4th Latin American Conference on Complex Networks

Book of Abstracts

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Book of Abstracts

LANET

4th Latin American Conference on Complex Networks

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Committees

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Invited Plenary Speakers

Evolution of triangulations: Hausdorff and spectral dimensions

José Fernando Mendes

University of Aveiro, Portugal.

We investigate complex networks generated from triangulations and higher-dimensional simplicial complexes that model closed, evolving manifolds. In our approach, networks evolve through local transformations that preserve triangular faces, leading to a variety of random architectures. Through extensive simulations, we analyze both growing and equilibrium states of these networks, focusing on their geometric and structural properties - including Hausdorff and spectral dimensions, degree distributions, and structural correlations. Our findings uncover a wide range of network geometries: some resemble small-world networks, while others are finite-dimensional with Hausdorff dimensions equal to or greater than the dimension of their building blocks. Spectral dimensions vary broadly, from around 1.4 up to infinity. We also present models with evolving topologies, such as a torus gaining holes over time, which displays strong small-world behavior and a heavy-tailed degree distribution.

Network theory to understand ecological changes

Guadalupe Peralta

Instituto Multidisciplinario de Biología Vegetal (IMBIV, CONICET - Universidad Nacional de Córdoba), Argentina.

Network theory is used in ecology to understand changes in biological communities and ecosystems, and has allowed researchers to move the focus from species to their interactions. For instance, the study of species interaction patterns help us understand how plant and pollinator species, as well as their interactions, respond to habitat disturbances. This approach further provides new directions to explore which species characteristics make them more or less resilient to habitat changes. Furthermore, the identification of those species characteristics can also be used to simulate species extinction under different environmental change scenarios. Moreover, studying ecological networks allows tackling key unresolved questions, such as why there are so many rare plant species on earth despite their expected extinction due to low population abundances. Unravelling the assembly and disassembly mechanisms of ecological networks can be used to develop conservation and management actions, and to predict changes in the ecosystem functions and services we depend on.

Emergent social coordination and collective bias in human and LLM populations

Andrea Baronchelli

University of London, United Kingdom.

Social conventions are the foundation of social coordination, shaping how individuals come together to form a society. In this talk, I will present theoretical and experimental findings that demonstrate the spontaneous emergence of social coordination in decentralized networks, as well as the existence of tipping points in social convention. I will then focus on the case of populations of large language models (LLMs). As AI agents increasingly communicate using natural language, understanding how they develop conventions is crucial for interpreting and managing their collective behaviour. I will show that LLM populations can establish social conventions and highlight how collective biases can emerge even when individual agents appear unbiased. I will conclude by stressing how the ability of AI agents to develop norms without explicit programming has significant implications for designing AI systems that align with human values and societal goals.

Exploring spatial segregation induced by competition avoidance as driving mechanism for emergent coexistence in microbial communities

Alex Arenas

Universitat Rovira i Virgili, Spain.

In this talk, we present the role of spatial segregation, prompted by competition avoidance, as a key mechanism for emergent coexistence within microbial communities. Recognizing these communities as complex adaptive systems, we challenge the sufficiency of mean-field pairwise interaction models, and we consider the impact of spatial dynamics. We developed an individual-based spatial simulation depicting bacterial movement through a pattern of random walks influenced by competition avoidance, leading to the formation of spatially segregated clusters. This model was integrated with a Lotka-Volterra metapopulation framework focused on competitive interactions. Our findings reveal that spatial segregation combined with low diffusion rates and high compositional heterogeneity among patches can lead to emergent coexistence in microbial communities. This reveals a novel mechanism underpinning the formation of stable, coexisting microbe clusters, which is nonetheless incapable of promoting coexistence in the case of isolated pairs of species.

The role of timing on waning immunity in epidemics: The Rebound Effect

Clara Granell

Universitat Rovira i Virgili, Spain.

In this talk, I explore how the timing of vaccination campaigns interacts with waning immunity to shape epidemic dynamics. Using an SIRS model, we uncover a counterintuitive "rebound effect", whereby misaligned timing in vaccination efforts can inadvertently lead to a larger secondary peak of infections. This effect is driven by the interplay between vaccine-induced immunity decay and the replenishment of the susceptible population, particularly when campaigns conclude as immunity wanes. By testing different start times and campaign lengths, we demonstrate how the timing of vaccination can either increase or prevent this resurgence. These findings highlight the importance of precise vaccination timing to avoid unintentional spikes in infections and offer guidance for future epidemic control strategies.

A theoretical framework for representing ideological bias through sentiment analysis

Pablo Balenzuela

Universidad de Buenos Aires, Argentina.

The quantification of ideological bias -understood as the systematic tendency of actors such as media outlets or social media users to express consistently favorable or unfavorable views toward specific political positions- remains a central challenge in the analysis of public discourse. Despite significant progress in natural language processing (NLP), especially with the advent of large language models (LLMs) that have greatly enhanced the accuracy of tone and sentiment detection in political texts, there is still a pressing need for metrics that are not only reliable and interpretable but also capable of effectively summarizing complex patterns of evaluative language. In this work, we introduce a novel approach to measuring political bias by conceptualizing it as a latent variable, embedded within a framework inspired by statistical physics. In our model, bias is treated as a quantity formally analogous to temperature, which allows for its systematic estimation using observed textual data. This analogy enables us to move beyond surface-level sentiment analysis and toward a deeper, more structural characterization of evaluative tendencies. We apply this modeling framework to a dataset comprising mentions of political actors across a range of media outlets. By analyzing the tone associated with each mention, our method infers the relative bias of different sources in a consistent and interpretable manner. The results demonstrate the capacity of the model to capture meaningful variations in political orientation and highlight its promise as a tool for the automated, scalable analysis of political communication. Our findings suggest that combining LLM-based sentiment extraction with physics-inspired modeling offers a powerful route for advancing the measurement of bias in complex discursive environments.

Towards Network Geometrodynamics. Directed Networks

Ernesto Estrada

Institut de Física Interdisciplinària i Sistemes Complexos, Spain.

I will define a new dynamical system on directed graphs based on a reaction-diffusion equation. The diffusion is controlled by the standard Laplacian of the undirected underlying graph and the reaction is controlled by a complex-valued term which respects the directionality of the edges in the digraph. I will show some of the advantages of this model for the study of directed graphs. Here the main focus will be on the complex Euclidean geometry induced by this dynamics. It induces a Euclidean distance as well as complex, and Euclidean angles between positions vectors for directed or mixed graphs. I introduce Kähler and Hermitian angles between different planes among position vectors and holomorphic and projection planes, respectively. To illustrate the usability of some of these indices in the study of real-world networks I will study the Kähler angle for finding hierarchies and detecting hierarchical clusters of vertices in several real-world networks.

