms. Finally, we establish an algorithm to identify the configuration of teams in such networks. We find that as the number of teams in a network increases, non- hybrid steady states (having the entirety of exactly one team being expressed and all other teams entirely repressed) become increasingly less dominant, and observing such states is very difficult in networks with more than three teams. Steady states of networks with more than two teams are much more "frustrated" than their two- team counterparts and are hence much less robust to perturbation. Further, directly transitioning between non-hybrid phenotypes is far harder if more than two teams are present, requiring much stronger and much more specific perturbation in terms of the teams targeted. We also find that our team-identification algorithm becomes increasingly more accurate at correctly predicting teams the more two-team-like a network is. Overall, our results indicate that decision networks governing choices between more than two fates are not biologically favourable due to their lack of robustness and the inefficiency of phenotypic switching on such networks, a possible reason why we do not find many examples of the same.

Keywords: Cellular decision making; multi-stability; design principles; cell-state transitions;



(This work is yet to be published)

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Breaking Down the Quantum Circuit for Influence Maximization

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Social network analysis (SNA) has significantly emerged in the last two decades as it has vast real-world applications. Influence maximization (IM) in SNA aims to find top k nodes that maximize the expected influence in the network. The LT (Linear Threshold), IC (Independent Cascade), and SIR (Susceptible-Infectious- Recovered) are the widely used classical diffusion models for simulations. However, performing simulations in large-scale networks is still a challenge due to the high complexity of these models. To the best of our knowledge, the existing studies do not perform the IM simulations using quantum computing, and recent studies have shown efficient computations of quantum computers.

This work suggests a quantum-enabled community-based IM algorithm to find the most influential seed nodes. This work finds the community to break down the graph into subgraphs to represent it with the available qubits. This work utilizes Pauli-Z strings along the reward and penalize coefficient to handle the inter and intra-community strength. Further, this work suggests a mechanism to embed the diffusion rules of LT, IC, and SIR models into the quantum circuits. Based on the edges and influence weight, this work encodes the respective gates on the quantum circuit, reflecting the rule of these diffusion models. The encoded diffusion models handle the progressive nature using Toffoli gates.

In the end, we integrate the proposed community detection algorithm with suggested quantum-based diffusion models to solve IM. Further, this work presents the analysis of experimental results on several datasets. However, due to the initial phase of quantum computing emergence, the proposed work has limitations such as inadequate availability of quantum simulators, less number of qubits in the existing quantum computers, etc. This work further discusses the potential challenges and future direction of IM concerning quantum computing.

Keywords: Quantum Computing, Influence Maximization, Community Detection, Social Networks.

Semantics of creativity: identifying LLM-authored fanfiction stories with Latent Personal Analysis

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The recent progress in the development of Generative Artificial Intelligence (GAI) has created a technology disruption yet to be fully understood. GAI-based Chatbots automate content generation, improve content quality, and increase diversity [1]. While the technology has advanced rapidly, relatively little research has been conducted on its impact on creative communities, such as fanfiction [2]. With the introduction of ChatGPT and its capabilities in content creation [3], several fanfiction community members started experimenting with it, as depicted in Figure 1. Here, we study the semantic differences between human and GAI-created fanfiction stories. We leverage Latent Personal Analysis (LPA) [4, 5], an unsupervised learning method that utilizes Information theory to identify the most surprising elements of entities in a population and semantic differences between stories created by humans or GAI. LPA is a methodology for (a) identifying latent, unknown-known attributes of entities and (b) identifying the elements whose Shannon information differs most from their counterparts in the population. These elements contribute to the entity's LPA's divergence attribute and determine its LPA's *signature* attribute. Thus, LPA signatures consist of corpus popular terms missing from or underused in the authors' vocabulary and overused rare terms. The data in this study consists of both human-written fanfiction stories retrieved from a 2017 public fanfiction archive [6] and synthetically LLM-created fanfiction stories based on zero-shot published prompts from the fanfiction community.

We demonstrate the strength of LPA signatures by using them as the training set for a GAI authorship classifier, showing that LPA gives an easy-to-understand, interpretable explanation of the semantic differences between human and GAI-generated stories. We show how, in this case, LPA is an easy and fast alternative to SHAP values [7].

Keywords: Entropy, Latent Personal Analysis, LLM-authored, Creativity.

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Comparing molecular changes among breast cancer subtypes through network-based approach

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Breast cancer remains a leading cause of mortality among women, characterized by its complex and diverse nature, comprising various molecular subtypes, each demonstrating distinct treatment responses and clinical outcomes. Addressing the complexity of tumor heterogeneity and advancing precision medicine are key objectives in current breast cancer research. This study aims to deepen understanding of the disease complexities at the molecular subtype level. RNA sequencing data for luminal A, luminal B, HER2-positive, and triple-negative breast cancer (TNBC) subtypes, with corresponding normal samples, were obtained from the Gene Expression Omnibus (GEO) database. We identified modules containing unique and significantly correlated genes with each subtype using weighted gene co-expression network analysis (WGCNA). Subsequently, genes within each subtype-specific module were explored by constructing and analysing protein–protein interaction (PPI) networks. The prognostic and diagnostic potential of the identified crucial proteins for each subtype was evaluated through survival and ROC curve analyses. We identified crucial proteins specific to each molecular subtype that exhibited significant associations with adverse survival outcomes in breast cancer patients and also demonstrated remarkable diagnostic efficacy in differentiating tumor and normal samples. The present study offers new insights for advancing research on breast cancer subtypes.

Keywords: Protein–protein interaction network analysis · Network topology · Survival analysis · ROC curve analysis.

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Topology aware Optimization of Encrypted Gradient Aggregation in Differentially Private Federated Learning via Broadcast Encryption for Enhanced Security in Multi-Party Network Transmission

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Federated Learning (FL) facilitates decentralized model training while safeguarding data privacy. However, secure and efficient gradient aggregation, particularly under Differential Privacy (DP) constraints, remains a critical challenge in multi-party networks. This paper introduces a novel protocol for secure gradient aggregation in Differentially Private Federated Learning (DPFL) that leverages topology-aware broadcast encryption, tailored to the underlying network structure, to enhance both security and communication efficiency.

The proposed protocol models the network topology as a graph $G = (V, E)$, where V represents clients and E denotes secure communication links. By harnessing topological features such as cliques, spanning trees, and articulation points, the protocol optimizes broadcast encryption to minimize communication redundancy, thus significantly improving the security of gradient transmissions. The broadcast encryption scheme is specifically adapted to the network's structure, reducing ciphertext size and the number of transmission rounds, leading to superior scalability and

communication efficiency. This reduction is quantified by a communication overhead factor proportional to log n, where n is the number of participating clients.

A key contribution of this work is the integration of a Gaussian noise mechanism within the broadcast encryption process to enforce ε-differential privacy. Noise sampled from $N(0, \sigma^2)$ is injected into the aggregated gradients, with the standard deviation σ determined by $\sigma = \frac{C.\sqrt{2\log log\left(\frac{1.25}{\delta}\right)}}{\varepsilon}$, where C represents the gradient clipping norm, and δ is the failure probability. This approach guarantees robust privacy, effectively thwarting adversarial attempts to infer sensitive information from the encrypted outputs.

Another significant contribution of this study is the mathematical characterization of the noise impact, which scales inversely with the square root of the number of clients, $O\left(\frac{1}{\sqrt{n}}\right)$. This finding indicates that as the client count increases, the detrimental effect of noise on model accuracy diminishes, thereby preserving the fidelity of the global model while ensuring stringent privacy standards.

Synchronization Analysis in Kuramoto Oscillator System in the Presence of Phase Lag and Noise

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The study of collective synchronization phenomena in a coupled oscillatory system is widely researched and essential for various natural and engineered systems [1]. Previous studies on synchronization analysis in the presence of phase lag in 1 and 2-simplex interactions show a dilated onset of synchronization [2]. Additionally, the order parameter diminishes when a low level of noise is introduced into the system [3]. In our study, we investigate how the interplay between phase lag and noise affects the synchronization phenomena in coupled Kuramoto oscillatory systems. We use the generalized Fokker-Planck equation [4], which describes the evolution of the probability density function of the phases over time to gain a deeper understanding of the system's collective behavior. We analyze the collective dynamical behavior of coupled Kuramoto oscillators in the presence of phase lag and noise analytically and numerically. The results of our study offer deeper insights into the mechanisms driving synchronization in complex systems. Understanding the influence of phase lag and noise will enable us to design control systems more effectively based on coordinated activity.

Keywords: Kuramoto oscillators; Fokker-Planck equation; Synchronization; Bifurcation analysis

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$$\frac{\partial P}{\partial t} = \frac{\partial}{\partial \theta}\left[K_1 \sin(\theta - \theta' - \beta) + K_2 R^2 \sin^2(\theta - \theta' - \beta)\right] P + D\frac{\partial^2 P}{\partial \theta^2}$$

Dynamic stability of complex systems using Gershgorin disc theorem

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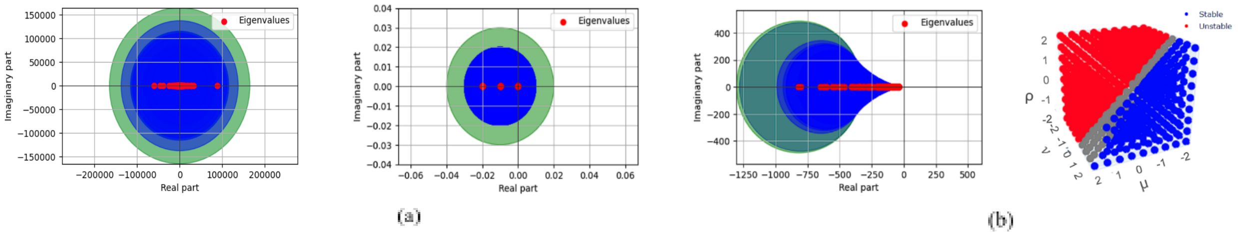
Prediction of the stability of large complex networks ranging from ecological, biological, chemical and mechanical systems to electrical grids and financial markets is a challenging task. In our research work, to determine the stability of complex dynamical networks, we have developed a comprehensive framework that integrates the Dynamical Jacobian Ensemble[1] and the Gershgorin Disc Theorem[2]. We extracted the Jacobian matrices for a complex dynamical network using the Dynamical Jacobian Ensemble[1] approach and corresponding to the ensemble, we generated Gershgorin Discs. As we know from the previous study, the Dynamical Jacobian Ensembles for the various networks are fundamentally different from each other and depend on the dynamics through dynamical exponents η, μ, ν and ρ and on the network topology through the degrees and average nearest neighbour degree as $J_{ii} = -C d_{nn}^{\eta} d_i^{\mu}$ and $J_{ij} = d_i^{\nu} A_{ij} G_{ij} d_j^{\rho}$ which are the diagonal and off-diagonal entries of the Jacobian respectively. These fundamental changes in the Jacobian Ensembles, we can also observe through the Gershgorin Discs as well (Fig.1.a). Further, using the Gershgorin Disc Theorem, we establish a criterion, $S = \beta\eta - \xi\rho + \psi(\mu - \nu)$, that helps to classify the dynamical stability of the system into the regions of stability and instability. We can clearly see these stability regimes in the parameter space (μ, ν and ρ) plotted in 3D (Fig.1.b). Thus, the integration of the Dynamical Jacobian Ensemble with the Gershgorin Disc Theorem presents a novel and effective theoretical method for predicting the stability of complex dynamical systems. This framework not only advances theoretical knowledge but also has practical implications for improving the stability and control of systems across various fields.



(a) (b)

Figure 1: (a) Gershgorin Discs for three stability regimes. (b) Stability regimes: stable (blue), unstable (red), and grey (less effective analysis) in the parameter space of dynamical exponents (μ, ν, ρ).

Keywords: Gershgorin Discs, Dynamical Jacobian Ensemble, Dynamic Stability.

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Spectral and network analysis of the financial markets

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Complex systems are extensively studied through spectral and network properties, which acknowledge many real-world challenges. It has proven successful in offering insights into the structure and dynamics of physical, biological, social, financial, and numerous other natural systems. The complexity of the financial market arises from the interplay among its constituent stocks, resulting in dynamic correlation patterns. These patterns undergo significant changes during critical market events. This work focuses on eigen-entropy and network properties of financial correlation matrices. It is crucial to detect their signatures for timely intervention or prevention. We extract information about market disorder by evaluating the eigenvalue centrality of correlation matrices. Various market events, such as bubbles or crashes, form a phase space that exhibits phase separation. The dynamics of correlation matrices among these phases indicate ordered and disordered movements. We capture the phase separation constructed from the spectral and network analysis. Our methodology would help in understanding and foreseeing tipping points or fluctuation patterns in complex systems. Preliminary findings suggest:

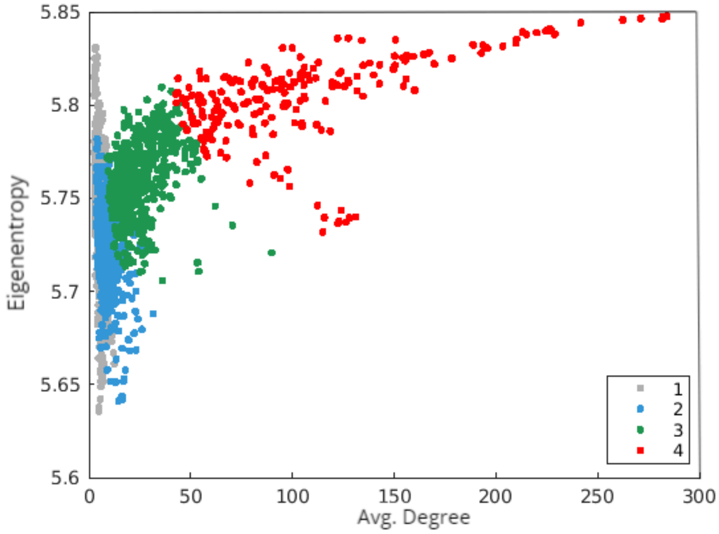

Figure 1: The plot illustrates the phase separation of the S&P 500 market in 4 different phases: Normal (1), Bubble (2), Anomaly (3), and Crash (4) states of the markets. Each event is segregated into different regions of the scatter plot, based on eigenentropy and the average degree of the network.

Keywords: Correlation; Entropy; Clustering; Network analysis.

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Chimeric states induced by higher-order interactions in coupled prey–predator systems

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Higher-order interactions are instrumental in characterizing the intricate com- plex dynamics in a diverse range of large-scale complex systems. Higher-order interactions are responsible for the promotion of a myriad of collective dynamics e.g., synchronization, oscillation death, chimera states and others. Our study investigates the effect of attractive and repulsive higher-order interactions in globally and non-locally coupled prey-predator Rosenzweig–MacArthur systems. We observe the emergence of spatiotemporal chimeric states, while the model system with only pairwise interactions exhibit synchronized oscillations. Our system exhibits a second-order transition from a chimera-like state (mixture of oscillating and steady state nodes) to a chimera-death state through a supercritical Hopf bifurcation. We discuss the origin of these states in detail and also investigate the effect of a higher-order non-local topology on the dynamics of the system. This network structure leads to the rise of a unique dynamical state termed as “amplitude- mediated chimera-like state” (Fig. 1). This state is characterized by randomness in both amplitude and phase among the oscillating nodes, whereas the rest of the nodes show steady state. Our study observes that the introduction of higher-order attractive and repulsive interactions exhibits incoherence and promotes persistence in consumer-resource population dynamics as opposed to the susceptibility shown by synchronized dynamics with only pairwise interactions. Our results should be of interest to conservationists and theoretical ecologists studying the effect of competing interactions in ecological networks.