Can we reproduce real networks? A generative latent position model for weighted random graphs

Paola Bermolen

Universidad de la República, Uruguay.

Complex networks are ubiquitous in real-world applications, from social networks to the Internet or brain connectomics. Using graph models as natural abstractions of such complex networks, the development of machine learning techniques has experienced an accelerated increase for tasks such as node classification, link prediction, or community detection. While Graph Neural Networks have demonstrated remarkable performance to this end, advancing expressive statistical models for graph data that capture properties of real-world networks is still an active area of research. This talk introduces a nonparametric latent position model for random weighted graphs. The key innovation is to relate the inner product of the nodal latent position vectors with the moment generation function of the edge weights' distribution. As a result, we show that considering higher moments can increase the model's discriminative power. Appropriately modified adjacency spectral embeddings can be used to estimate the nodal latent positions from a given weighted adjacency matrix. We derive statistical guarantees for this embedding algorithm: consistency and asymptotic Normality. We also show how these spectral embeddings can be used to generate new graphs with statistically similar structure and edge weight distribution.

Capturing the linguistic diversity of societies

Jose Javier Ramasco

Institut de Física Interdisciplinària i Sistemes Complexos, Spain.

Cultural diversity encoded within languages and linguistic varieties is decreasing in a context of growing globalization. It is thus important to understand what drives linguistic variation, and which mechanisms might enable coexistence of different languages and varieties. In these works, we study the coexistence of different languages in multilingual societies and also the presence of linguistic varieties in the UK English. In both cases, we first characterize the situation with a large scale empirical analysis in terms of the spatial distribution of the different languages and dialectal variants and the emerging mixing patterns. For example, in the case of languages we find that it ranges from a mixing of language speakers to segregation with multilinguals on the boundaries of disjoint linguistic domains, while in the UK cities we find an inverse connection between mobility mixing and the segregation of varieties. We introduce a model that with slight adaptation is able to handle both languages and varieties coexistence. Modifying the model parameters, it is possible to find the different regimes observed in the spatial empirical data for both cases.

Role of waning immunity for epidemic spreading on networks

Silvio C. Ferreira

Departamento de Física, Universidade Federal de Viçosa, Brazil National Institute of Science and Technology for Complex Systems, Brazil

Keywords: Spreading Phenomena; Criticality; Waning immunity

Network epidemiology involves the investigation of compartmental epidemic models on structured populations, where individuals are represented by nodes and their interactions by edges of a graph that defines the contact network of the system. The basic epidemic models on networks are the susceptible-infected-susceptible (SIS), where infection does not confer immunity, and the susceptible-infected-recovered (SIR), where individuals acquire permanent immunity after infection. Biologically, immunity is usually conferred for a finite time (waning of immunity), and the dynamics is better described by the susceptible infected-recovered-susceptible (SIRS) model. The SIRS model is much less addressed than its simpler SIS and SIR counterparts in the context of phase transitions and network epidemiology, as temporary immunity is often assumed to play only a minor role, merely introducing a delay between the infected and susceptible states. On the other hand, in neuroscience, the refractory state – where neurons stop firing for a while - is known to play an important role in neuronal dynamics and brain criticality. In this talk, I will show that waning immunity can drastically alter the nature of epidemic spreading on heterogeneous networks with power-law degree distributions, compared to case without immunity (SIS dynamics). I will discuss the activation mechanism in the presence of waning immunity [1,2], analyze theoretical mean-field approaches and epidemic localization for SIRS dynamics [3], and finally, show how epidemic dynamics with non-Markovian healing are affected by the presence of waning immunity [4].

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- [2] Cota, W., Mata, A. S., & Ferreira, S. C. (2018). Robustness and fragility of the susceptible-infected-susceptible epidemic models on complex networks. Phys. Rev. E 98, 012310.
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theoretical approaches for epidemic processes with waning immunity in complex networks. Phys. Rev. E 106, 034317.

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Smart Grids: (complex) power system networks

Pablo Monzón

Universidad de la República, Uruguay.

Power systems have evolved to advanced networks that use digital communications technologies to monitor, analyze and manage electricity flow in a more efficient way. Their response lies in enhancing energy efficiency, integrating renewable energy sources, improving reliability and reducing risks of instabilities and outages. Along with optimization tools, they enable better demand-response management and the reduction of carbon emissions, playing an important role in building sustainable energy infrastructure, improving the quality of life and supporting environmental conservation. In the talk we will highlight the main characteristics of smart grids with focus on some demand-response schemes.

Exploring concepts of complex networks with living neurons grown in the laboratory

Jordi Soriano-Fradera

Universitat de Barcelona, Spain.

Neurons grown in vitro (neuronal cultures) are an excellent model system to investigate a wealth of intriguing questions from a physics of complex systems perspective [1]. Neuronal cultures are spontaneously active, i.e., they elicit network-wide action potentials without any external input. This activity is grounded on the intrinsic neuronal dynamics, biological noise, and connectivity between neurons. The latter can be dictated and perturbed by using neuroengineering tools, offering the possibility to alter structural network layout and observe the corresponding changes in network activity [2]. Such activity can be monitored by using different experimental techniques that allow us to track the behavior of thousands of neurons. Although neuronal cultures offer a fascinating 'network neuroscience' playground, full controllability of connectivity is very difficult and experimentalists have to deal with unexpected surprises, such as plasticity or homeostatic behavior. In this talk I will present some examples of engineered neuronal cultures and their monitoring through either calcium imaging or high-density multielectrode arrays. Next, I will show how the analysis of the repertoire of activity patterns serves as proxy to quantify neuronal network connectivity and its changes upon development or even disease. Finally, I will provide examples of the use of chemical or electrical stimulation to alter the dynamic repertoire of the networks and induce plasticity, an aspect of great importance to investigate computation in vitro.

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- [2] Montalà-Flaquer M., López-León C.F., Tornero D., Houben A.M., Fardet T, Monceau P., Bottani S., Soriano J. Rich dynamics and functional organization on topographically designed neuronal networks in vitro. iScience 26, 105680 (2022). DOI: 10.1016/j.isci.2022.105680.

Consistent community detection and model selection in the Stochastic Block Model

Florencia Leonardi

Universidade de São Paulo, Brasil.

In this talk, I will present recent results on the consistency of methods based on maximum and integrated likelihood to detect communities and estimate the number of communities in the Stochastic Block Model. The results are optimal in the sense that strong consistency is achieved above the phase transition threshold, in the logarithmic degree regime.