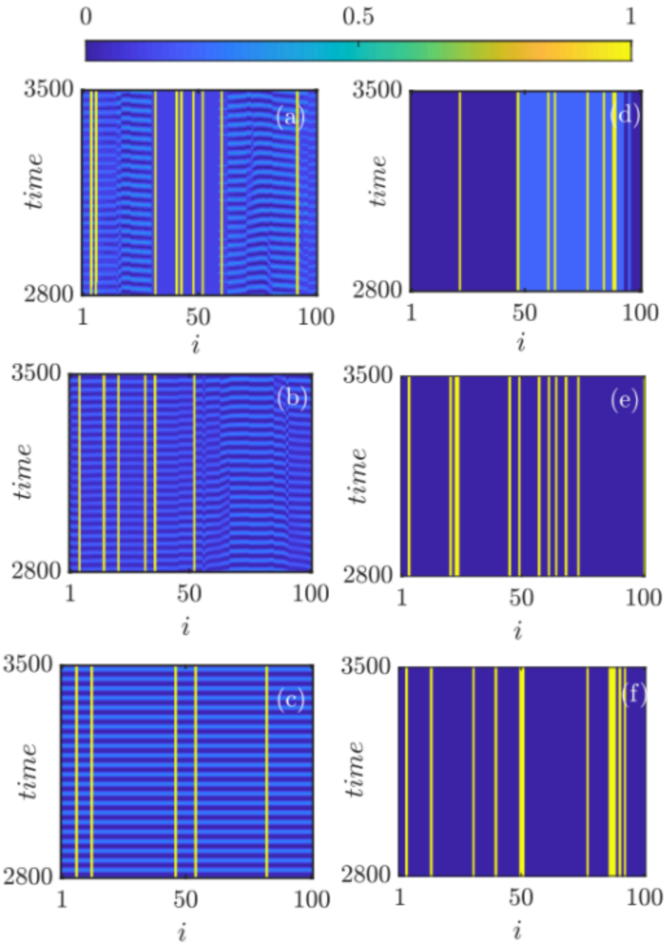

Figure 1: Spatio-temporal plots of nodes i vs time to show chimeric states. Left panel: (a)-(c) Amplitude-mediated chimera-like states under various coupling conditions before oscillation death. Right panel: (b)-(d) Chimera death states at various coupling parameters after oscillation death.

Impact of weight thresholding on the robustness of complex networks to central node attack strategies

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Dense complex networks often lead to time-consuming and cumbersome analyses in real-world applications such as finance, neuroscience, climate science, and transportation systems. Weight thresholding (WT) is a simple method to decrease the number of links in the weighted network. Here, we assess the impact of WT on the robustness of real-world networks against different node attack strategies. We implement two WT methods:

one that removes a fixed fraction of weak links and another that removes a fixed fraction of strong links. This allows us to investigate the role of both strong and weak links in maintaining the robustness of networks under node attack strategies.

The robustness of the thresholded network is measured in terms of the size of the largest connected component (LCC). We find that WT by either weak link removal or strong link removal does not affect the LCC of the network, and the resulting thresholded networks show robust connectivity structures against node attacks. Generally, real-world networks subjected to WT hold a comparable connectivity structure to node attack, even for higher WT values. Therefore, these WT procedures can be used as a method for network sparsification in cases where robustness to node attacks is crucial.

In addition, we analyze the change in the top 30% of central nodes with WT and find that WT by strong link removal may trigger a greater change in node centrality rank than WT by removing weak links. Also, both WT procedures change the efficiency of node attack strategies. Network science research to find important/influential nodes in the network has to consider that simplifying the network with WT methodologies may also change the node importance evaluated by different node centrality indicators in the network.

Keywords: Complex networks; Robustness; Weight thresholding; Node attack strategies.

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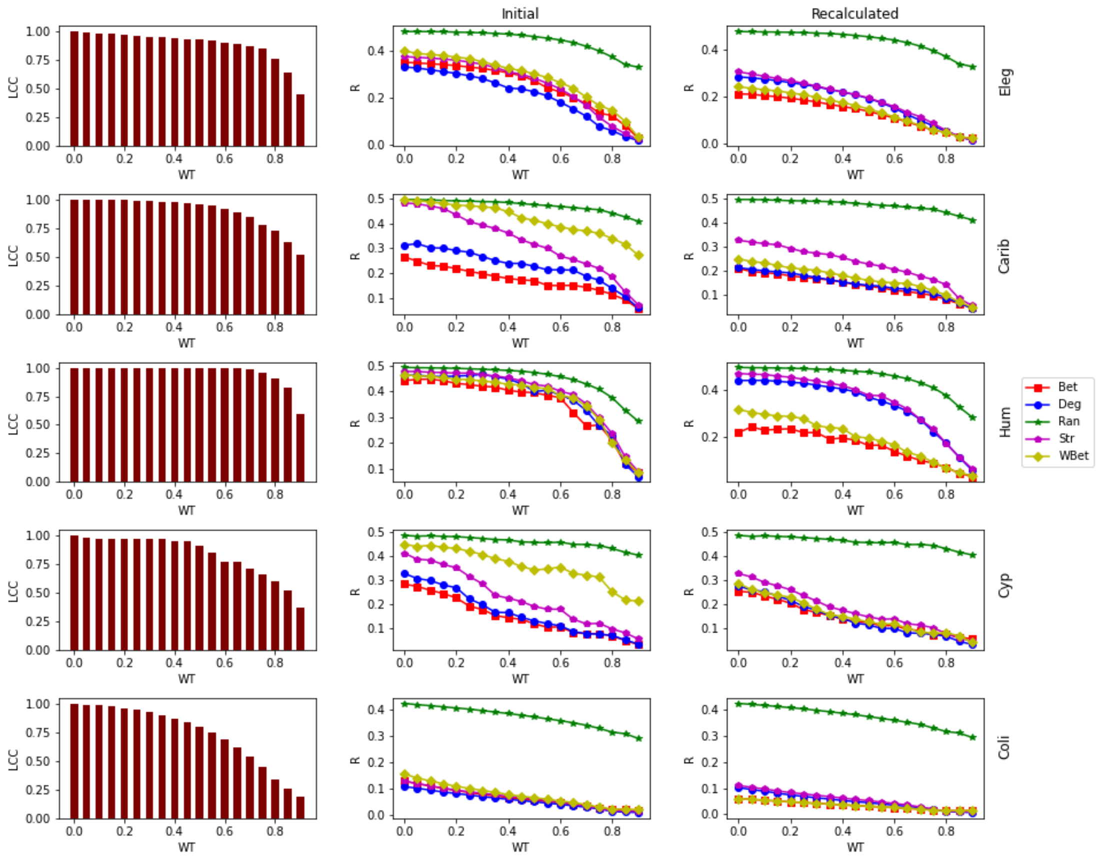

Figure 1. LCC after each weight thresholding (WT by weak link removal) value (left column), robustness (R) of the network under initial (middle column), and recalculated attack strategies (right column) as a function of weight thresholding (WT) value for the networks C. elegans (Eleg), Caribbean(Carib), Human12a (Hum), Cypdry (Cyp), and E.coli (Coli).

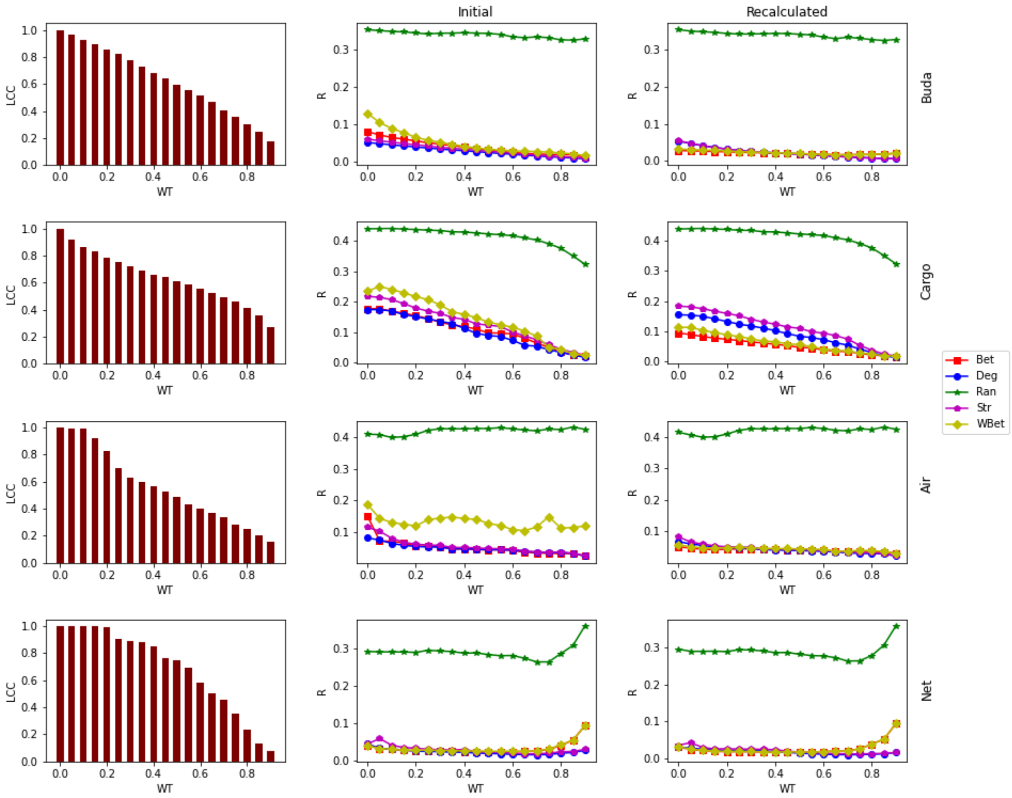

Figure 2. LCC after each weight thresholding (WT by weak link removal) value (left column), robustness (R) of the network under initial (middle column), and recalculated attack (right column) strategies as a function of weight thresholding (WT) value for the networks Budapest (Buda), Cargoship (Cargo), US Airports (Air), and Netscience (Net).

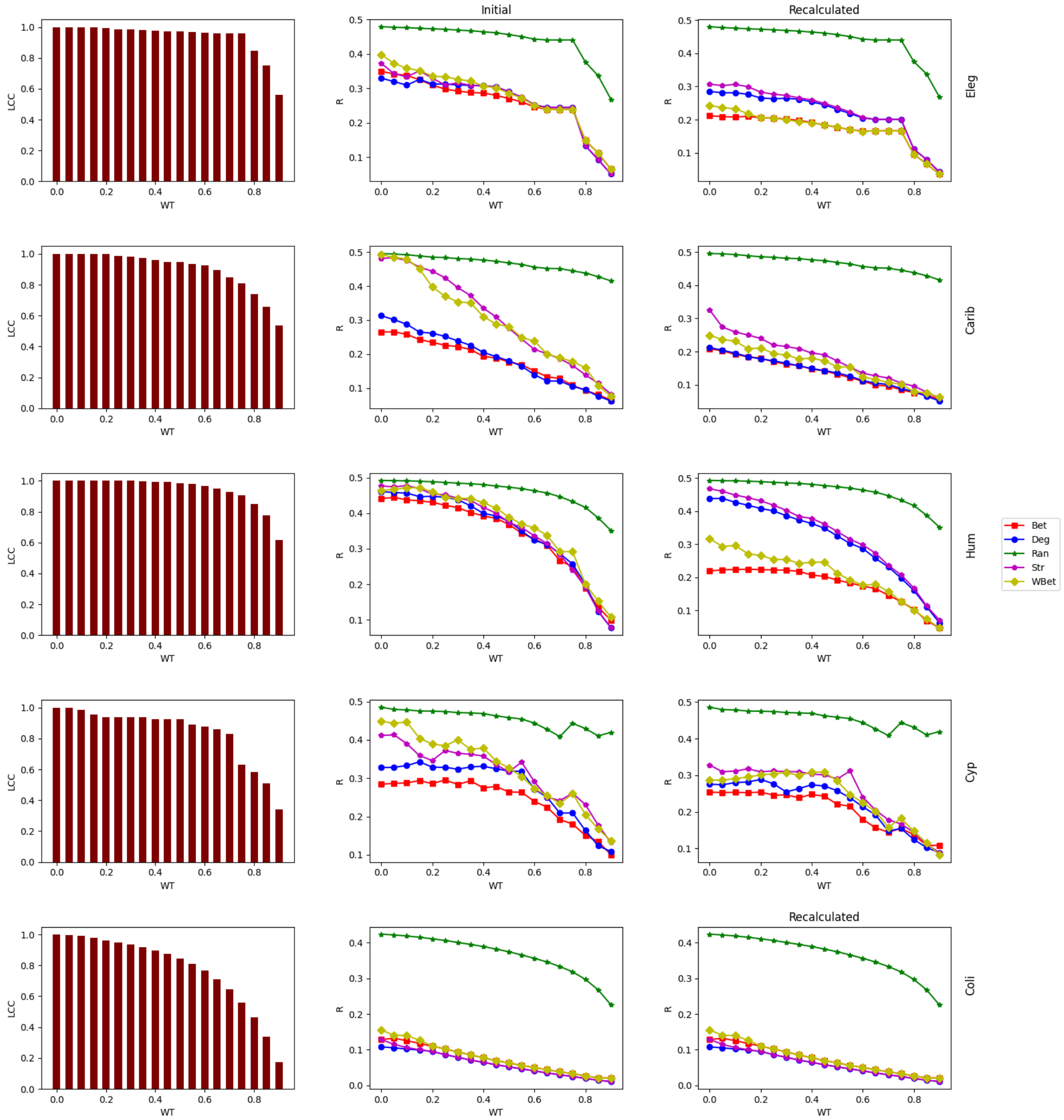

Figure 3. The LCC after each weight thresholding (WT by strong link removal) value (left column), the robustness (R) of the network under the initial (middle column), and the recalculated attack strategies (right column) as a function of the weight thresholding (WT) value for the networks C. Elegans (Eleg), Caribbean (Carib), Human12a (Hum), Cypdry (Cyp), and E. Coli (Coli).

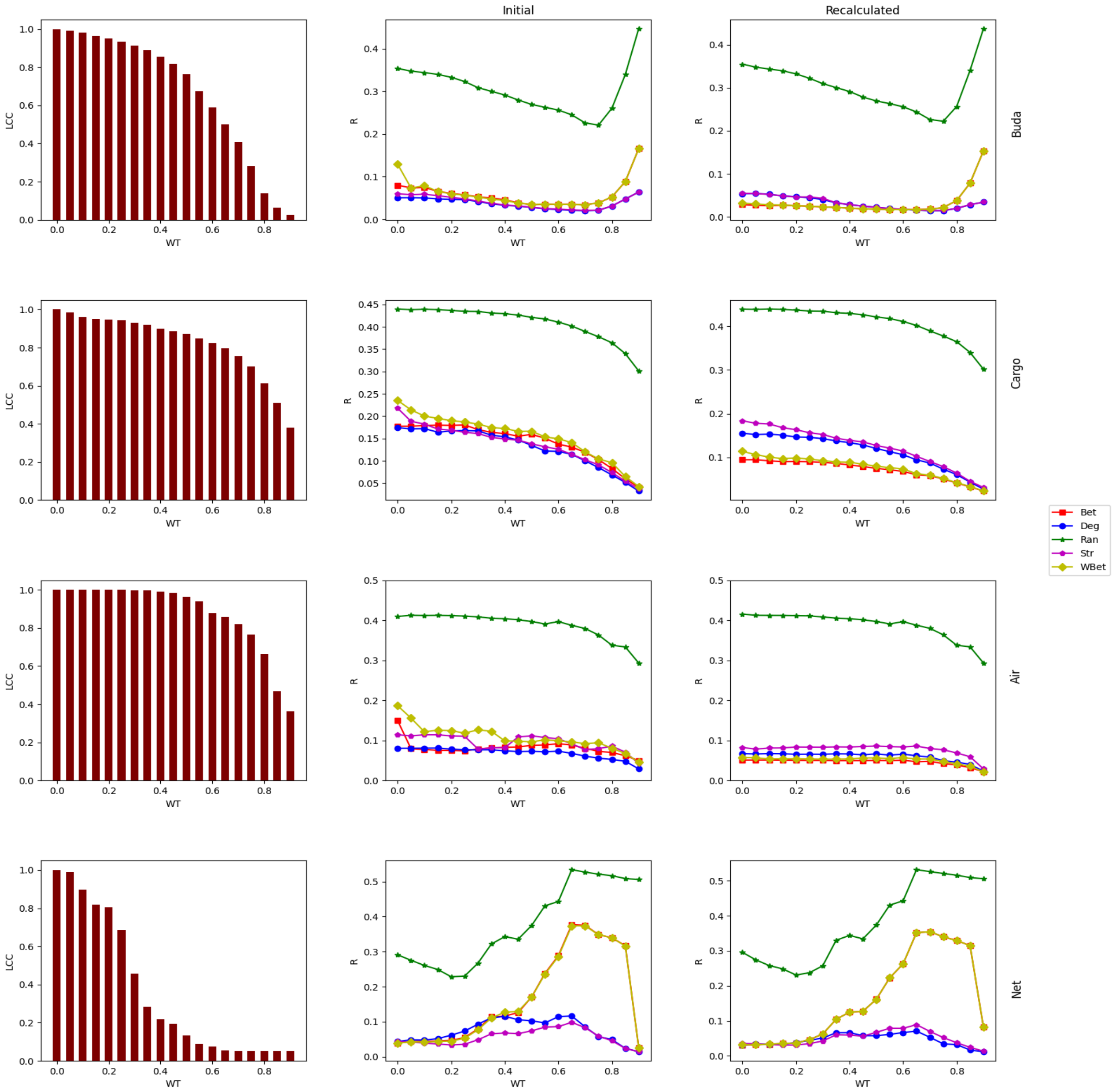

Figure 4. The LCC after each weight thresholding (WT by strong link removal) value (left column), the robustness (R) of the network under the initial (middle column), and the recalculated attack (right column) strategies as a function of the weight thresholding (WT) value for the networks Budapest (Buda), Cargoship (Cargo), US airports (Air), and Netscience (Net).

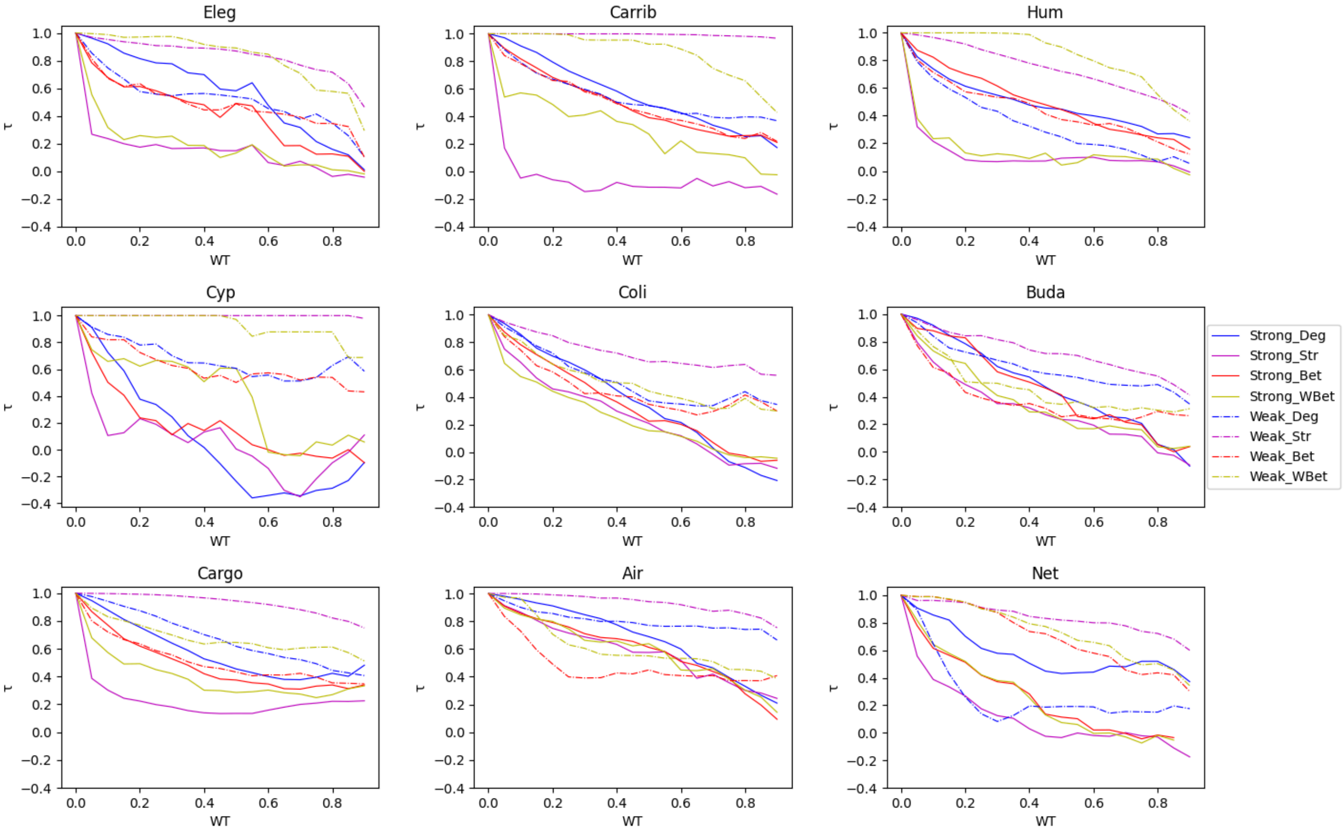

Figure 5. Kendall's tau coefficient (τ) for centrality measures Deg, Str, Bet, and WBet. Correlation is measured between the initial network's node rank and the network's node rank after WT. We compute τ using the top 30% of nodes of the network. Solid lines indicate τ for WT with strong link removal; dashed lines indicate τ for WT with weak link removal.

Synchronization in adaptive higher-order networks

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Many natural and man-made complex systems feature group interactions that adapt over time in response to their dynamic states. However, most of the existing adaptive network models fall short of capturing these group dynamics, as they focus solely on pairwise interactions. In this study, we employ adaptive higher- order networks to represent these systems by proposing a general framework incorporating both adaptivity and group interactions. We demonstrate that complete synchronization can exist as an invariant solution within these complex structures and provide the necessary conditions for the emergence of a stable synchronous state. Additionally, in certain pertinent cases, this necessary condition resembles the master stability function approach by separating the dynamical and structural properties. We illustrate our theoretical findings through examples involving adaptive higher-order networks of coupled generalized Kuramoto oscillators with delay. We also show that the interplay of group interactions and adaptive connectivity results in the formation of stability regions, which can induce transitions between synchronization and desynchronization.

Deep Learning based Link Prediction for Minimizing Maximum Betweenness of Networks

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Centrality measure is a tool to identify key nodes/links in networks having higher importance/control/load than other nodes and links [5]. Betweenness centrality determines how frequently a node in the network is on the shortest path between all other pairs of nodes. It is typically used in node ranking to locate the nodes with maximum control of information flow or nodes heavily loaded due to information flow happening through shortest paths [5]. The highest value of betweenness centrality observed among all the nodes in a given network is termed as *maximum betweenness* of the network. It signifies the maximum load or traffic in a network, which can be a notion of the required amount of maintenance and resources for the proper functioning of the network. One of the possible ways to reduce the load on nodes is by diverting traffic through new pathways created by adding missing links. Therefore, we consider the problem of finding a missing link in a network, adding which minimizes the maximum betweenness of the network. Identifying such a link deterministically in a network turns out to be computationally expensive due to several rounds of betweenness score computation.

In this work, we propose a graph neural network (GNN) [3] based approach with rank loss [4] that attempts to predict a missing link in a network, adding which can maximally reduce the maximum betweenness of the network. To construct our dataset, we introduce the missing links one at a time into the network and compute the difference between the maximum betweenness of the altered network and the original network. A positive difference suggests that the missing link can potentially reduce the maximum betweenness of that network, and we label such links as 1. Otherwise, if the difference is zero or negative, the link is labeled as 0. This difference is also used to rank all missing links.

The proposed model is shown in Figure 1. We begin by generating node features derived from different centrality scores of nodes. These features are provided as input into a graph neural network (GNN) to produce initial node embeddings. For each missing link, an edge embedding is created by concatenating the embeddings of the corresponding nodes. Two distinct multi-layer perceptron (MLP) neural networks subsequently process these edge embeddings. The first MLP predicts the classification label of the links, while the second

MLP assigns a score for ranking the missing links. This score is further utilized in computing the triplet margin loss adapted from [6]. The entire neural network architecture is being trained end-to-end using the Adam optimizer, optimizing a combined loss function using an unweighted summation that incorporates classification and ranking objectives.

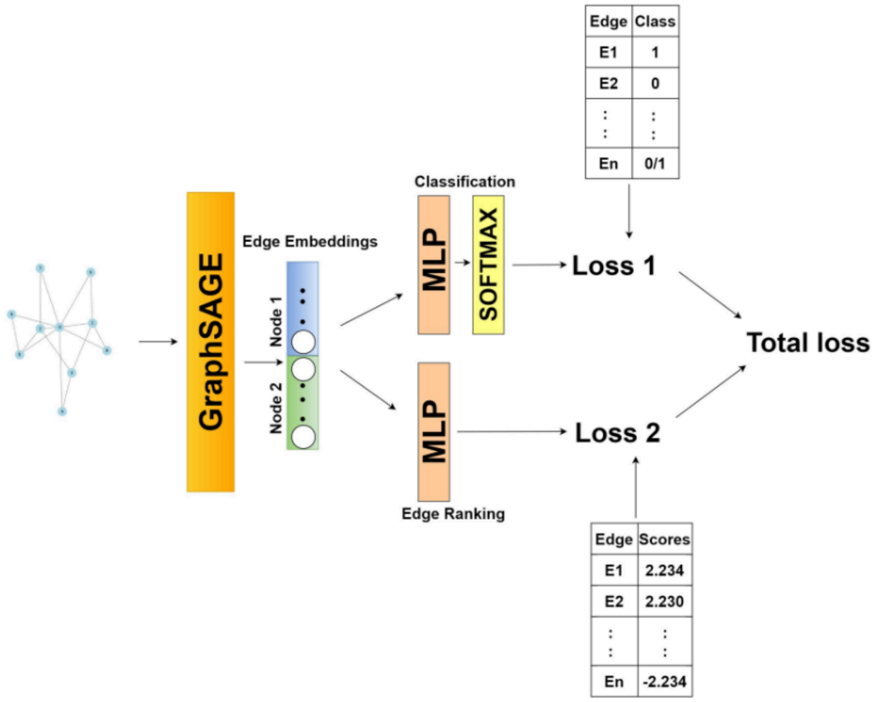

Figure 1: Workflow of the proposed model.

Experiments are conducted on various synthetic networks (Barabasi-Albert [1] and Erdos-Renyi [2]) with different diameters. The learning of the proposed model is observed better on Barabasi-Albert networks compared to Erdos-Renyi networks. For Barabasi-Albert networks, Our model achieved a mean average precision(mAP) of 0.74 in the top-10 and 0.88 in the top-100 missing links, which highlights the efficiency of the proposed model in predicting the best links.

Keywords: Graph Neural Network, Betweenness Centrality, Link Prediction.

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Heterogeneity induced control of chaotic systems

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We explore the behaviour of coupled chaotic oscillators where one unit has intrinsically dissimilar dynamics. Our main findings are as follows: First, we find that the presence of a single dissimilar chaotic system in the network manages to drive all the chaotic oscillators to regular limit cycles. Additionally, the regular cycles that emerge are significantly smaller in size than the uncoupled chaotic attractors. Counterintuitively, the more geometrically dissimilar the single distinct system is from the other chaotic oscillators, the stronger is the emergent control [1]. So surprisingly, enhanced heterogeneity in coupled systems leads to more pronounced and robust controllability.

We further explore this idea by considering a diverse set of network topologies, to determine the effect of position of dissimilar node [2]. The key property is determined to be the sum of the path lengths between the dissimilar node and all the other nodes (or its maximum, if coupled to unconnected networks), denoted by L_d. We find that there exists a linear relation between this quantity and the critical coupling strength for the onset of a spatiotemporal fixed point. This holds true for a chain with the dissimilar node at different locations, a ring and complete network with one embedded dissimilar node, as well as star networks with a dissimilar hub or dissimilar peripheral node. Furthermore, we show that networks with high average degree and high clustering coefficient are more resilient to the influence of an external dissimilar system. These findings will potentially aid in the design of optimally placed dissimilar nodes for controlling chaos in complex networks.

Keywords: Chaotic oscillators; Chaos control

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Identification of Depression Markers in the resting state by Functional Brain Networks

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Depression, clinically termed major depressive disorder (MDD), is a pervasive mental health condition affecting over 264 million individuals globally (**WHO, 2020**). It manifests through persistent sadness, loss of interest in activities, changes in appetite and sleep, fatigue, and difficulty concentrating, significantly impairing daily

functioning (**American Psychiatric Association, 2013**). Depression symptom severity is a key predictor of short-term risk for hospital encounters. We intend to highlight the importance of considering multiple aspects of severity in clinical assessment and treatment of MDD, as well as the potential of brain functional connectivity patterns as biomarkers for depression severity. This work explores network theory approaches to address dynamic network connectivity as a significant biomarker for early detection and prediction of depression.

Electroencephalography (EEG) is a critical tool in the study of Major Depressive Disorder (MDD), providing real-time, non-invasive monitoring of brain activity with high temporal precision. Studies have revealed resting state eeg data to be more suitable for predicting depression than task based data (**Kaushik et. al., 2023**) . In this study, we conducted a detailed analysis of 128 channel resting state EEG data, to identify significant brain channels involved in depressive states (**Cai., et. al., 2022**). We performed spectral and complexity measures to identify channels with significant differences between MDD and normal controls. The figures shown below demonstrate the difference in power spectral density (PSD) and Higuchi fractal dimension (HFD), respectively, for each channel among MDD and Normal subjects. Notably, channels exhibiting statistically significant differences in their PSD values, suggests that left frontal lobe is more active than central or right lobe in individuals with MDD. Further to understand the underlying network and dynamics at these sensor locations, we employed the visibility graph approach to generate visibility graphs (**Lacasa et. al., 2008**). We have performed an advanced topological characterization of brain activity in these significant channels by quantifying levels of connector hubs and non-hubs (**Guimera and Amaral, 2005**). The within-module and between module connectivity provides deeper insights into the differential brain activity associated with depressive states. By integrating these insights, our research contributes to a more deeper view of the topological changes in brain activity related to depressive states, potentially guiding future interventions and therapeutic strategies.

Keywords: Major Depressive Disorder (MDD) ; visibility graph approach; Connector hubs; Dynamic network attributes.

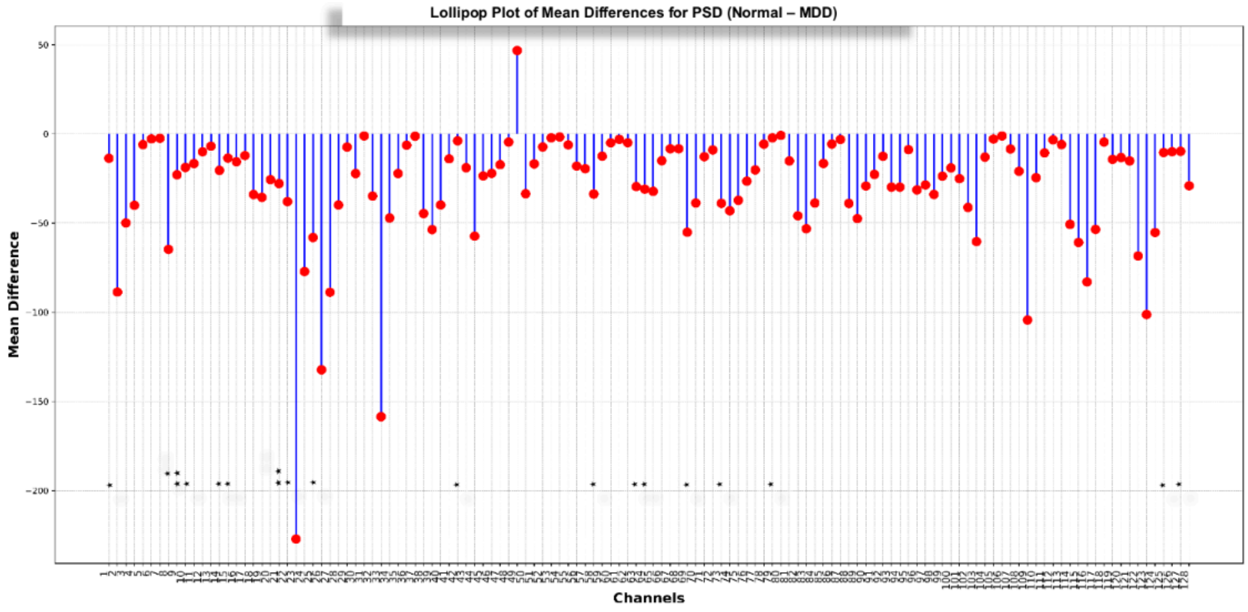

Fig8 : Lollipop plot illustrating the mean difference of PSD values between MDD and normal condition, with significant channels at 1, 8, 9, 10, 14, 15, 21, 22, 42, 58,63, 64, 69, 79, 125, 128, while 9, 21 being the most significant.