This is a joint work with Andressa Cerqueira (UFSCAR) and Catherine Matias (Sorbonne Université).

Violence, City Size and Geographical Isolation in African Cities

Ronaldo Menezes

University of Exeter, United Kingdom.

Violence is commonly linked with large urban areas, and it is presumed to scale superlinearly with population size. This study explores the hypothesis that smaller, isolated cities in Africa may experience a heightened intensity of violence against civilians. It aims to investigate the correlation between the risk of experiencing violence, a city's size and its geographical isolation. Over 20 years, the incidence of civilian casualties has been analysed to assess lethality in relation to varying degrees of isolation and city sizes. African cities are categorised by isolation (number of highway connections) and centrality (the estimated frequency of journeys). Findings suggest that violence against civilians exhibits a sublinear pattern, with larger cities witnessing fewer events and casualties per 100,000 inhabitants. Remarkably, individuals in isolated cities face a quadrupled risk of a casualty compared to those in more connected cities.

Lost in averaging: local and global intermittencies in complex networks

Inmaculada Leyva

Complex Systems Group & GISC - Universidad Rey Juan Carlos, Spain.

Laboratory of Biological Networks - Centre for Biomedical Technology, Spain.

The study of collective dynamics in complex networks has significantly advanced our understanding of how local interactions give rise to emergent phenomena such as synchronization, criticality, and pattern formation. Most research to date, however, has focused on the strongly coupled regime, where coherent global behaviors dominate. This emphasis has overshadowed the rich and complex dynamics that unfold in weakly coupled systems, where many natural and engineered systems actually operate. In this regime the systems exhibit a diverse repertoire of transient and intermittent behaviorsâĂŤincluding on-off synchronization, metastable switching, and, most notably, chaotic itinerancy. These intermittent regimes play essential functional roles in systems ranging from sensory processing in the olfactory cortex to perceptual switching and adaptive locomotion in robotics. We aim to address this gap by investigating how the topological features of complex networks shape the emergence, structure, and persistence of the intermittencies in weakly coupled oscillator systems. Our results highlight how structural heterogeneity and connectivity patterns modulate the system's ability to explore diverse dynamical states, offering new insights into the interplay between network architecture and functional complexity.

Eco-evolutionary constraints shape the endemicity and epidemic trajectories of rapidly evolving viruses

David Soriano-Paños

Universitat Rovira i Virgili, Spain

Antigenic escape constitutes the main mechanism allowing rapidly evolving viruses to achieve endemicity. Beyond granting immune escape, empirical evidence also suggests that mutations of viruses might increase their inter-host transmissibility. While both mechanisms are well-studied individually, their combined effects on viral endemicity remain to be explored. In this talk I will introduce a minimal eco-evolutionary framework to simulate epidemic outbreaks generated by pathogens evolving both their infectiousness and immune escape.

With this model, I will first show that contagions at the population level constrain the effective evolution of the virus, accelerating the increase in infectiousness in the first epidemic wave while favoring antigenic variation in the transition to the endemic phase. I will explain why the interplay between both evolutionary pathways favours the endemicity of viruses with lower baseline infectiousness. Finally, I will show that the networked structure of the antigenic space produces seasonal epidemic trajectories which capture the evolution of rapidly evolving viruses such as the H3N2 virus.

Structure, Dynamics, and Prediction in Political Corruption Networks

Sebastián Gonçalves

Instituto de Física - Universidade Federal do Rio Grande do Sul, Brasil

Political corruption networks are complex and evolve dynamically, with gender-related structural differences emerging only under specific conditions. In this talk, we present an integrated analysis of recent studies on corruption networks in Brazil and Spain, spanning nearly three decades of political scandals. We uncover universal structural features -including exponential degree distributions, significant modular structure, and assortative mixing patterns- as well as dynamic mechanisms driven by recidivist actors that govern network evolution. We examine gender disparities in participation and centrality, showing that although women are underrepresented, their structural roles are similar to those of men, and gender has no significant effect on network resilience under node removal. Leveraging graph-based machine learning and deep learning techniques, we demonstrate that it is possible to recover missing links, predict future criminal associations, and infer the intensity and type of interactions among agents with high accuracy. We also identify key agents whose central roles influence the cohesion and evolution of the networks. Our findings not only enhance the understanding of political corruption as a networked phenomenon but also suggest algorithmic tools for early detection and prevention of systemic corruption.

LANET School Sessions

Introducción a los sistemas complejos y redes - Johann Martínez

Universidad Rey Juan Carlos, Spain

Belief-propagation algorithm: application of the Ising model on

networks with arbitrary distributions of motifs - José Fernando

Mendes

University of Aveiro, Portugal

We extend the belief-propagation algorithm to random networks that contain complex structures

like triangles, loops, and cliques. These networks are modeled as hypergraphs, where each motif

(such as a loop or clique) is treated as a hyperedge connecting multiple nodes. This approach

keeps the networks sparse and tree-like at a higher level, making it possible to apply belief

propagation even in the presence of loops. Using this framework, we study the ferromagnetic

Ising model and derive exact results, including the critical temperature for the phase transition.

Interestingly, we find that higher clustering and larger motifs lead to an increase in the critical

temperature compared to traditional tree-like networks. However, small amounts of clustering

do not qualitatively affect the phase behavior. Our method also allows us to pinpoint the exact

emergence of the giant connected component in these networks.

Dinámica de redes - Jesús Gómez-Gardeñes

Universidad de Zaragoza, Spain

Implementación Electrónica de Redes Complejas. Experimentos

y Ciencia abierta - Ricardo Sevilla Escoboza

Universidad de Guadalajara, México

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Parallel Sessions

Tuesday morning - PA01 (Room 7)

Distributed Saddle Point Dynamics for Constrained Resource Allocation Problems in Multiplex Networks

Christian D. Rodriguez-Camargo, Andres F. Urquijo-Rodriguez, and Eduardo Mojica-Nava

Universidad Nacional de Colombia

Resource allocation in multiplex networks is a critical challenge in various domains, including transportation, communication, and energy systems. This paper investigates the problem of constrained resource allocation for multiplex networks, where resources must be optimally distributed across multiple interconnected layers while adhering to system constraints. We present a mathematical formulation of the problem, incorporating capacity limitations, priority constraints, and inter-layer dependencies. To address computational complexity, we propose an efficient optimization framework that utilizes a saddle-point dynamics algorithm. In this work, we extend previous results on saddle point dynamics in multiplex networks to address the resource allocation problem, incorporating coupling constraints between inter- and intra-layer nodes. We provide a theoretical analysis proving the convergence of the proposed algorithm with the optimal solution. A multienergy system as a multiplex network is used to illustrate the applicability of the proposed theoretical results.