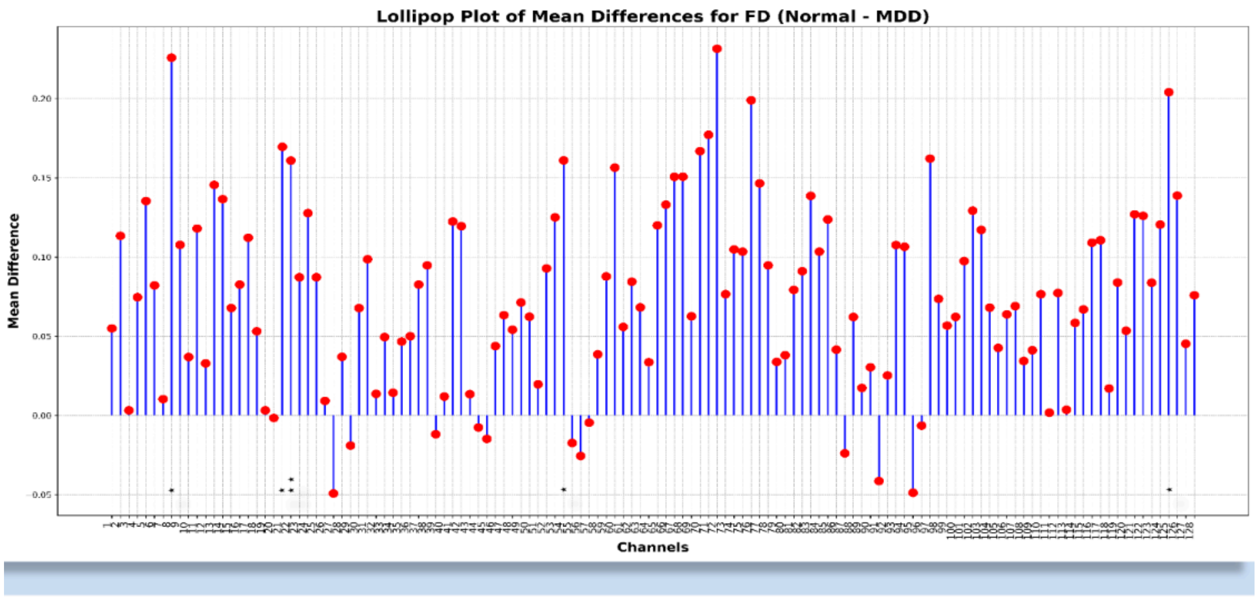

Fig7 : Lollipop plot illustrating the mean difference of FD values between MDD and normal condition, with significant channels at 8, 21, 22, 54, 125, while 22 being the most significant.

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Ethics In Rotten Apples: A Network Epidemiology Approach For Active Cyber Defense

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The widespread use of Internet of Things (IoT) devices has led to increased connectivity, raising concerns about cybersecurity, particularly regarding malware infections. While researchers have explored methods for detecting malicious “black worms”, some have suggested active defense mechanisms like the concept of “white worms” that self-propagate to patch vulnerable systems. However, ethical and legal considerations surrounding such interventions remain debatable. In this paper we examine the implications of integrating ethical elements into white worms, focusing on their effectiveness rather than on their ethical or legal dimensions. We use network epidemiology tools to model the simultaneous spread of black and white worms in IoT networks. We investigate the impact of varying ethical parameters and network topologies on the dynamics of worm propagation.

Our model examines the spread of two worms within a network of vulnerable devices: a malicious black worm (B) and a benign white worm (W). The black worm spreads at a rate of β_B, while the white worm, which aims to secure devices, spreads at β_W. The white worm is designed to be ethical; it notifies the device owner of the breach and then enters a dormant state (D) without using resources. Owners may patch their systems at a rate of γ, after which the white worm erases itself. If the user doesn't act, the white worm may exit dormancy at a rate of ϵ and become active (W), propagating to other devices at a rate of μ.

Our findings suggest that ethical constraints may hinder not only the efficacy of white worms in preventing large-scale botnet formation but also their ability to protect the entire system. Additionally, we identify the importance of network structure in shaping the effectiveness of white worm deployment strategies. The results indicate that while white worms hold promise as a countermeasure against black worms, their deployment requires careful consideration of the tradeoff between being ethical and practical.

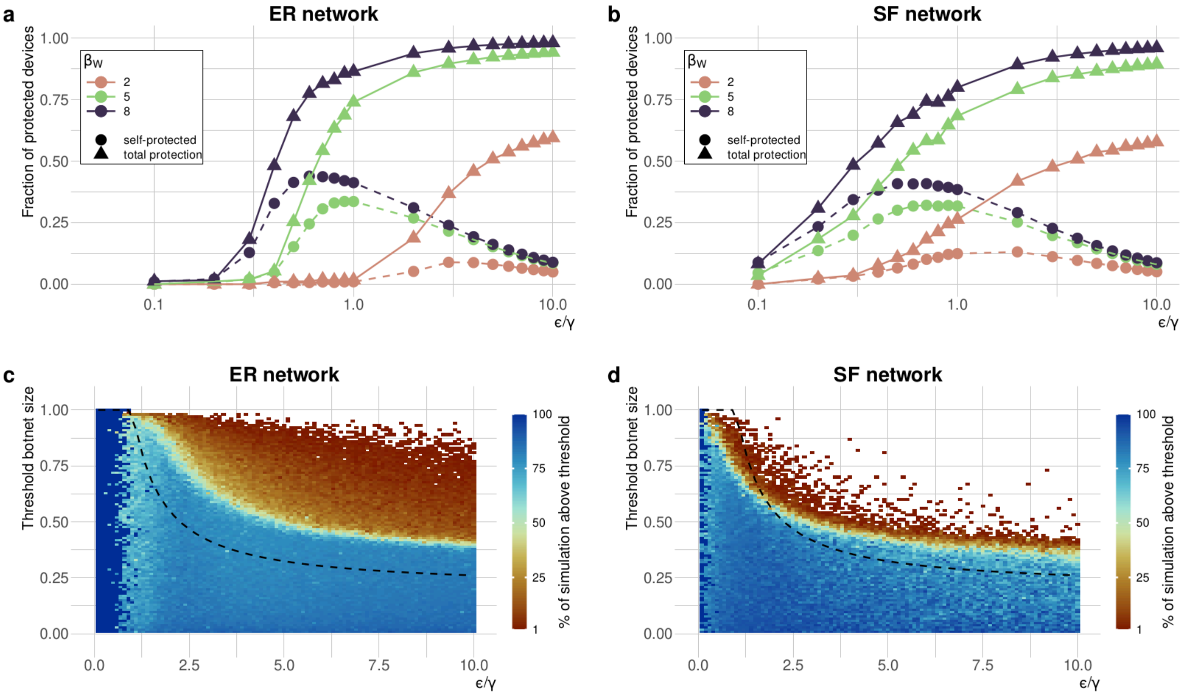

Fig 2: ***Impact of Network Topology on Worm Dynamics and Protection*** *- The figure illustrates the dynamics of worm propagation and device protection under different network topologies. The first row shows the fraction of protected devices as a function of worm roughness,* $\epsilon' = \epsilon/\gamma$*, with* β_W *varied and* β_B *fixed at 1. Triangles indicate the total fraction of protected devices (by owner updates or forced by the worm), while circles show the fraction protected by owner updates alone. In panel (a), the ER network exhibits behavior similar to the homogeneous case, while panel (b) shows that in the SF network, the white worm spreads more easily at low roughness, though its overall reach is limited. The second row highlights the percentage of simulation time where the botnet size exceeds a certain threshold. Panel (c) demonstrates that in the ER network, botnet presence is significantly reduced, with only a narrow range of roughness values below 1 maintaining a botnet throughout the simulation. In panel (d), the SF network shows that only as* ϵ' *approaches 0 does the botnet cover the entire system for the entire simulation. These results emphasize the influence of network topology on the efficacy of white worm deployment and botnet containment.*

Keywords: Cybersecurity; Internet of Things (IoT); Network Epidemiology; Ethical Constraints.

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Rich club prominence as a novel early biomarker of cognitive decline

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Dementia is poised to become a global health crisis. A significant contributor to the failure of therapeutic treatments is that diagnosis can only be reliably established late in the course of the disease, when neuronal loss and neurosynaptic degeneration have taken hold, and years after irreversible damage to the brain has occurred. This calls for novel biomarkers that are sensitive for dementia development before its clinical symptoms start to manifest. Patients with a history of transient ischemic attack (TIA) have a higher risk of post-stroke dementia, and are thus a suitable cohort to study preclinical dementia.

It has been shown that the rich club organization of the brain – densely interconnected hub nodes thought to be central to the brain's information processing capabilities – is disrupted in established dementia [1]. Yet, little is known about the process of the degradation of the rich club, and specifically the timing of these network changes in relation to clinically detectable manifestations of cognitive decline. Therefore, rich club analyses have the potential to provide promising biomarkers of preclinical dementia and aid our understanding of the microstructural mechanisms that underlie late life dementia development.

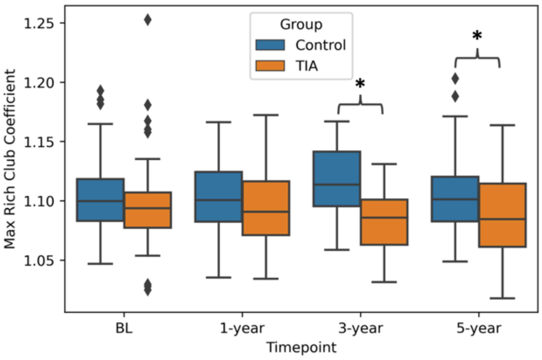

*Fig. SEQ Figure * ARABIC 1: Boxplots of the maximum normalized rich club coefficient (Φmax) for TIA patients and controls over time.*

In this study, we examine the rich club organization of TIA patients by looking at the prominence of the rich club effect in these patients at various timepoints, along with measures of cognition. Patients with TIA and non-TIA controls underwent DTI imaging at baseline, 1-year, 3-year, and 5-year post TIA or recruitment [2]. Whole-brain tractography utilizing constrained spherical deconvolution (CSD) was performed to construct connectomes at all available timepoints. The maximum normalized rich club coefficient (Φ_{max}) was used as an indicator of the prominence of the rich club effect for each individual. The prominence of the rich club was not significantly different between TIA patients and non-TIA controls at baseline or 1-year follow-up ($p > 0.05$). However, TIA patients showed a significantly less prominent rich club effect at 3-years and 5-years compared to controls ($p = 0.048$ and 0.017, respectively). TIA patients exhibited a significantly higher decrease in rich club prominence over time, relative to controls ($p=0.014$). Importantly, these network level effects are observable before any differences in cognitive performance can be identified. The decrease in rich club prominence seen in TIA patients relative to controls may be a novel biomarker for future cognitive decline. This potential biomarker might play an important role in early detection of dementia, and patient selection for future vascular risk reduction trials or trials of novel dementia therapeutics.

Keywords: Network neuroscience; Cognitive decline; Rich club; TIA.

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Functional hyper-graphs of stock markets

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In stock markets nonlinear inter-dependencies between various companies result in nontrivial time-varying patterns. The interdependence of various companies in a stock market affects the overall dynamics of the market. A network representation of these inter-dependencies has successfully analysed the evolution of stock prices and events. However, these studies have revolved around the assumption that correlations are pair- wise. Whereas, in a system as intricate as the stock market, the interactions need not be limited to pairwise. Here, we present a methodology to construct higher-order inter- action hyper-graphs from stock market data. Here, we introduce a general methodology using information-theoretic tools to construct a higher-order representation of the stock market data, which we call *functional hyper-graphs*. This framework enables us to examine the stock market events by analyzing the functional hypergraph quantities: Formann-Ricci curvature and Von Neumann entropy. We compare the corresponding quantities of networks and hyper-graphs to understand the applicability of functional hyper-graphs in stock markets further. We find that the pairwise network structure is more robust in comparison to hypergraphs.

Keywords: *functional hyper-graphs*, *Stock markets*, *Complex systems*

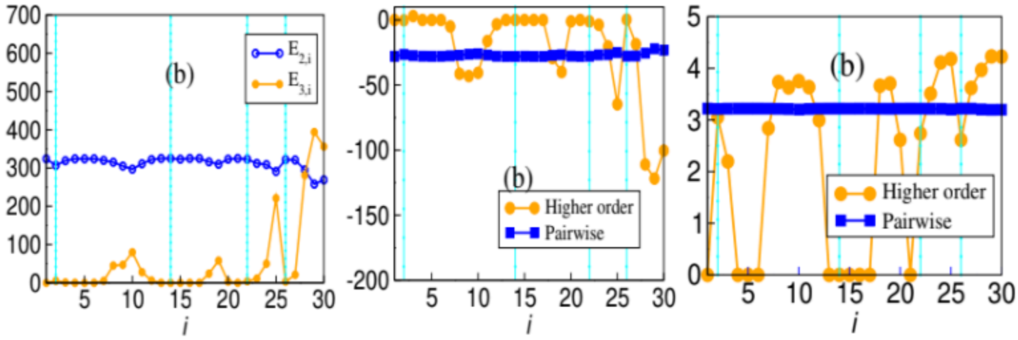

Figure 1: (a) Number of pair-wise $E_{2,i}$ (blue open circles), and hyperedges $E_{3,i}$ (orange solid circles) as a function of window index i for DAX. (b) Pairwise Formann-Ricci curvature (blue open circles), and higher order Formann-Ricci curvature (orange solid circles) as a function of window index i for DAX (c) (b) Pairwise Von Neumann entropy (blue open circles), and higher order Von Neumann entropy (orange solid circles) as a function of window index i for DAX. Vertical lines mark the windows with large volatility. Hyperedges have more variability than the pairwise edges and they are less robust than pairwise networks.

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Continuous Time Quantum Walks on Complex Network Topologies

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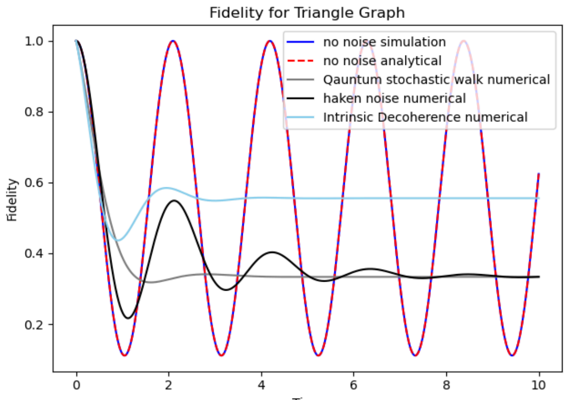
We study the stability of continuous time quantum walks(CTQWs) on complex network topologies like scale-free, Erdos-renyi and small world networks. Quantum walks are quantum analog for classical random walks. Our work focuses on analyzing metrics such as fidelity of initial and evolved states, inverse participation ratio and von neumann entropy. We also study the density matrix visualization to get a better understanding of populations in each node and quantum coherences. We present a comprehensive study of how different network topologies influence the behavior of CTQWs through simulation results. Our findings reveal the variations in quantum walk dynamics across different network topologies and provide insights into the impact of network topologies on stability of quantum walks. Through detailed simulations and comparisons, we aim to get a better understanding of the stability of quantum networks, which can impact both theoretical research and practical applications in quantum computing and network analysis.



Keywords: Fidelity; Inverse Participation Ratio; Von Neumann Entropy; Coherence

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Fairness-aware Analysis of Centrality Measures in Social Networks

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Analyzing a network derived based on a social system helps us understand the basis on which the relationships have been formed, detect the structure of relationships, and how individual nodes are affecting the whole social system. Social networks consist of nodes and edges, where nodes are individuals and edges depict the relationships among the nodes. Nodes in social networks can be further divided into communities based on common factors such as religion, gender, ethnicity, ideology, etc. Further, these communities are treated as majority and minority based on their size, occupation, and other social stigma. Due to their smaller size, the nodes of minority communities are generally overshadowed by nodes of the majority community and remain deprived of job opportunities, beneficial schemes, ideas, education, etc., due to relatively less exposure and connections than their counterparts nodes of the majority community. One of the primary reasons for this disparity is the absence of a fairness notion in policies implemented for the social systems when it comes to providing opportunities or resources. Similarly, it also becomes essential to design policies for spreading awareness related to beneficial schemes, etc., while keeping fairness in check so that the disparities in the context of exposure to spreading information can be reduced significantly.

The prominent nodes in social networks have been observed to get exposed to information about opportunities and schemes early and play an essential role in spreading such information by acting as seed nodes. Centrality measures are a tool to identify these prominent nodes by assigning higher ranks to them[6, 5]. Centrality measures are classified into local, global, and modular. Each category of centrality measures gives us different aspects of node’s connections in the network and rank nodes differently. Some centrality measures may assign a higher ranking to very few nodes or none of the minority communities. In this work, we investigate the fairness capacity of various centrality measures for information spread. The motivation is to identify those measures which, when used for selecting seed nodes for information spread, expose an equal fraction of nodes in the minority and majority communities, i.e., the fraction of nodes getting exposed to information in majority and minority communities should have low parity.

We use a network generation model given in [2] to generate synthetic networks with majority and minority nodes while tuning the homophily parameter to vary the network structure. We implement an influence propagation model motivated from [3] to estimate the amount of spread of information in both communities of considered networks when the seed nodes are chosen as per the top-ranking nodes according to the considered centrality measures. We used a standard metric to determine the statistical parity difference [1, 4] between these centrality rankings and identify specific ones that are unbiased and more fair than their counterparts for different values of homophily.

Figure 1 summarizes the results. We observed that for different values of homophily, different rankings are more fair compared to other centrality rankings.

Keywords: Social Networks, Minority nodes, Majority nodes, Centrality Mea- sures, Information Diffusion, ICM model, Local Centrality Rankings, Global Centrality Rankings, Modular Centrality Rankings, SPD.

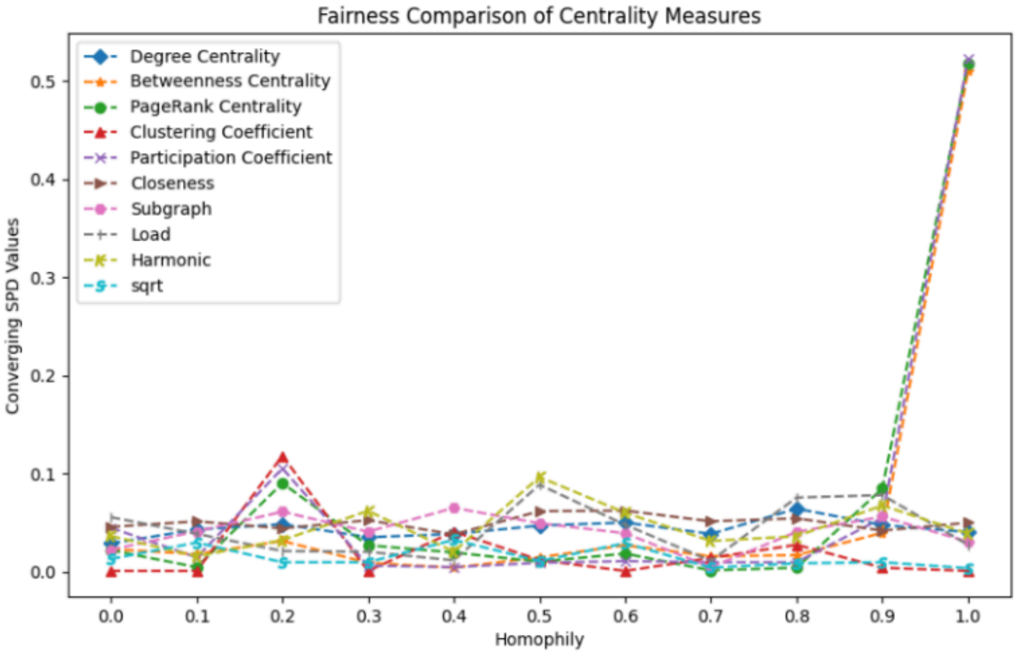

Figure 1: Fairness-aware comparative analysis of centrality measures. The results show that for the network to be extreme heterophily or extreme homophily, the Clustering Coefficient outperforms other centrality measures; similarly, for the homophily parameter tuned between 0.4 to 0.8, Betweenness Centrality, Page Rank Centrality outperforms others considering fairness as a constraint. For the homophily parameter to be 0.5, the Participation Coefficient is more fair than others.

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Spatiotemporal Dynamics and Bifurcation Analysis On Network And Non-Network Environments Of Dangerous Prey And Predator Model

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Within ecological systems, predators frequently come into contact with deadly or toxic prey, placing their own lives in jeopardy as a result of this interaction. The goal of predators is to maximize the likelihood of successful reproduction while simultaneously reducing the risks they face. In this work, a two-dimensional predator-prey model is presented considering the impact of predators interacting with one another. The model also takes into account the losses that are incurred as a result of coming into contact with poisonous prey as well as the negative impact that fear has on the reproduction of prey. The model displays a number of different types of bifurcations, such as transcritical, saddle-node, Hopf, Bogdanov-Takens, cusp, Bautin, and homoclinic bifurcations. Additionally, the model demonstrates multistability. The critical parameters may result in the extinction of predators if encounters with risky prey cause them to suffer excessive losses. It sheds light on the fragile balance that predators must maintain in order to flourish. In this study, the spatial patterns are investigated in both network and non-network contexts. More specifically, a comparison is made between the generation of Turing patterns in network models with continuous media and various network topologies. These patterns are influenced by the combination of predator loss, diffusion coefficients, and network topologies. The effect of critical parameters leads to the gradual development of a variety of patterns, such as spots and stripes. The simulation illustrates how the distribution of node density and the amount of time it takes for patterns to stabilise are affected by a number of different network topologies, including Watts-Strogatz (WS), Barabási-Albert (BA), and LA (Lattice) networks. The intricate dynamics of interactions between predators and prey in ecological systems could be better understood as a result of these discoveries, which bring critical new understandings.

Key words: Prey Predator model, Bifurcation analysis, Network environment, Turing pattern

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Gene expression noise due to phase separation of transcription factors

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Phase separation of proteins and RNA into dense protein rich phases, known as biomolecular condensates, has emerged as a means to spatially organize the intracellular environment. Transcription factors have also been shown to phase separate which could regulate the dynamics of gene expression. Hence, there is a need to study the role of phase separation of transcription factors on transcriptional bursting and the resultant noise in gene expression. Here, we used computational models to study the role of phase separation of transcription factors on reaction kinetics for transcription. Phase separation of proteins (transcription factors) results in different density, material and transport properties depending on the approach to the critical temperatures. We used coarse-grained models of transcription factors to generate percolated two-phase systems of dense and dilute transcription factors. Then, we used kinetic Monte Carlo simulations to study reaction kinetics of transcription as a function of the approach to critical temperatures. Taken together, our work helps to draw mechanistic insights into how phase separation and percolation of transcription factors affect gene expression noise.

Keywords: Gene expression noise; Transcription bursting; Phase separation; Biomolecular condensates

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Fairness Metrics for Community Detection Methods in Social Networks

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In social networks, the nodes are organized into communities. As per the definition proposed by Barabási in his book, “In network science, we call a community a group of nodes that have a higher likelihood of connecting to each other than to nodes from other communities” [1]. The understanding of community structure has played an essential role in understanding the network evolution as nodes join communities, and these communities are further connected with each other to form a large-scale complex network. In real-world networks, nodes are often organized into communities based on ethnicity, gender, race, or wealth, which leads to structural biases and inequalities. If these inequalities are not considered while designing SNA algorithms, they frequently lead to a biased outcome, especially for minorities [4]. For e.g., community detection methods use network structure and nodes’ attributes to identify communities in a given network. If these methods overlook structural inequalities, they cannot efficiently identify small size groups [3], that might further impact the fairness of other SNA methods. Therefore, it is crucial to consider structural inequalities while designing SNA methods to ensure fairness and mitigate bias for or against all users and groups, irrespective of their size or type.
Ghasemian et al. [3] compared 16 community detection methods and showed that the number of identified communities varies a lot across different methods. The authors did not study the impact of different community detection methods on different types of nodes or communities having varying sizes and densities. In the community detection domain, many metrics exist to compute the quality of identified communities; however, there is no metric to quantify the fairness of a method if it is biased towards minorities. Fairness is not yet well defined and studied for community detection (CD) methods, given that it has a vast literature [2].

In our work, we propose fairness metrics for community detection methods and then perform a comparative analysis of existing community detection methods using the performance-fairness trade-off. The community detection methods are classified into the following six classes: (i) Modularity Optimization, (ii) Label Propagation, (iii) Spectral Characteristics, (iv) Dynamical methods, (v) Representation Learning, and (vi) Miscellaneous. We observe that the fairness of different community detection methods is consistent for different metrics. However, it is not the case that a specific class of methods always performs better. The performance-fairness trade-off is highly dependent on particular methods, and some of the best- performing methods having high NMI (Normalized Mutual Information) and fair- ness are FairWalk, Node2Vec, Fluid, Infomap, Walktrap, RSC-V, RSC-K, Significance, CPM, and RSC-SSE, as shown in Figure 1.

To the best of our knowledge, this is the first work of its kind. In this talk, we will discuss the proposed fairness metrics for community detection, their characteristics, and suitability, followed by the fairness results of different types of community detection methods on real-world and synthetic networks that have minorities and majorities. The talk will be concluded with various open research questions in this direction.

Keywords: Community Detection, Fairness, Social Network Analysis

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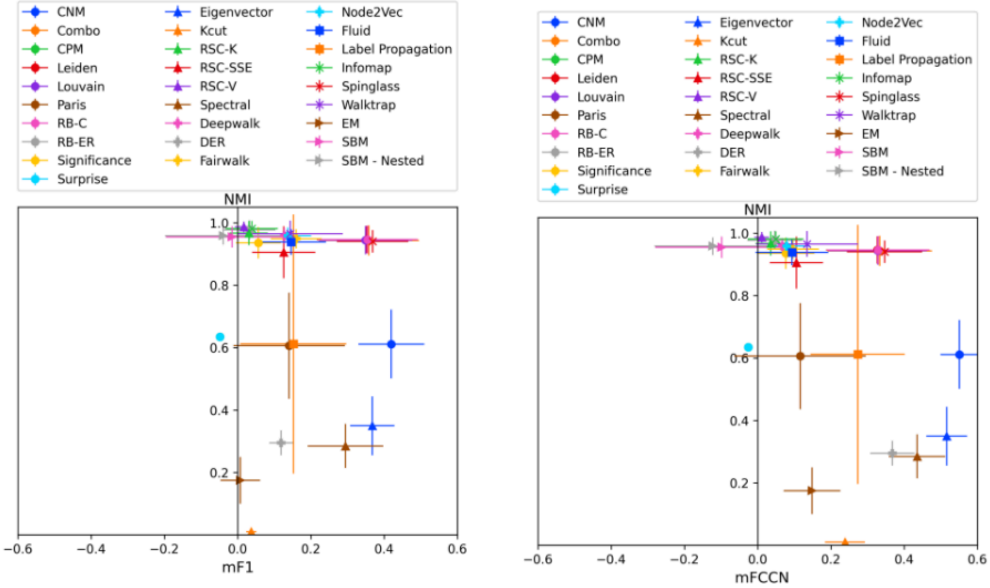
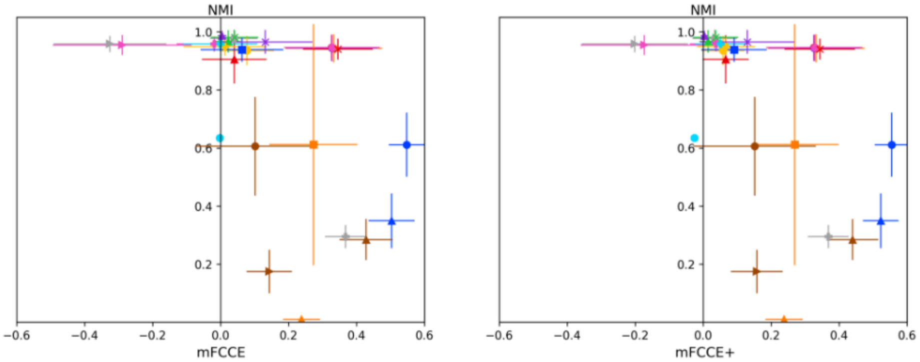


(a) mF1

(b) mFCCN



(c) mFCCE

(d) mFCCE+

Figure 1: Performance vs. Fairness trade-off analysis of various community detection methods on LFR networks of 1000 nodes, tau1 = 2, tau2 = 2.5, average degree = 20, Maximum degree = 100, and minimum community size = 20. Performance is measured using NMI, and fairness is measured using the four proposed metrics: (a) mF1, (b) mFCCN, (c) mFCCE, and (4) mFCCE+.

Evaluating Sparsification Algorithms for Gene Regulatory Networks: Effective Resistance, Random, K-Neighbor, and Forest Fire Approaches

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Gene regulatory networks (GRNs) are a critical area of systems biology re- search, providing insights into fundamental biological mechanisms underlying disease emergence, progression, development, and evolutionary processes. GRNs derived from complex organisms can be extensive, presenting significant challenges for researchers in terms of efficient computation and data management. These challenges can be mitigated by identifying sparsification algorithms that reduce the size of the graph without compromising the essential structural properties that define GRNs. While sparsification algorithms have been evaluated for general purposes, the unique contribution of this project is an extensive search and evaluation for sparsification algorithm applicable for GRNs, focusing on preserving the net- work properties that are particularly relevant for this type of biological network.

In this study, we evaluate four sparsification algorithms—Effective Resistance sparsifier [1], Random sparsifier [2], K-neighbor sparsifier [3], and Forest Fire [4]—applied to gene regulatory networks of E. coli, Multiple Sclerosis blood cell mRNA transcriptome, and gene regulatory data from another human system. We chose three of the sparsifying algorithms that are found to be superior for directed graphs and one that is fastest (Effective Resistance) based on findings by Chen *et. al.* in their evaluation of sparsifiers on a wide range of datasets from different domains [5].

Preservation of key network properties during the sparsification process is imperative. Depending on the end goal of the research project, various network properties may be deemed essential. In this study, we have identified and consolidated fundamental network properties recognized as critical for maintaining the fidelity of GRNs across a range of research domains. In cancer biology, immunology, and neurological disorder research, elucidating the pathways and mechanisms involved in disease progression is a prevalent strategy. [6] In developmental biology, GRNs are characterized by structural variations that distinguish different developmental stages. [7] For cancer and immune system studies, the focus often lies on the nature of regulatory modules and the dynamic characteristics emerging within GRNs. [8, 9] Some of the most important network properties to preserve in these contexts are the distribution of path lengths, the prevalence of the 14 motifs [10], and the modularity of network communities. Additionally, core structural features of GRNs are indicated by metrics such as K_{nn}, PageRank, and degree distribution [11], which are also important to preserve within acceptable thresholds. Given that GRNs exhibit scale-free properties [12], retaining a power-law degree distribution under sparsification is also crucial. In this project, we evaluate the extent to which each of these properties is retained under sparsification by the selected algorithms. Using the K-S statistic test and Chi-squared test, we compare the distribution of K_{nn}, PageRank, selected motifs, clustering coefficient, and the degrees of each sparsified graph against the original graph's properties. This analysis reveals the extent to which a sparsifier retains network properties.

Initial findings suggest that Effective Resistance based sparsifier retains degree distribution well for the human gene but not so well for the Multiple Sclerosis GRN. In contrast, K_{nn} and random sparsifier are superior in terms of retaining PageRank of nodes in the Human Gene data. Sparsifiers that prune nodes significantly alter the motif distribution and may therefore be unsuitable for GRNs. On the other hand, the Effective Resistance-based algorithm is among the faster algorithms but is not designed for undirected networks, making it less ideal for GRNs, which are defined by directionality. This paper presents an extensive experimentation on sparsification algorithms and match them with the multitude of research goals involving GRNs, thus providing guidance for the research community in choosing appropriate sparsifier for their work.