Anticipating Explosive Synchronization via Local Ordinal Entropy Measures

Juan A. Almendral^{1,2}, I. Leyva^{1,2}, C. Letellier³, I. Sendiña-Nadal^{1,2}

- (1) Universidad Rey Juan Carlos, Complex Systems Group & GISC, Móstoles, Spain.
 - (2) Universidad Politécnica de Madrid, CTB, Pozuelo de Alarcón, Spain.
- (3) Rouen Normandie Universite-CORIA, Campus Universitaire du Madrillet, Saint-Etienne du Rouvray, France.

Explosive synchronization (ES) in complex networks poses major challenges for prediction due to their abrupt nature and lack of early signs in global system observables. In this work [1], we introduce a local, data-driven approach based on ordinal pattern transition (OPT) entropy to anticipate ES in a range of networked dynamical systems. Focusing on time series from individual nodes, we show that OPT entropy measured at central or highly connected nodes rises well before the onset of synchronization, outperforming traditional early warning indicators such as autocorrelation and fluctuation amplitude. We demonstrate the method's effectiveness in systems of coupled phase oscillators, Chialvo maps, and chaotic Rössler oscillators, including real-world experiments with chaotic electronic circuits. The results underscore the power of ordinal-based methods for capturing subtle changes in temporal dynamics and highlight their relevance in scenarios where global observables are inaccessible or unreliable. This framework holds promise for real-time monitoring of critical transitions in diverse fields including neuroscience, climate science, and infrastructure networks.

[1] Leyva, I.; Almendral, J.A.; Letellier, C.; Sendiña-Nadal, I. Local Predictors of Explosive Synchronization with Ordinal Methods. Entropy 2025, 27, 113 (doi.org/10.3390/e27020113).

Una Nueva Medida para Caracterizar las Estructuras de Ciclos en Redes Complejas

Kevin Nicolás Ramos Guasca, <u>María Elizabeth Mesa Pineda</u>, Juan Camilo Higuera Calderón

Universidad Nacional de Colombia, Colombia

Este artículo propone una nueva medida llamada Enredamiento (R) para cuantificar el grado de acoplamiento entre ciclos irreducibles en redes complejas, definidos como aquellos ciclos simples que no pueden descomponerse en ciclos más pequeños. A diferencia de las métricas tradicionales basadas en caminos (como centralidad de grado, intermediación o cercanía), que suelen correlacionarse fuertemente entre sí, R captura información estructural independiente al medir el solapamiento de aristas entre ciclos, revelando nuevos patrones que no capturan las anteriores medidas. Utilizando redes de Watts-Strogatz, demostramos que R aumenta con la densidad y aleatoriedad de la red, pero se satura tras un umbral crítico, mostrando un comportamiento que contrasta con las medidas clásicas. Esta métrica ofrece una perspectiva innovadora para analizar sistemas donde los ciclos son funcionalmente relevantes (como redes biológicas o tecnológicas), proporcionando insights sobre robustez, modularidad y dinámicas emergentes aproximaciones alto. que otras pasan

Tuesday morning - PA02 (Room 8)

Network metrics reveal ecosystem age as a key driver of food web assembly in Greenland ponds

<u>Anahí López-Rodríguez</u>^{1,2,3}, Erik Jeppesen^{4,5,6,7}, Thomas A. Davidson^{4,5}, Luc De Meester^{8,9,1}, Iván González-Bergonzoni², Nicolás Vidal¹¹, Ruben Sommaruga¹², Korhan Özkan^{4,13}, Hartmut Arndt¹⁴, Klaus Jürgens¹⁵, Mariana Meerhoff^{1,4,8}

- (1) Department of Ecology and Environmental Management, Centro Universitario Regional del Este, Universidad de la República, Uruguay.
 - (2) Departamento de Ciencias Biológicas, CENUR Litoral Norte, Universidad de la República, Uruguay.
- (3) Departamento de Ecología y Biología Evolutiva, Instituto de Investigaciones Biológicas Clemente Estable, Uruguay.
 - (4) Department of Bioscience, Aarhus University, Denmark.
 - (5) Arctic Research Centre, Aarhus University, Denmark.
 - (6) Sino-Danish Education and Research Centre Beijing, China.
 - (7) Limnology Laboratory, Department of Biological Sciences and Centre for Ecosystem Research and Implementation, Middle East Technical University, Ankara, Turkey.
 - (8) Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB), Germany.
 - (9) Laboratory of Freshwater Ecology, Evolution and Conservation, Belgium.
 - (10) Institute of Biology, Freie UniversitÃdt Berlin, Germany.
 - (11) Departamento de Ecología y Evolución, Facultad de Ciencias, Universidad de la República, Uruguay.
- (12) Lake and Glacier Research Group, Department of Ecology, University of Innsbruck, Innsbruck, Austria.
 - (13) Institute of Marine Sciences, Middle East Technical University, Turkey.
 - (14) University of Cologne, Institute for Zoology, Germany.
 - (15) Leibniz Institute for Baltic Sea Research, Germany.

Arctic ecosystems are undergoing major changes as a result of climate change that in many cases results in habitat loss for many species. However, glacial retreat also creates new habitats, such as lakes and ponds, providing an opportunity to test how communities and food webs assemble. Here, we studied the network structure of the food webs analysing potential drivers such as environmental variables in 16 fishless ponds of contrasting age (8 young <50 years, 8 old >150 years) located in an area of rapid glacial retreat on the west coast of Greenland. We tested for differences in beta diversity and nestedness of prey and consumers related to the age class of the ponds. Based on gut content analysis of zooplankton and benthic macroinvertebrates we

constructed food webs and investigated the extent to which network metrics related to pond age and environmental variables. The food items of pelagic and invertebrates in the young ponds represented a subset of those present in the old ponds' food webs. Food webs of old ponds had higher taxonomic richness, higher linkage density and lower connectance, indicating higher stability. Pond age class was the main explanatory factor for most food web metrics followed by productivity, here assessed by proxies total nitrogen (TN) and phytoplankton chlorophyll-a (Chl-a). Food webs in old ponds did not show any significant association with environmental factors. In contrast, in young ponds, connectance, trophic niche overlap, and trophic web length were significantly related to TN and Chl-a, and trophic web length was also related to pond surface area. The different complexity patterns indicate that food web structure in newly created ponds becomes more complex and independent of environmental conditions as ponds age. These differences likely make food webs of new ecosystems more unstable and vulnerable to external disturbances than those of older ecosystems

Hotspot areas of mass effect and regional connectivity throughout the freshwater landscapes of South America

<u>Ana I. Borthagaray</u>^{1,2}, Reichmann Florencia¹, De León Agustin^{1,2}, Agosto Bruno^{1,2}, Cunillera-Montcusí David³, Bou Jordi⁴ & Arim Matias^{1,2}.

- (1) Departamento de Ecología y Gestión Ambiental, Centro Universitario Regional del Este, UdelaR, Uruguay.
 - (2) Centro Interdisciplinario en Ciencia de Datos y Aprendizaje Automático (CICADA), UdelaR, Uruguay.
 - (3) Institute of Aquatic Ecology. HUN-REN Centre for Ecological Research, Hungary.
 - (4) LAGP, Flora and Vegetation, Institute of the Environment, University of Girona, Spain

Connectivity is key for biodiversity persistence and the maintenance of ecological functions in the long term and at a global scale. Well-connected landscapes enable individuals to move and respond to climatic changes. However, explicit approaches for quantifying the functional role of different areas in biogeographic connectivity have been elusive. Freshwaters are spatially structured ecosystems critically endangered because of human activities and global change. Mass effects-the increase in local diversity by immigration- and corridor effects-the connections with distant communities- are basic and relevant mechanisms connecting diversity with landscape configuration. Herein, we used a network-based approach to identify freshwater hotspots areas for mass and corridor effects across South America. Using satellite images, we represent the landscape structure of ephemeral, temporal and permanent freshwaters as directed graphs with weighted links by the distance between cells and the water cover. Three centrality metrics were used to rank freshwater areas with respect to their potential role in dispersal-mediated mechanisms. Out-degree represents the potential of an area to operate as a diversity source to other regions, in-degree reflects the importance that incoming dispersal may have in local diversity, and betweenness refers to the importance of local areas for connecting other distant areas. We identified main rivers acting as ecological corridors for all freshwater types, and a mixed distribution of connectivity hotspots in southern-west ecoregions, associated with lentic and lotic systems. We propose a broad scale connectivity map of the freshwater habitats of South America, identifying potentially relevant areas for dispersal-mediated mechanisms. While many conservation strategies focus on identifying isolated areas based on focal species, our study identified regions based on their role in promoting freshwater connectivity at a continental extent.

Animal Social Networks and the Dynamics of Information Transmission

Bárbara Seaman¹, Cristobal Quiñinao¹, Pablo Marquet^{1,2,3}

- (1) Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile.
- (2) Centro de Modelamiento Matemático (CMM), Universidad de Chile, International Research Laboratory, CNRS, Chile.
 - (3) Santa Fe Institute, 1399 Hyde Park Road, Santa Fe, NM 87501, USA.

The role of animal social networks (ASN) in maintaining efficient communication within groups has been of growing interest in recent years. Here, we test the hypothesis that ASNs, exhibit structural patterns that optimize the efficiency and fidelity of information transmission. To test this, two approaches are used. Firstly, structural patterns and dynamics of ASN of different taxa and group sizes are explored, with the aim of determining regularities associated with group living. Secondly, temporal explicit simulations are used to test optimal topologies in relation to different rates of communicational noise and group sizes. The results indicate that ASNs generally present structural regularities in line with social selection pressures, suggesting that they play an important role in group communication. These findings have implications for understanding the stability and survival of social groups.

Tuesday afternoon - PA03 (Room 7)

Anticipating explosive synchronization in networks of Kuramoto oscillators

Juan Gancio¹, Giulio Tirabassi², Cristina Masoller¹

(1)Universitat Politècnica de Catalunya, Spain.

(2)Universitat de Girona, Spain.

Many complex systems experience sudden changes in their dynamics as they transition between different states when a control parameter is varied. The threshold value of the parameter for which an abrupt transition occurs is known as "tipping point". For real-world systems, such as animal populations, vegetation fields, and the climate, there is a particular interest in being able to detect if a tipping point is approaching, since once crossed the systems may not recover the previous stable state. An example of a sudden change is explosive synchronization (ES), an abrupt transition between a disorder state and a synchronous one, characterized by being of first-order. In this work, we propose several quantifiers based on the permutation entropy (PE) that present a particular behavior when the network approaches a synchronous state. PE is a time series analysis technique that uses symbols (ordinal patterns) defined by the ordering of the data points, disregarding the actual values, and has recently been proposed as a new indicator for critical transitions. We test this new method in different networks of Kuramoto phase oscillators linked in such a way that they present ES. We observe substantial and characteristic changes in these quantities as the networks approach synchronization, even when the synchronization is explosive. Therefore, PE-based quantities can serve as early warning signals (EWS) of this class of transitions. Our results complement previous findings regarding PE methods for EWS of critical transitions, expanding their applications to systems characterized by complex temporal behaviors.

Online Change Point Detection for Weighted and Directed Random Dot Product Graphs

 $\underline{\text{Bernardo Marenco}}^{1,2},$ Paola Bermolen 1,2 , Marcelo Fiori $^{1,2},$ Federico Larroca $^{1,2},$ Gonzalo $\underline{\text{Mateos}}^3$

- (1) Facultad de Ingeniería, Universidad de la RepÞblica, Uruguay.
- (2) Centro Interdisciplinario en Ciencia de Datos y Aprendizaje AutomÃątico (CICADA), Universidad de la República, Uruguay.
 - (3) Deptartment of Electrical and Computer Engineering, University of Rochester, USA

Given a sequence of random (directed and weighted) graphs, we address the problem of online monitoring and detection of changes in the underlying data distribution. Our idea is to endow sequential change-point detection (CPD) techniques with a graph representation learning substrate based on the versatile Random Dot Product Graph (RDPG) model. We consider efficient, online updates of a judicious monitoring function, which quantifies the discrepancy between the streaming graph observations and the nominal RDPG. This reference distribution is inferred via spectral embeddings of the first few graphs in the sequence. We characterize the distribution of this running statistic to select thresholds that guarantee error-rate control, and under simplifying approximations we offer insights on the algorithm's detection resolution and delay. The end result is a lightweight online CPD algorithm, that is also explainable by virtue of the well-appreciated interpretability of RDPG embeddings. This is in stark contrast with most existing graph CPD approaches, which either rely on extensive computation, or they store and process the entire observed time series. An apparent limitation of the RDPG model is its suitability for undirected and unweighted graphs only, a gap we aim to close here to broaden the scope of the CPD framework. Unlike previous proposals, our non-parametric RDPG model for weighted graphs does not require a priori specification of the weights' distribution to perform inference and estimation. This network modeling contribution is of independent interest beyond CPD. We offer an open-source implementation of the novel online CPD algorithm for weighted and direct graphs, whose effectiveness and efficiency are demonstrated via (reproducible) synthetic and real network data experiments.