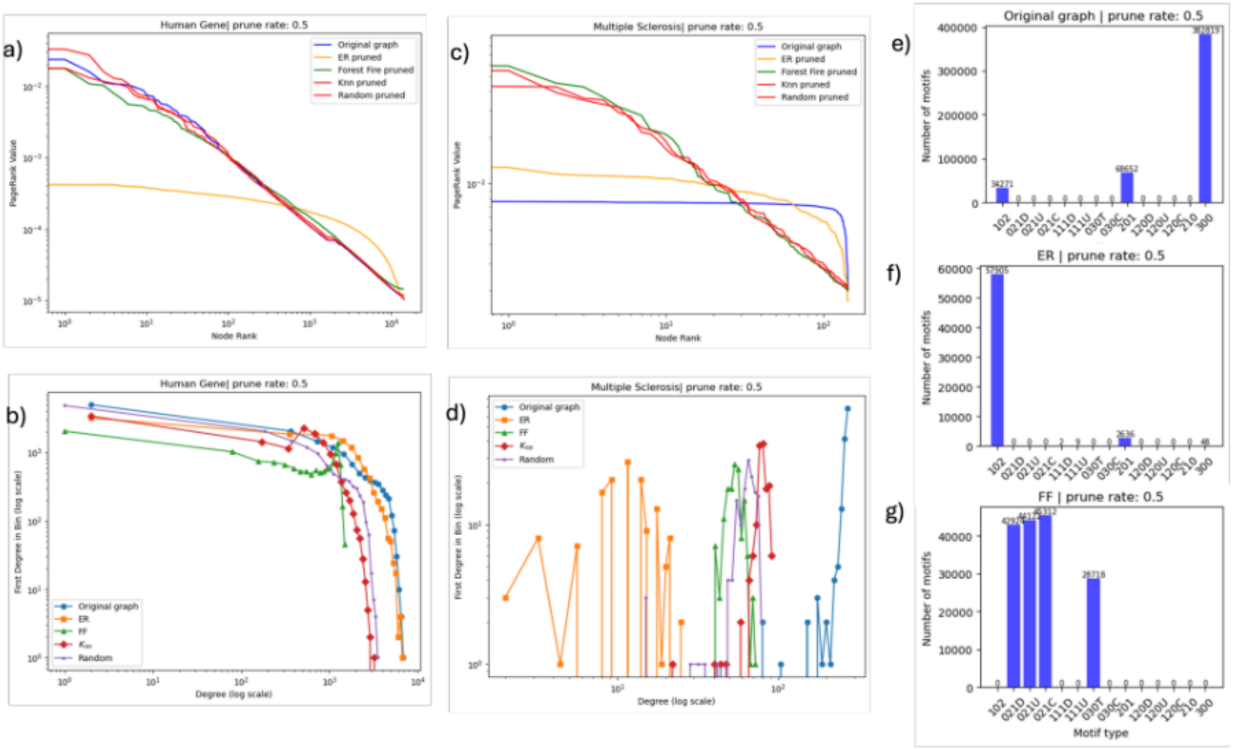

Figure 1: (a) The PageRank distribution of graphs produced after sparsification by the four algorithm juxtaposed with the PageRank distribution of the original graph of human genes. (b) The degree distributions of the original graph and the four sparsified graphs for human gene. (c)The PageRank distribution of graphs produced after sparsification by the four algorithm juxtaposed with the PageRank distribution of the original graph of Multiple Sclerosis (MS) blood cells. (d) The degree distributions of the original graph and the four sparsified graphs for MS. (e) The motif distribution of the original MS graph. (f) and (g) are the motif distributions of MS graph after sparsification by Effective Resistance sparsifier and Forest Fire sparsifier.

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Aging in Weighted Ensemble of Excitable and Self-oscillatory Neurons: The role of Pairwise and Higher-order Interactions

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We investigate the aging transition of a mixed population comprising spiking and excitable Morris-Lecar (ML) neurons on the top of a weighted complex network [1]. We investigate two different network interaction models: a scale-free network and a 2-dimensional simplicial complex [2]. We conducted an in-depth analysis of a scale-free network, revealing that under weak coupling, only self-oscillatory neurons maintain rhythmic dynamics, resulting in partial oscillation death. This suggests that an aging transition can occur even with the quiescence of a few neurons. At moderate coupling strength, collective oscillation is observed when the proportion of quiescent neurons is low, but as this proportion increases, partial oscillation occurs [3]. At higher coupling strengths, a sudden and complete oscillation death is observed at a critical ratio of excitable neurons. This transition is consistent regardless of the weight tuning parameter, although increasing it expands the region of partial oscillation. Additionally, 2nd-order interactions reduce the network's robustness, and partial oscillation is absent even at moderate levels of 2nd-order coupling strength. Furthermore, we observe the presence of

inhomogeneous steady states within the complete oscillation death regime, regardless of the network interaction models.

Keywords: Aging transition, Neurons, Higher-order interaction

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Pattern formation in a two-compartment rumor model under dispersion

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We investigate formation of Turing patterns in a generalized two-compartment (Innocent-Spreader) model for rumor spreading through spatial dispersion. Pattern formation in reaction diffusion systems can be triggered by certain instabilities present in the system. These instabilities offer important insights regarding the dynamics and interactions driving the emergence of patterns in numerous animate and inanimate systems. We find that the presence of diffusion in the rumor model is significantly responsible for the evolution of spots from stripes and a continuous growth of spots as well. We further explore the role of some important system parameters, such as, the rate of media correction, inhibition, forgetting, and self-correction on controlling the spread of rumors. Lastly, we investigate how initial conditions can influence the emergence of mixed-mode patterns characterized by low rate of diffusion.

Keywords: Rumor model, Turing pattern, Instability, mixed-mode pattern.

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Frustrated Quantum Magnetism on Complex Networks: What Sets the Total Spin

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Consider equal antiferromagnetic Heisenberg interactions between qubits sitting at the nodes of a complex, nonbipartite network. We ask the question: How does the network topology determine the net magnetization of the ground state and to what extent is it tunable? By examining various network families with tunable properties, we demonstrate that (i) graph heterogeneity, i.e., spread in the number of neighbors, is essential for a nonzero total spin, and (ii) the key structure governing the total spin is the presence of (disassortative) hubs, as opposed to the level of frustration. We also show how to construct simple networks where the magnetization can be tuned over its entire range across both abrupt and continuous transitions, which may be realizable on existing platforms. Our findings pose a number of fundamental questions and strongly motivate wider exploration of quantum many-body phenomena beyond regular lattices.

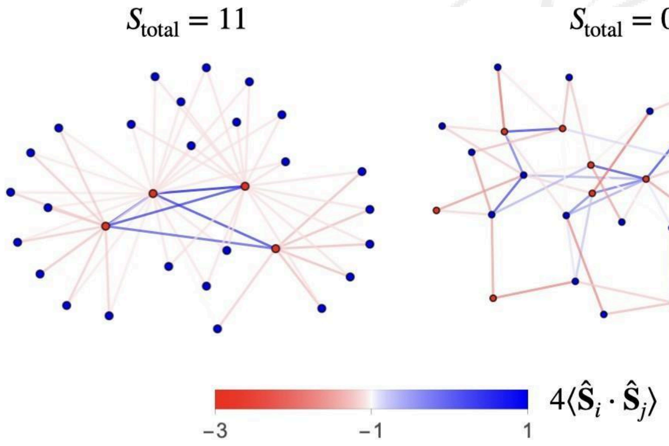

Figure 1: Two graphs with the same number of sites and bonds but very different ordering, showing the impact of heterogeneity. Blue bonds are highly frustrated.

Keywords: Complex quantum networks; Frustrated magnetism; Tunable graphs

Reference: G Preethi and Shovan Dutta, arxiv:2403.09116.

Identifying dynamical transitions and temporal structure of complex systems dynamics

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Keywords: Transition networks, Quasi distance-based measures, Chaos-chaos transition

Complex systems can exhibit a diverse set of dynamics and bifurcations, with each dynamical state exhibiting distinct temporal structure at different time scales. Developing frameworks to catalog the temporal ordering of various dynamics will help predict critical transitions in complex systems such as physiology, climate and engineering [1, 2]. Most real-world systems lack governing equations, making it difficult to predict their behavior for a different parameter subspace. In this work, we study the temporal structure of various dynamics exhibited by the Logistic map ($x_{n+1} = rx_n(1 - x_n)$), which demonstrates period-doubling route to chaos, chaos-chaos transitions (also referred to as interior crisis) and intermittency dynamics for a wide range of control parameter r. At certain values of r, the attractor undergoes a sudden expansion, leading to different types of chaotic fluctuations, a phenomenon referred to as an interior crisis [3]. Such dynamical states and transitions exhibited by this map are also observed in chemical reactions, electrical circuits, heartbeat dynamics, and fluid mechanical systems, making it a suitable model to investigate its dynamics [4, 5, 6, 7, 8]. To capture these structures, we encode the temporal fluctuations onto a complex network topology by considering the amplitude levels as nodes and the transition between the amplitude levels as directed edges of the network [9]. These edges are also given a weight that is equal to the probability of Markov transition between amplitude levels. We derive the average network entropy, local, and global quasi-distance measures from the network constructed at each control parameter to decipher the temporal ordering of different dynamical states. Global distance measures such as the characteristic path length (CPL) and the average betweenness centrality ($\langle C_{BC} \rangle$) quantify the diversity of amplitude jumps associated with the orbit, whereas the average network entropy μ_S quantifies the number and the uncertainty of transition between amplitude levels. Figure 1 shows the orbit diagram, Lyapunov exponent, and the trend of global network measures with r. We observe that all the measures approach zero for periodic dynamics and attain non-zero values for chaotic regimes, consistent with the trend of the Lyapunov exponent of the map. The average network entropy shows a spike at r corresponding to a period-doubling bifurcation (such as $r = 3.544$, 3.654, and so on). All these measures attain a non-zero value at the accumulation point ($r = 3.569 \ldots$), which corresponds to the first onset of chaos or end of period-doubling cascade. Also, the distance-based measures exhibit a spike at $r = 3.857$, 3.745, 3.635, 3.961, which coincides with the boundary of a chaos-chaos transition (interior-crisis). We further look into the local network properties such as node-wise in- and out-degree to characterize the local structural properties of the time series. We discover that the unstable periodic orbits (UPOs) evolve towards certain regions of the attractor, revealing interesting patterns across the control parameter range. In summary, we propose a framework to encode the temporal transitions onto a complex network, and we were successfully able to detect most of the prominent dynamics exhibited by the Logistic map.

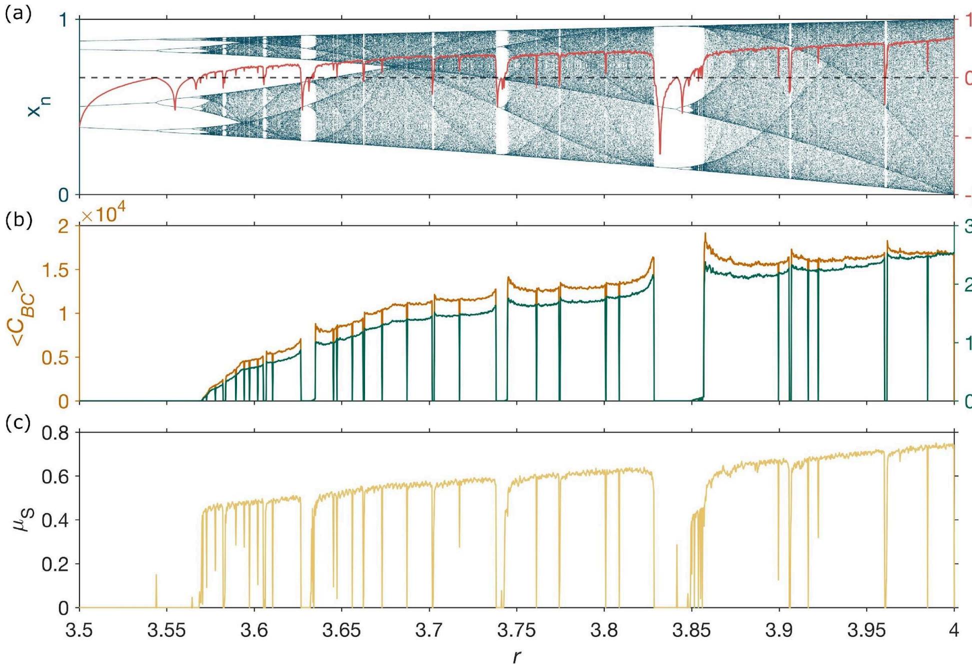

Figure 1: (a) The orbit diagram of the Logistic map between the control parameter 3.5 and 4 (left axis) and the Lyapunov exponent λ (right axis) for each control parameter. (b) Variation of the characteristic path length (CPL) and average betweenness centrality ($< C_{BC} >$) of the network with parameter r. (c) Variation of the average network entropy μ_S with parameter r.

Universality in the self-similar hierarchical organization of real-world networks

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Keywords: Real-world networks, Self-similarity, Hierarchical communities, Horton's laws

Many real-world networks, for example, several social and biological networks, exhibit self- organization in the form of hierarchical community structure [1–13]. We show that such hierarchical topology is self-similar and follows scaling laws common across networks derived from several real-world complex systems.

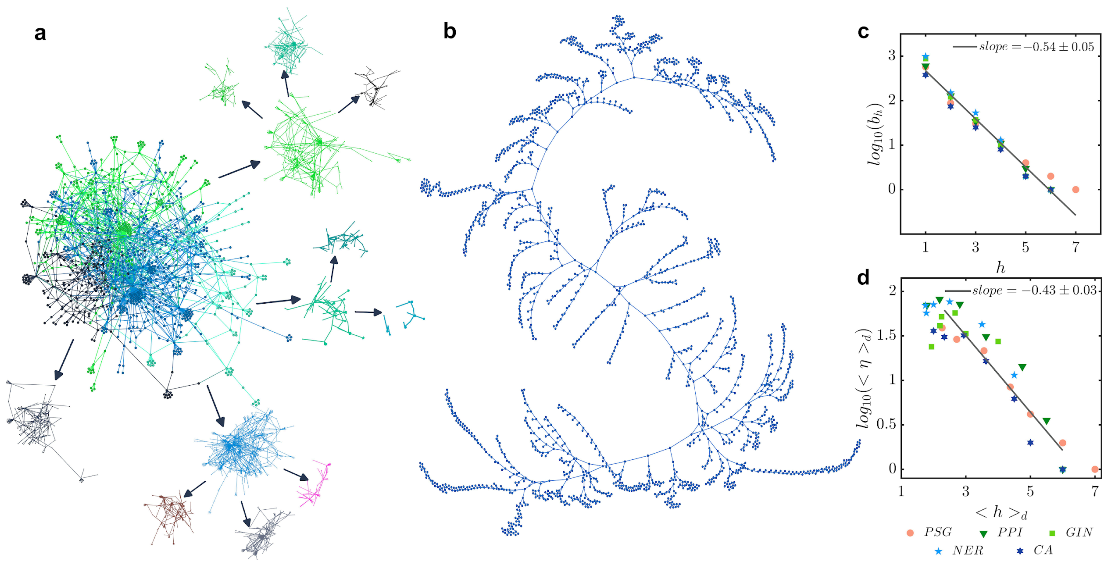

Fig. 1. Universal scaling observed in the hierarchical community structure of different real systems. (a) Com- munity within community structure in the neural network of mouse. **(b)** Binary tree representation of the hierarchical community structure of the network in figure 1(a). **(c)** Exponential scaling between the number of branches of a certain index h with the Horton-Strahler index h satisfying Horton's law of branch numbers for the binary tree representations of different real-world networks. **(d)** Plot of mean relative link density ($< \eta >d$) with order $< h >d$ at a fixed hierarchical depth d as evaluated for binary tree representations of different datasets.

Here, we investigate diverse biological systems such as protein structure graph (PSG), protein- protein interactions (PPI), gene interaction network (GIN) and network of nerve fibre tracts in mouse (NER), and social networks such as the co-author network (CA). Figure 1(a) shows the multi-scale community structure of the network of nerves in mouse. We map the hierarchical community structure generated by Girvan-Newman's algorithm [14] onto a binary tree representation as shown in figure 1(b). We quantify the self-similarity of the binary tree representation using a topological index (denoted by h) introduced by Horton and Strahler in the context of river networks [15, 16]. Horton's laws state that the number of branches and mean attributes of the tree follow a geometric progression with h [17, 18]. Thus, if the number of branches b_h having index h follows a geometric progression, i.e., the bifurcation ratio $R_b = b_h/b_{h+1}$ is a constant then the tree is considered Hortonian [17]. This law can imply a topologically self-similar community structure in a complex network [19]. We however assert that topological self-similarity is implied only if the binary tree is structurally Hortonian [17], i.e., each sub-basin of the binary tree also exhibits Horton's law with the same R_b.

We show that Horton's laws are obeyed by community structure of several real systems as shown in figure 1(c). These networks exhibit common scaling law where the slope of $\log_{10}(b_h)$ versus h plot is -0.54 ± 0.05 with a 90% confidence level across distinct systems. This slope corresponds to $R_b = 3.48$, which is close to the R_b (3.5) observed in many river networks [17]. Furthermore, Horton's law of mean quantities is obeyed by mean relative link density $< \eta >_d$ with mean index $< h >_d$ at any fixed hierarchical depth d, implying that any subset of the tree representation is also Hortonian (figure 1(d)). Hence, the corresponding complex networks are topologically self-similar.

In summary, we discover universally self-similar structural organization across multiple real world systems. The discovery implicates a common governing mechanism that would be crucial in understanding the formation and organisation of these complex networks.

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Black Swan Events on Ethereum Blockchain Transaction Networks

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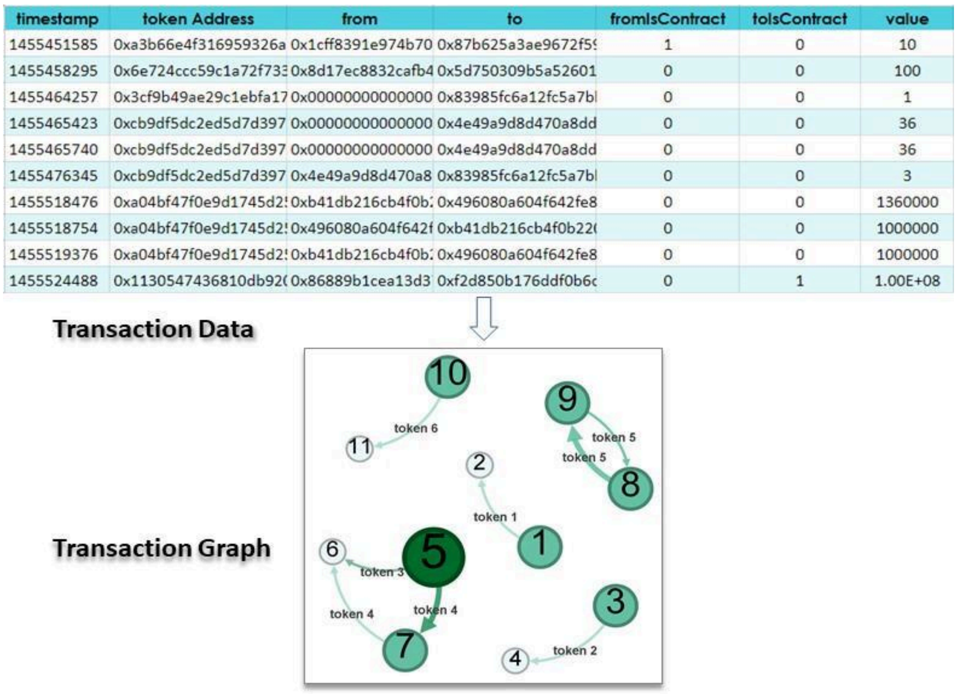

timestamp	token Address	from	to	fromIsContract	toIsContract	value
1455451585	0xa3b66e4f316959326a	0x1cff8391e974b70	0x87b625a3ae9672f5	1	0	10
1455458295	0x6e724ccc59c1a72f73	0x8d17ec8832cafb4	0x5d750309b5a52601	0	0	100
1455464257	0x3cf9b49ae29c1ebfa17	0x00000000000000	0x83985fc6a12fc5a7b	0	0	1
1455465423	0xcb9df5dc2ed5d7d397	0x00000000000000	0x4e49a9d8d470a8dd	0	0	36
1455465740	0xcb9df5dc2ed5d7d397	0x00000000000000	0x4e49a9d8d470a8dd	0	0	36
1455476345	0xcb9df5dc2ed5d7d397	0x4e49a9d8d470a8	0x83985fc6a12fc5a7b	0	0	3
1455518476	0xa04bf47f0e9d1745d2	0xb41db216cb4f0b	0x496080a604f642fe8	0	0	1360000
1455518754	0xa04bf47f0e9d1745d2	0x496080a604f642f	0xb41db216cb4f0b22	0	0	1000000
1455519376	0xa04bf47f0e9d1745d2	0xb41db216cb4f0b	0x496080a604f642fe8	0	0	1000000
1455524488	0x1130547436810db92	0x86889b1cea13d3	0xf2d850b176ddf0b6	0	1	1.00E+08

Figure 1: Illustrate the ERC20 token transaction data over the Ethereum blockchain and the associated transaction graph. For simplicity, we assign a unique integer number corresponding to the 'from', 'to', and 'token Address' columns. Here, 'from' is the seller's, 'to' is the buyer's wallet, and the edge label shows which tokens are traded. The edge thickness represents multiple transactions of the same tokens between buyer and seller. For instance, between node 5 and 7, two transactions of 'token 4'.

After several Black Swan events like the 2007-08 financial crisis, there is a growing enthusiasm worldwide to understand the financial ecosystem. Modeling a financial system as a network has helped us to understand a wide range of phenomena crucial for financial, professionals, economists, and researcher. We consider the Ethereum Blockchain transaction data to analyze the trader's behavior during the 2018 crypto crash and the COVID-19 pandemic. The Ethereum blockchain and its ERC20 token standard have revolutionized the landscape of digital assets and decentralized applications. ERC20 tokens are programmable and interoperable tokens, enabling various applications and token economies. Transaction graphs, representing the flow of the value between wallets within the Ethereum network, have played a crucial role in understanding the system's dynamics, such as to- ken transfers and the behavior of traders. Here, we explore the evolution of daily transaction graphs of ERC20 token transactions, which sheds light on the trader's behavior during the Black Swan Events – 2018 crypto crash and the COVID-19 pandemic. By using the tools from network science and differential geometry, we analyze 0.98 billion of ERC20 token transaction data from November 2015 to January 2023. Our analysis reveals an increase in diverse interaction among the traders and a greater adoption of ERC20 tokens in a maturing Ethereum ERC20 financial ecosystem after the Crypto Crash 2018 and the COVID-19 pandemic. Before the crash and the COVID-19 pandemic, most traders interacted with other traders in an isolated or restricted manner, with each trader focusing solely on either buying or selling activities. However, after the crash and during the pandemic, most traders diversely interacted among themselves by participating in both buying and selling activities. In addition, we observe no significant negative impact of the COVID-19 pandemic on user behavior in the financial ecosystem.

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Evolution of Social Networks in Kanzara Village: Changing Patterns of Social, Informational, Agricultural and Financial Interactions

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The study of social networks is vital for understanding the dynamics of rural communities, particularly in the evolving context of India's semi-arid tropics (SAT). social networks play a crucial role in shaping social, informational (Banerjee *et al.,* 2019), agricultural (Maertens & Barrett, 2013), labor, and financial interactions ((Banerjee *et al.,* 2024)) among households. This paper examines the evolution of household-level networks in Kanzara village, Maharashtra, over three decades, focusing on financial, agricultural, and labor interactions. Using balanced census panel data from one of the ICRISAT village (2007, 2013, 2022), we employ graph theoretical approaches for visualization and computation of network parameters and stochastic actor-oriented models (SAOMs) to analyze network changes. Our findings reveal significant shifts in network structure and group dynamics in the backdrop of agricultural mechanization, improved financial access, and changing labor patterns. While village networks remain sparse and exhibit caste-based homophily (Figure 1), there is a notable decline in the centrality of dominant castes, suggesting a weakening of traditional social hierarchies. Financial networks, in particular, show a transformation with the introduction of low-cost formal credit, altering the

frequency and structure of social interactions. These insights contribute to understanding how rural social organizations adapt to contemporary socio-economic challenges.

Keywords: Village network; Evolution; Financial networks; Agriculture information sharing networks.

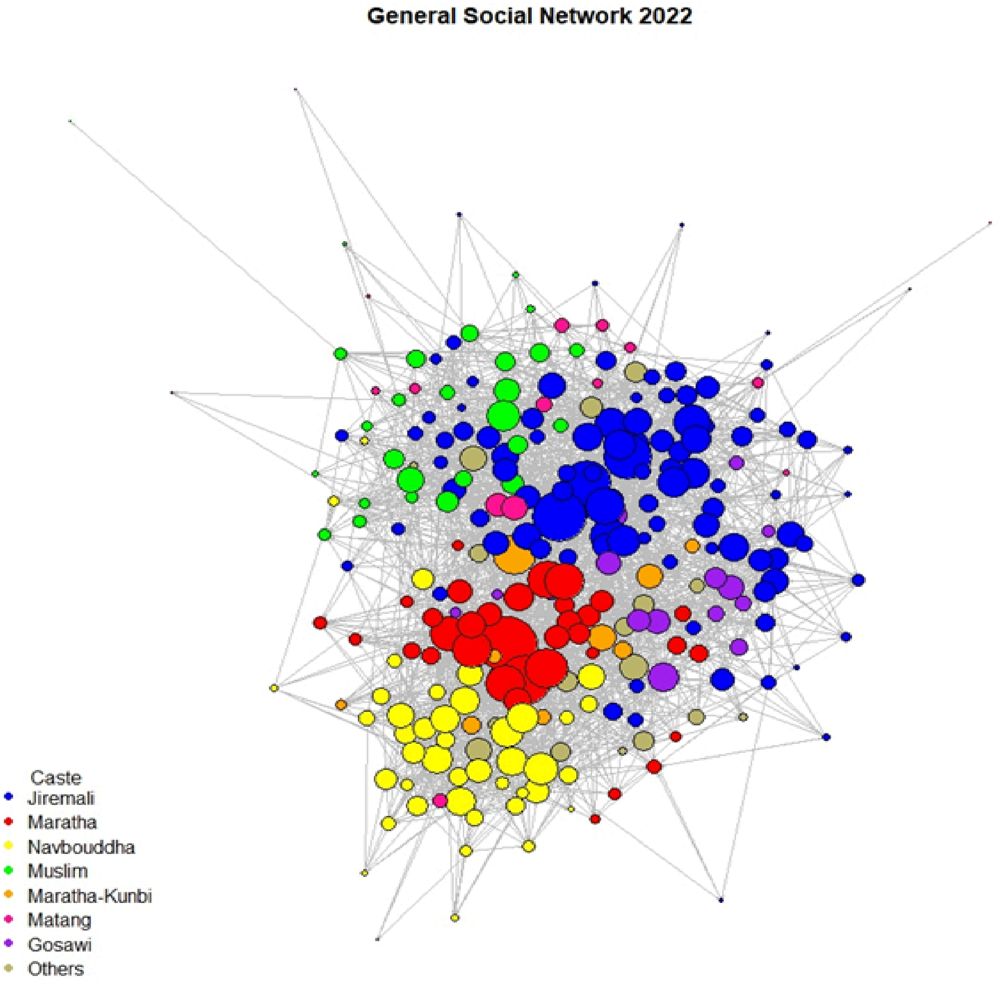

Figure 1: Graphical presentation of village networks for census round 2022. Note: Only provided network presentation for the latest round of census, other visual presentations are available in full paper

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Farthest-First Traversal For Identifying Multiple Influential Spreaders

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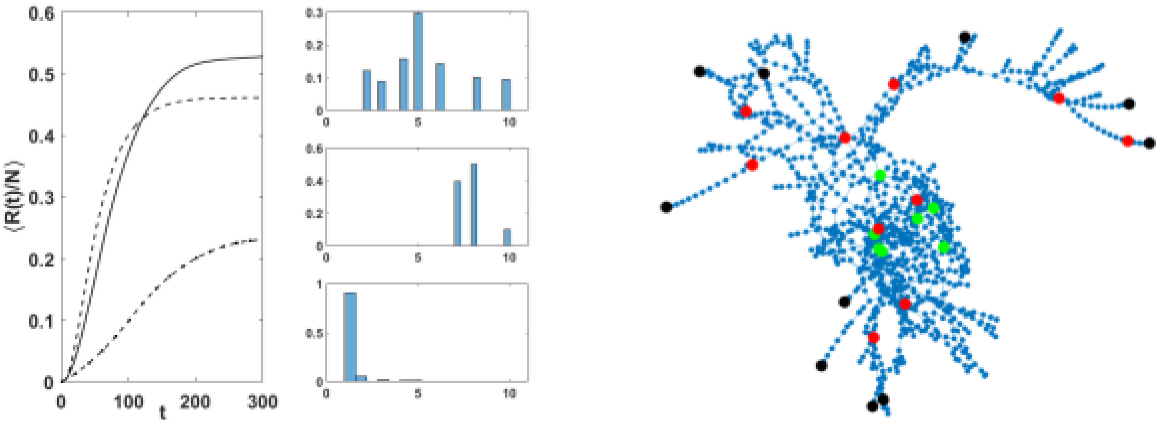
Understanding the influence of initial spreaders in spreading processes on complex networks is a challenging problem with wide-ranging practical applications. Selecting initial spreaders based on centrality measures alone often fails to achieve extensive network coverage. This arises from the heterogeneity of real-world networks and the overlap in influence among spreaders, leading to redundancy. To address this, we propose a method that identifies multiple influential initial spreaders that are well- dispersed across the network. Our approach utilizes the Farthest-First Traversal algorithm to select a set of widely separated nodes. These nodes then serve as centers, from which influential nodes in their local neighborhoods are identified and chosen as the initial spreaders. We numerically examine the effective- ness of the spread initiated from these nodes using the SIR epidemic spread model. We compare our results with influential nodes obtained using degree centrality, which does not guarantee dispersion, and with influential nodes obtained from a non-overlapping community detection-based method. We present the results for different network structures, including both synthetic and real-world datasets. Our numerical experiments show that initiating the spread from the nodes selected using the proposed method minimizes the time required to cover the entire network and maximizes the spread within a given time, particularly in the case of spatial networks.



(a) (b)

Figure 1: Panel (a) shows the average fraction of recovered individuals ($\langle R(t)/N \rangle$) in the SIR simulation on the euroroads dataset. The solid line represents the proposed method, the dashed line represents hub nodes, and the dashed-dotted line represents FF nodes. The right panel displays the degree distribution of initial spreaders for each method. Panel (b) illustrates a sample node selection: FF nodes (black), proposed method based nodes (red), and hub nodes (green).

Keywords: Influential spreaders, Diffusion in networks, Farthest-First Traversal

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Machine learning for phase ordering dynamics

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Forecasting the behavior of the dynamic system is a riveting task within the purview of complex systems theory. Reservoir Computing (RC)[1], is one of the recent computational paradigms that have been exploited for data-based forecasting of chaotic dynamical systems. Reservoir computers were developed as a type of recurrent neural network (RNN) that are a brain-inspired framework.

The rapid temperature quenching of a homogenous two-state mixture(binary mixture) into a broken-symmetry phase approached as phase-ordering kinetics or ‘domain coarsening’ continued as a center for interdisciplinary sciences and the study of statistical physics [2]. We endeavor to develop a reservoir computing approach to forecasting the phase ordering dynamics in a lattice system. To forecast phase ordering kinetics, the reservoir is trained using the input data, containing information about the order parameter at different times during the phase ordering process. The time-dependent Ginzburg-Landau(TDGL) equation and the Cahn- Hilliard equation(CHC) are the standard models for describing the order-parameter kinetics of a uniform two-phase mixture. Importantly, a single reservoir has been proven to be adequate in processing the information of a large number of state variables involved in the task. To summarize, we have studied the phase ordering dynamics for conserved and non-conserved order parameters[3]. The dimensionless form of TDGL and CHC equations without thermal noise for $H \neq 0$ can be expressed as:

$$\frac{\partial}{\partial t}\psi(r,t) = \psi - \psi^3 + \nabla^2\psi + H \qquad \frac{\partial}{\partial t}\psi(r,t) = \nabla.\left[-\psi + \psi^3 - \nabla^2\psi\right].$$

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Aggression Breeds Aggression: The Impact of Aggressive Feeds on User Behavior on Social Media Network

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The widespread use of aggressive behaviour on Twitter raises concerns about potential negative influences on user behavior. Despite previous research exploring aggression and negativity on the platform, the relationship between users’ aggressive behavior and that of feeds of followee being exposed to this user, remains underexplored. This study investigates whether exposure to aggressive feeds can lead to an aggressive behavior of an user. We formalize the problem using a heterogeneous network where nodes represent users and tweets, while edges denote following relationships and tweet-posting actions. We detected tweet nodes as aggressive or non-aggressive by developing a transformer-based aggression detection model (macro F1=0.92). User aggression was quantified using a proposed "user aggression intensity" metric based on their overall aggressive activity. Our analysis of 14M tweets from 63K user nodes revealed that aggressive feeds (incoming edges from followed users) can significantly influence users to behave more aggressively on online platforms (P-value < 0.05) (Fig.1a). This effect is also pronounced for event-specific behavior (Fig.1b). Furthermore, the study found that users tend to support and encourage aggressive behavior of their followee users (Fig.1c), which can contribute to the proliferation of aggressive behavior [1].