Robustness analysis of public transportation networks and the relationship between topology and mobility in latin american cities

Tomás Cicchini^{1,2}, Marta C. González^{5,6}, Inés Caridi^{1,4}, Leonardo Ermann^{3,4}

- (1) CONICET-Universidad de Buenos Aires, Facultad de Ciencias Exactas y Naturales, Instituto de Cálculo (IC), Argentina.
- (2) Universidad de Buenos Aires, Facultad de Ciencias Exactas y Naturales, Departamento de Física, Argentina (3) Dto FT, GIyA, Comisión Nacional de Energía Atómica, Argentina.
 - (4) CONICET, Argentina
 - (5) Department of Civil and Environmental Engineering, University of California, USA.
 - (6) Department of City and Regional Planning, University of California, USA

The systematic study of public transportation systems is essential to address the challenges faced by large cities nowadays. Analyzing these systems using complex networks allows for a focus on key aspects such as robustness, hubs detection, etc.. Given the nature of transport systems, several types of networks can be constructed [1], for example: the \mathbb{L}' -space, where nodes represent stops and edges connect consecutive stops along routes; and the C-space, where nodes represent routes and edges connect routes that share stops. This dual representation enables the study of robustness through a combined approach [2]: identifying central nodes in the C-space (routes with high centrality) and removing the corresponding edges in the L'-space to analyze topological effects, particularly the size of the giant component, S_1 , and the average shortest path length, aspl. This framework can simulate scenarios such as the discontinuation of a route due to operator bankruptcy, strikes, or public policy decisions. To assess how such disruptions affect urban mobility, origin-destination matrices can be used to evaluate the fraction of feasible, t_1 , trips and their efficiency t_2 . Interestingly, this comparative analysis of topology and mobility shows that t_1 behaves similarly to S_1 . Likewise, t_2 follows a trend analogous to that of the aspl. This structuralmobility relationship could be relevant for data-informed urban planning. We apply this framework to case studies from three Latin American cities: Buenos Aires, Mexico City, and Rio de Janeiro.

Tuesday afternoon - PA04 (Room 8)

Similarity, Complex Networks, and Machine Learning in Pharmacologically Relevant Molecule Discovery

Roberto Bernal Jaquez¹, Elliot Ridout-Buhl², Emiliano Montoya³, León Alday-Toledo^{3,4}, Felipe Aparicio²

- (1) Departamento de Matemáticas Aplicadas y Sistemas, Universidad Autónoma Metropolitana Cuajimalpa, México.
- (2) Departamento de Ciencias Naturales, División de Ciencias Naturales e Ingeniería, Universidad Auónoma Metropolitana, Unidad Cuajimalpa, México.
- (3) Posgrado en Ciencias Naturales e Ingeniería, División de Ciencias Naturales e Ingeniería, Universidad Autónoma Metropolitana, Unidad Cuajimalpa, México.

(4) Independent Researcher

In recent years, we have witnessed the emergence of vast structural databases containing billions of molecules, most of which lack detailed physicochemical or pharmacological data. The discovery of new materials and drugs now hinges on efficiently identifying candidate molecules within these immense search spaces-molecules that meet specific similarity criteria with compounds of known properties and validated bioactivity. To address this challenge, we employ both supervised and unsupervised machine learning techniques to extract structural patterns from bioactive molecules and cluster collections of compounds with shared properties. In this work, we demonstrate an innovative approach to molecular vectorization using natural language processing (NLP) methods, encoding chemical information into fixed-length numerical vectors. This facilitates the application of machine learning models to diverse chemical problems, complementing traditional methods such as extended connectivity fingerprints. Furthermore, we show that accurate classification and clustering of large molecular datasets can only be achieved in non-Euclidean spaces. Our findings reveal that the performance of common algorithms (such as k-means) is highly dependent on the choice of metric. By applying the Mahalanobis distance-which accounts for molecular correlationsto a subset of the GDB17 database, we construct complex networks with nontrivial topological properties (e.g., community formation). This approach yields well-defined clusters that group structurally similar molecules with closely aligned electronic properties. Our results highlight the critical role of metric selection and open new avenues for efficient large-scale molecular exploration.

Does the service sector stimulate economic growth? A novel approach with machine learning using US Input-Output data

Santiago Picasso

Universidad de la República, Uruguay

A stylized fact in modern economies is that the more developed a country is, the greater the weight of the service sector. In this sense, the study of economic complexity through the standard measure of complexity index presents an increasingly relevant omission to understand the economic process and its growth. This paper proposes a new methodology to retrieve information on economic complexity in services. For this purpose, the US input-output matrix is used. This work is novel because, thanks to the structure of the data as a network, it is possible to infer the missing information of complexity of services at a level of disaggregation that is strikingly higher than in other works. Using the k-NN method, it is possible to learn 146 services sector complexity index. The index recuperated by this method is consistent with previous work and this index is highly correlated with the GDP of States and US economy.

Redes complejas aplicadas al análisis del transporte público intermunicipal, Caso de estudio: el deparatamento del Quindío en Colombia

Mónica Jhoana Mesa Mazo, Jorge Mario García Usuga

Universidad del Quindío, Colombia.

Esta investigación presenta un análisis del sistema de transporte público intermunicipal en el departamento del Quindío en Colombia a partir del enfoque de redes complejas. Utilizando las librerías OSMnx y NetworkX en Python, se modeló la red vial del departamento para evaluar su conectividad, identificar rutas críticas y zonas vulnerables, y proponer estrategias que mejoren la toma de decisiones por parte de los organismos de tránsito. La metodología se dividió en dos fases: primero, se construyó un subgrafo que representa la zona centro de Armenia, y posteriormente, se modeló la red vial completa del departamento. El análisis reveló una red con 9132 nodos y 20.745 aristas, evidenciando características típicas de redes viales jerárquicas. Se aplicaron tres medidas clave de centralidad: centralidad de grado, que identificó nodos con muchas conexiones directas; centralidad de cercanía, que resaltó los nodos con acceso más eficiente al resto de la red; y centralidad de intermediación, que mostró qué nodos actúan como puentes cruciales en la conectividad global. Estas métricas permitieron detectar zonas estratégicas como Armenia, Calarcá y La Tebaida, y también municipios con baja conectividad como Génova y Salento, los cuales son más vulnerables a interrupciones y desastres naturales. El estudio concluye que, aunque el Quindío cuenta con una red vial funcional, enfrenta retos significativos en términos de interconectividad y resiliencia. Las rutas Armenia-La Tebaida, Armenia-Pereira, Calarcá-Valle y Armenia-Quimbaya son claves para mantener la cohesión vial. La teoría de redes se muestra como una herramienta eficaz para diseñar intervenciones en infraestructura y fortalecer la planeación estratégica del transporte, permitiendo una mayor eficiencia y sostenibilidad del sistema.