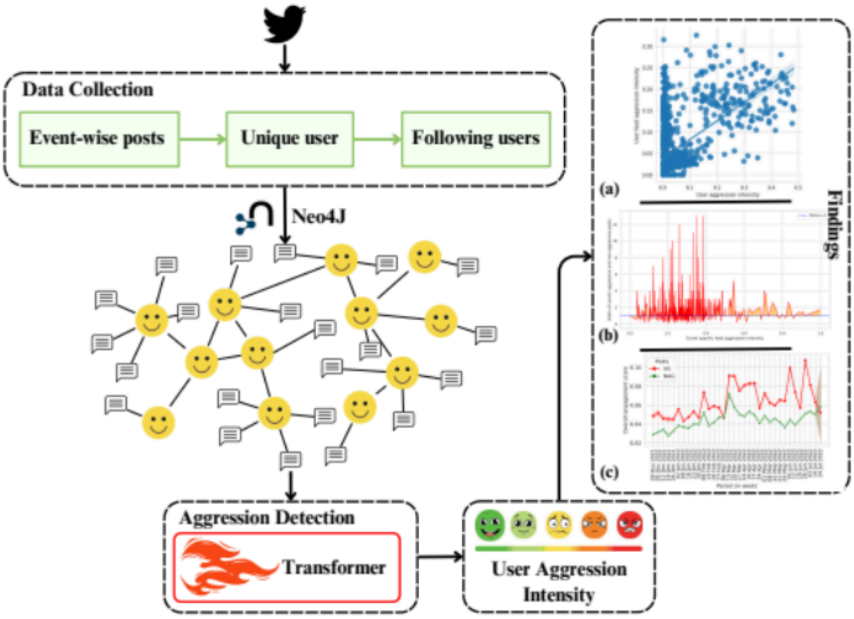

Figure 1: Flow of the methodology used to answer our research questions.

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Modelling protein complexes as multilayer networks

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Protein structure and dynamics play a crucial role in defining its function. Hence, understanding the protein structure-function paradigm has been an area of active research. While atomistic models and molecular dynamics simulations of the proteins provide detailed insights into interactions and dynamics, coarse-grained models have proven effective in understanding the folding and emergent properties of proteins. One such coarse-grained approach is modeling protein structures as complex networks (referred to as Protein Contact Networks or PCN) with amino acid residues as nodes and distance between them defining the edges. This approach decomposes the 3-D protein structure topology to a 2-D network topology and allows us to use graph theoretical measures to draw inferences about protein structure and function. Though quite useful in understanding protein folding, conformational changes and allosteric communication, the single layer representation fails to provide insights into interactions between different proteins in complexes. Considering, most important functions within cells involve formation of protein complexes, it is imperative to extend the network formalism to be able to capture the protein-protein interactions in the complexes. In this work, we have modeled protein complexes as multilayer networks. Multilayer networks represent complex systems as multiple levels by considering subsets of nodes as different layers. In the context of multimeric protein complexes, each monomer has been considered as a different layer. By modeling protein structures as multilayer networks, the information about the intralayer and interlayer edges is preserved. In our study, we have modeled homodimers and heterodimers as multilayer networks with two layers. Identifying important nodes and their influence on other nodes could be useful in understanding mutations in protein complexes. We have extended the centrality measures from single-layer networks to multilayer networks in order to identify influential nodes in multilayer PCNs. This has allowed us to study, how perturbing an influential residue can affect the long-range interactions. We then compare the network properties of the single-layer topology and the multilayer topology to benchmark the multilayer model of PCN. We have utilized this framework to understand the structure and function of CLOCK:BMAL1, a transcription factor that belongs to the bHLH-PAS domain family. Mutations in CLOCK:BMAL1 have been well studied due to their role in regulating circadian rhythms. Using the multilayer approach, we have been able to provide deeper insights into the structural and dynamical role of these mutations.

Keywords: Multilayer network; Protein Contact Network; CLOCK:BMAL1; Centrality Measures.

Information Localization in Complex Networks

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Networks are composed of interconnected units that interact with each other and form the infrastructure for different dynamical systems. The relationship between the interconnected architecture and nonlinear interaction is essential to understand – how the virus spreads nationwide, how information spreads through social networks, how economic shocks propagate from one financial institution to another, or how neurons interact to perform specific functions in the brain. We can encode different spreading phenomena as perturbation propagation in nonlinear dynamical systems. Predicting the information propagation pattern in dynamical systems is still an open problem. Characterizing dynamical properties to predict the perturbation propagation on network structures can help us reverse engineer the system architecture, enhance robustness, and provide insights into the underlying mechanism of their evolution. We uncover an emerging localization phase in the perturbation propagation in nonlinear dynamical systems where one node acquires a finite fraction of all the perturbations. We observe that sometimes perturbation is localized on the hub nodes, and for other dynamics, it diffuses over all the nodes. What are the dynamical signatures of localization? What are the consequences of localization of nonlinear dynamics? For two sets of parameter values, Fig. 1, representing two classes of dynamical patterns in a specific scenario, illustrates the family of challenges that we tackle here to understand the information propagation pattern.

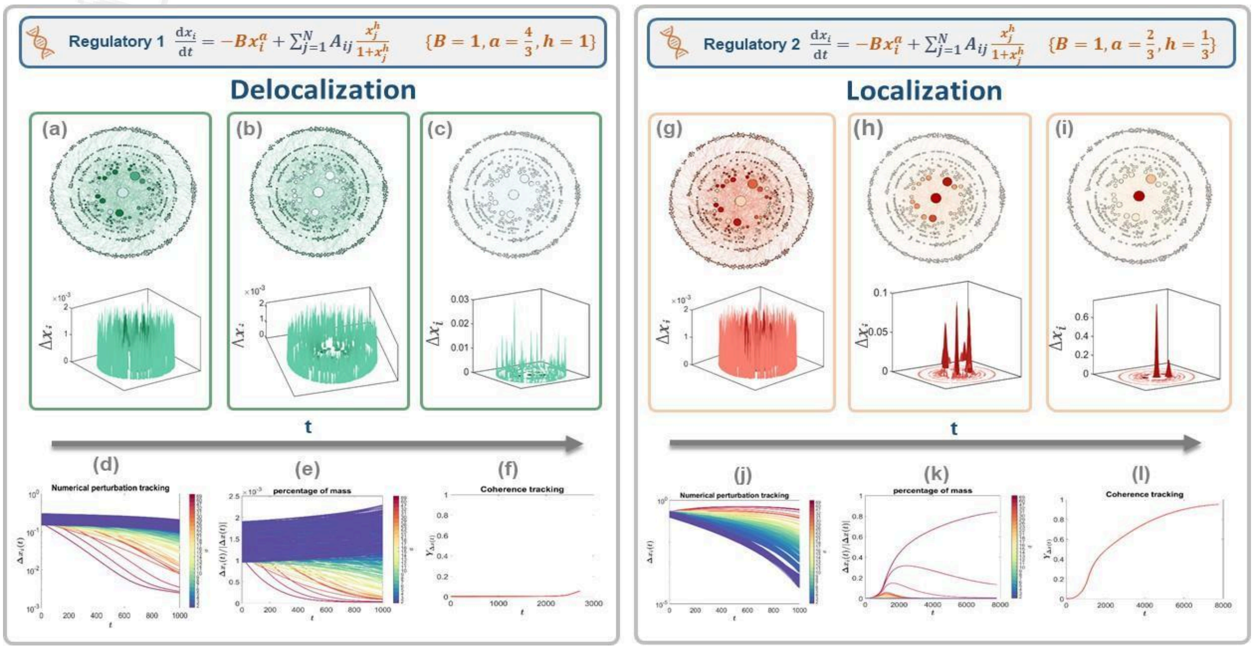

Fig. 1: Information localization in complex networks. We consider a regulatory dynamical model and choose two sets of parameter values (Regulatory 1 and Regulatory 2). We perturbed around the fixed point and tracked the perturbation propagation pattern. Starting the perturbation from randomly selected nodes as time progress, perturbation goes away from the hub node (a-d). In contrast, for other cases, perturbation decay fast for the peripheral nodes and gets condensed to the hub nodes (g-j). One can observe that the perturbation propagation pattern is entirely different (c, i) when the network structure is identical, and the initial perturbation pattern is the same (a, g). Here, localization occurs from nonlinear interactions. (e, k) Illustrate the percentage of perturbation left on the nodes, and (f, l) is a measure for the localization of perturbation in networks.

Compartmental Framework for Prebunking Misinformation

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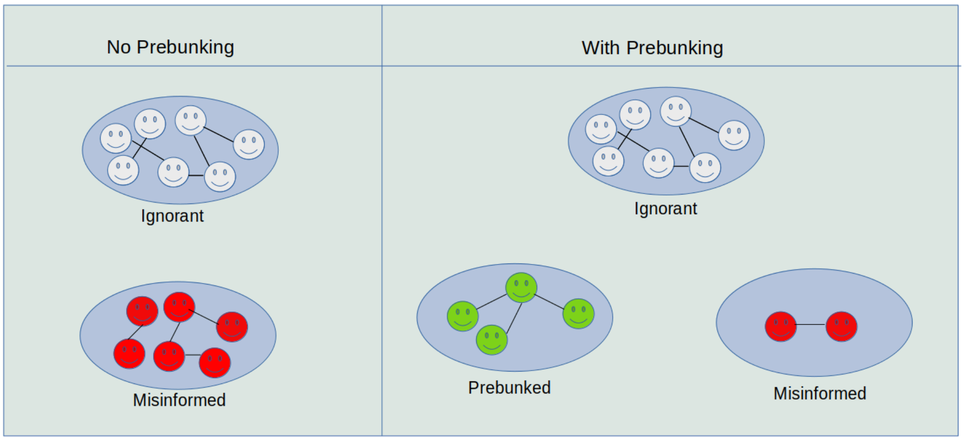
The rapid proliferation of misinformation in the digital age poses severe risks to public understanding and decision-making processes. Prebunking[1], an initiative to equip people with cognitive resilience to misinformation before encountering it, has recently garnered support from both psychologists and policymakers.

Inspired by the psychological theory of inoculation, our work adapts the compartmental model from epidemiology to model prebunking as an equivalent to vaccination[2] and develops effective prebunking strategies against misinformation. Interventions rooted in inoculation theory can transform individuals from being susceptible to becoming resistant to misinformation, thereby reducing its spread. Numerically, we demonstrate the efficacy of prebunking across various network platforms and dynamics-dependent parameters. Our model provides a practical framework for comprehending and combating misinformation, offering valuable insights for policymakers and technology developers to strengthen public resilience against false information.



Keywords: Prebunking, Misinformation, Social Network, Compartmental model.

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Mitigation and Enhancement of Neuronal Extreme Events:Impact of coupling and random links

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We explore a collection of aperiodic neuronal maps [1], diffusively coupled to nearest neighbours, as well as globally coupled through the collective mean field of the action potentials. We focus on the possible emergence of temporal as well as spatial extreme events in such coupled neuronal systems [2]. Our central finding is that local diffusive coupling enhances the probability of occurrence of both tem- poral and spatial extreme events whereas global mean field coupling suppresses extreme events (See figure 1).

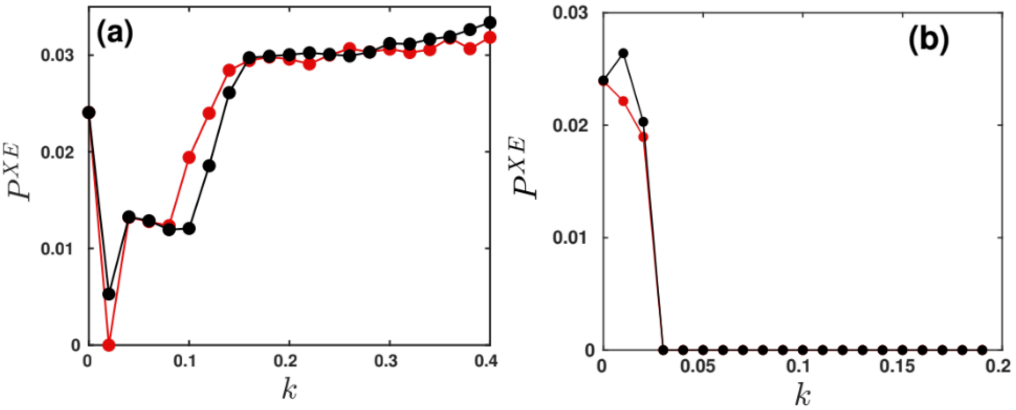

Figure 1: Probability (P^{XE}) of extreme events in time versus coupling strength for a ring of sizes 100 (red), 500 (black) with (a) diffusive local coupling and (b) meanfield global coupling [2].

We also explore the influence of random connections on the creation of extreme events in the spiking patterns of the action potentials of model neurons diffusively coupled in networks. We find that the presence of a small fraction *p* of static random links in the network suppresses extreme events, while a high fraction of such links induce extreme events for sufficiently high coupling strengths. Interestingly, when the random links are time-varying, even a small number of such links can make the network prone to extreme events in a significant range of coupling strength [3].

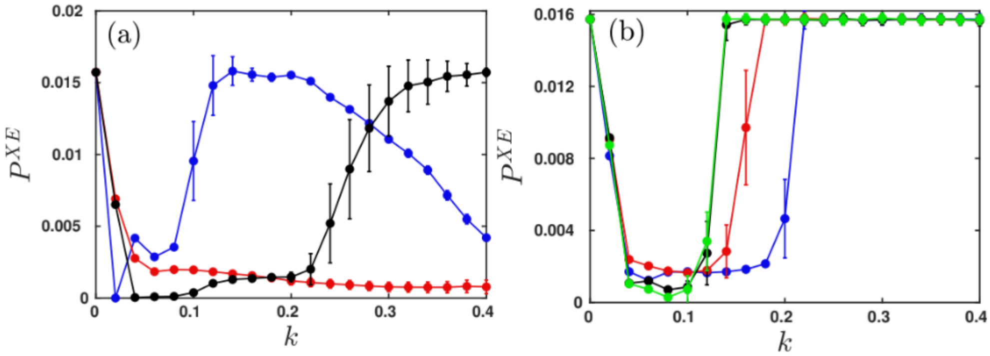

Figure 2: Probability (P^{XE}) of extreme events in time as a function of coupling strength (k) for a ring of size 100, with (a) static random links and (b) time-varying random links. The data presented here for the fraction of random links $p = 0$ (blue), 0.2 (red), 0.9 (black) for the static case, and $p = 0.02$ (blue), 0.1 (red), 0.5 (black), 0.9 (green) for the time-varying case [3].

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Collective dynamical states in adaptively coupled identical phase oscillators

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In this work, we investigate the interplay of an external forcing and an adaptive network, whose connection weights co-evolve with the dynamical states of the phase oscillators. In particular, we consider the Hebbian and anti-Hebbian adaptation mechanisms for the evolution of the connection weights. The Hebbian adaptation manifests several interesting partially synchronized states, such as phase and frequency clusters, bump state, bump frequency phase clusters, and forced entrained clusters, in addition to the completely synchronized and forced entrained states. Anti-Hebbian adaptation facilitates the manifestation of the itinerant chimera characterized by randomly evolving coherent and incoherent domains along with some of the aforementioned dynamical states induced by the Hebbian adaptation.

Keywords: Adaptive network; Dynamical states; Kuramoto oscillators.

Reference:

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Dynamical phase transitions in post-ictal generalized EEG suppression

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The post-ictal generalized EEG suppression is a neurological condition usually occurring in patients with generalized tonic-clonic seizures. It consists of marked suppression of low-frequency waves before returning to normal brain function. Moreover, often, the path of return to normal brain function is accompanied by a mixed state consisting of suppression and high amplitude oscillation. We explain these phase transitions from the standpoint of bifurcation theory to attain a proper dynamical model that mimics similar behavior. We find that various stages of postictal generalized EEG suppression are best modelled via the normal form of sub-critical Hopf bifurcation.

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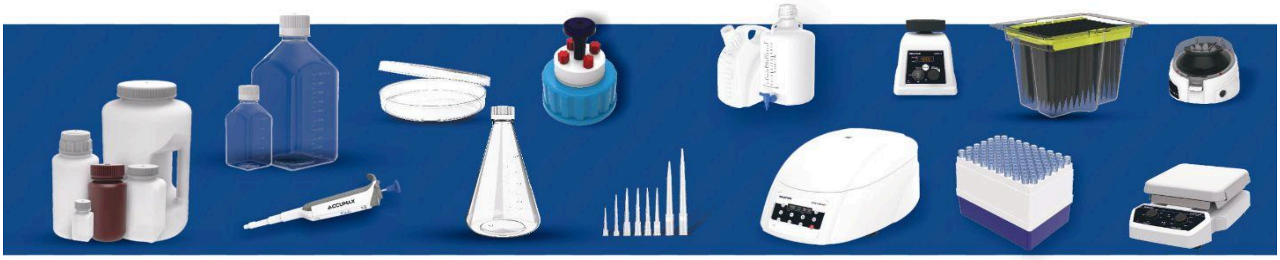

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