Modelamiento de parámetros físico químicos de aguas superficiales con Redes Complejas: de estudio Departamento del Quindío-Colombia

Jorge Mario García Usuga¹, Mónica Jhoana Mesa Mazo²

(1)Universidad del Quindío, Colombia.

(2) Corporación Universitaria Empresarial Alexander von Humboldt, Colombia.

La medición de nitrógeno y fosfato en cuencas hidrográficas es fundamental para la gestión y conservación de los recursos hídricos, ya que estos parámetros son indicadores clave de la calidad del agua. El exceso de nitrógeno y fosfato puede causar contaminación y eutrofización, sumado a que la temperatura del agua refleja los efectos del cambio climático y actividades humanas. Monitorear estos elementos ayuda a proteger la biodiversidad, asegurar la calidad del agua potable y mitigar los impactos del cambio climático. Estos datos son cruciales para tomar decisiones informadas en la gestión de los recursos hídricos, y desarrollar herramientas de software para predecir su comportamiento es esencial para los organismos de control. Es por esta razón que evaluar el contenido de estos parámetros y desarrollar una herramienta de software que permita predecir y modelar su contenido y comportamiento es esencial para la toma de decisiones de los organismos de control.

Para la creación de la red compleja se tomaron como punto de partida la red o grafo construido en [1,2,3], el cual presenta una red dirigida de 409 nodos y 408 aristas que representa la red hidrográfica del departamento del Quindío. Para modelar el transporte de partículas en el agua en específico el Nitrógeno, se utiliza el modelo de Nitrificación [4,5].

$$\frac{dN_0}{dt} = -k_{oa}N_0$$

$$\frac{dN_a}{dt} = k_{oa}N_0 - k_{ai}N_a$$

$$\frac{dN_i}{dt} = k_{ai}N_a - k_{in}N_i$$

$$\frac{dN_n}{dt} = k_{in}N_i$$
(1)

Donde N_o , N_a , N_i , N_n denotan nitrógeno orgánico, amoniaco, nitritos y nitratos respectivamente. K_{oa} , k_{ai} , k_{in} son constantes de nitrificación. Ahora bien, con respecto a los fosfatos Chapra [5] proponen un modelo basado en ecuaciones diferenciales ordinarias para el fósforo orgánico:

$$\frac{dp_{org}}{dt} = \pi p A - K_{p,org} P_{org} - K_{p,settl} P_{org}$$
 (2)

Donde P_{org} es la concentración de fósforo orgánico, A es la concentración de amoníaco, π es el porcentaje de fósforo contenido en algas, $k_{P,org}$ la velocidad de decaimiento del fósforo orgánico, $k_{P,settl}$ la velocidad de sedimentación del fósforo orgánico. Con estas ecuaciones se modela ambos parámetros de calidad del agua, dando informaci \tilde{A} şn a la red sobre cómo estas se distribuyen en toda la cuenca.

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Wednesday morning - PA05 (Room 7)

Exact solutions of the Kuramoto model with asymmetric higher order interactions of arbitrary order

<u>Guilherme S. Costa</u>¹, Marcel Novaes^{2,3}, Marcus A. M. de Aguiar^{1,3}.

- (1) ICTP South American Institute for Fundamental Research & IFT UNESP, Brasil.
 - (2) Instituto de Física, Universidade Federal de Uberlândia, Brasil.
 - (3) Instituto de Física Gleb Wataghin, Universidade Estadual de Campinas, Brasil.

Higher order interactions can lead to new equilibrium states and bifurcations in systems of coupled oscillators described by the Kuramoto model. However, even in the simplest case of 3-body interactions there are more than one possible functional forms, depending on how exactly the bodies are coupled. Which of these forms is better suited to describe the dynamics of the oscillators depends on the specific system under consideration. Here we show that, for a particular class of interactions, reduced equations for the Kuramoto order parameter can be derived for arbitrarily many bodies. Moreover, the contribution of a given term to the reduced equation does not depend on its order, but on a certain effective order, that we define. We give explicit examples where bi and tri-stability is found and discuss a few exotic cases.

Semantic Networks from Word Free Association: Structure and Psycholinguistic Applications

Álvaro Cabana.

Facultad de Psicología and CICADA, Universidad de la República, Montevideo, Uruguay.

Semantic networks built from free association data offer an ecologically valid and empirically grounded approach to modeling the structure of meaning in the mental lexicon. In these networks, nodes represent words and links encode spontaneous associative responses collected in word production tasks (Nelson, McEvoy & Schreiber, 2004; De Deyne & Storms, 2008). Unlike co-occurrence-based networks, free association captures direct semantic relationships grounded in speakers' subjective experience. These networks exhibit hallmark features of complex systems-including heavy-tailed degree distributions, semantic modularity, short path lengths, and high clustering-and network metrics such as degree, betweenness, and eigenvector centrality have been shown to strongly correlate with lexical frequency and predict behavioral data such as lexical decision times, reaction times in naming tasks, and memory retrieval (De Deyne et al., 2013; Cabana et al., 2024). Beyond their structural properties, these networks enable the construction of word embeddings through dimensionality reduction techniques such as singular value decomposition, resulting in high-dimensional vector spaces that reflect cognitively meaningful semantic structure. These embeddings have high psycholinguistic validity and can be used to model semantic similarity, priming effects, and lexical access. Moreover, applying unsupervised clustering methods to these embeddings allows for the derivation of objective, corpus-free measures of lexical ambiguity-capturing, for instance, the number and distribution of distinct semantic senses associated with a given word-thus providing a novel approach to studying polysemy and meaning dominance in natural language. We present recent normative data for Rioplatense Spanish (Cabana et al., 2024) and show how alternative construction strategies (e.g., single vs. multiple response formats, weighted vs. binary edges) influence both the topological structure of the network and the distributional properties of the embeddings.

Wednesday morning - PA06 (Room 8)

Diffusion analysis of inflationary shocks in the Mexican economy. A study using dynamic network analysis

Martha Alatriste-Contreras¹, Emiliano Alvarez².

(1) Departamento de Economía, UNAM, Mexico;

(2) FCEA, UdelaR, Uruguay

This paper analyzes the impacts of shocks on the price system of the economy. We investigate how variations in retail prices, in the exchange rate, and policy interventions affect the diffusion of inflationary pressures in Mexico, based on open data from the Consumer Price Index. We propose to analyze the processes of price formation and diffusion through network techniques. Empirical results allow us to identify the most relevant nodes in the price network of the Mexican economy. Results also show a dynamic network structure that evolves according to a core-peripheric structure, with important implications for the policies that are usually applied against inflation. The network analysis based on price correlations using the T-MDS methodology and a sensitivity analysis revealed that results are robust to adjustments in the threshold value. Finally, the examined dynamic network measures are related to the rate of inflation and rapid fluctuations in the official exchange rate. We found that staple foods are highly relevant to the network's structure based on several centrality measurements.

Measuring the structural evolution of street networks

Juan Antonio Pichardo-Corpus

El Colegio de la Frontera Norte, México.

The proposal examines the evolution of cities through their street networks by utilizing centrality measures, particularly betweenness centrality. These measures relate to economic activity distribution, architectural changes, and urban mobility. Although significant findings support the use of centrality measures in urban analysis, questions remain about the underlying structures within street networks. This research focuses on quantifying structural changes in the form of central loops. Topological methods such as persistent homology are applied to quantify visual patterns, with Betti numbers proposed to measure holes in urban structures. The study examines Paris's street network before and after the 19th-century Haussmann project, comparing the number of fundamental cycles with Betti-1 to analyze structural changes. It finds stable patterns of Betti-1 in the network before and after Haussmann's changes, while fundamental cycles show large variations. The approach effectively highlights differences in structural evolution, particularly when comparing the networks before and after Haussmann's interventions.

Connectivity can increase biodiversity resistance to pollution or magnify its impact if equalizing mechanisms are eroded

Agustin de León^{1,2}, Ana I. Borthagaray^{1,2}, Matías Arim^{1,2}.

- (1) Departamento de Ecología y Gestión Ambiental, Centro Universitario Regional del Este, UdelaR, Uruguay.
 - (2) Centro Interdisciplinario en Ciencia de Datos y Aprendizaje Automático (CICADA), UdelaR, Uruguay.

The environmental impact of pollutants on biodiversity is often viewed as a local process, neglecting the role of organism dispersal across landscapes. Pollutants dissolve into the environment, creating a disturbance gradient across communities. Dispersal can mitigate local impacts or propagate changes to the larger metacommunity. However, there is no comprehensive framework to understand the interplay between local and regional pollutant effects through metacommunity processes. We used the Maldonado River basin in Uruguay as a model, focusing on a wetland ecosystem influenced by pollutants from four wastewater treatment plants. Using metacommunity simulations with varying pollutant discharge and species dispersal ability, we explored two mechanisms linking pollutant concentration to community assembly: a reduction in community carrying capacity, equally affecting all species, and traitbased filtering due to differences in species tolerance. The interaction between pollutant impact mechanisms, species dispersal capacity, and community connectivity emerged as a key determinant of regional biodiversity outcomes. Notably, the connectivity-pollutant interaction changed depending on whether the pollutant affected species performance or reduced carrying capacity, driving either degradation or resistance to diversity. Furthermore, the extent of the pollutant's geographic impact influenced how connectivity affected biodiversity. Dispersal capacity also influenced these alternative effects. Finally, biodiversity changes due to pollutants were not monotonically related to distance from the pollution source. These results provide important insights for ecosystem management. Biodiversity impacts are influenced by species vulnerability and dispersal patterns. Local bioassays cannot be scaled to assess biodiversity threats without considering metacommunity dynamics. Distance from pollutant sources may not accurately reflect true biodiversity impacts. Lastly, connectivity should be integrated when evaluating disturbance effects. Our findings suggest that pollutant impacts on biodiversity may be misrepresented in monitoring programs that fail to account for metacommunity effects.

Thursday morning - PA07 (Room 7)

Modelo matemático para la propagación del VIH en una población con estructura de edad y condiciones de riesgo asociadas

<u>Francisco Andrés Betancourt Arteaga</u>, Hernán Darío Toro Zapata, Jorge Mario García Usuga Universidad del Quindío, Colombia.

La Teoría de Redes Complejas es un área de la matemática con bases en la teoría clásica de grafos de las matemáticas discretas. En las últimas décadas, y gracias al surgimiento de los métodos computacionales, se ha dado un desarrollo acelerado de las técnicas de análisis y se han encontrado múltiples aplicaciones a diversos problemas de la Ciencia y la Tecnología. En este sentido, en este trabajo se pretende mostrar la utilidad de las redes complejas para estudiar la dinámica de propagación del VIH en una población susceptible con estructura de edad, donde los vértices de la red representan personas; adicionalmente, se incorpora en cada vértice infectado la dinámica de infección por VIH en la escala inmunológica, en la cual se modela la interacción del virus de inmunodeficiencia humana (VIH) con el sistema inmune. Consiste en un sistema de ecuaciones diferenciales que incluye células T no infectadas, células T infectadas, células de respuesta citotóxica y partículas virales infecciosas y no infecciosas; además, el modelo considera dos intervenciones de terapia antirretroviral diferentes (ITI e IP) evaluando su efectividad. Se estudia el comportamiento de la población con la evolución de una red en la que se consideran diferentes escenarios en los que interactúan diferentes grupos de edad y se identifica su estado inmunológico en el transcurso del tiempo. Esta estructura multiescala del modelo permite condicionar la dinámica de propagación en la escala poblacional al estado particular inmunológico de los individuos y viceversa.

Impact of risk perception and mobility preferences on epidemic spread in spatially embedded agent populations

Andrés Anzo Hernéndez

SECIHTI - Investigadoras e Investigadores por México -Benemérita Universidad Autónoma de Puebla - Facultad de Ciencias Físico-Matemáticas, México.

In this study, we propose an agent-based epidemiological model implemented on a cellular automata framework to investigate how human behavior, media influence, and mobility patterns jointly affect the spread of infectious diseases. Each agent is embedded in a spatial grid and exhibits adaptive behavior based on a fuzzy risk perception mechanism. Agents assess the local risk level and, depending on their behavioral type-cooperator or defector-decide whether to increase their precaution level, which reduces infection probability at a personal cost. Mobility is modeled through two mechanisms: random movement and gravity-based relocation, where agents probabilistically choose destinations according to spatial distance and a social preference function. This reflects realistic movement constraints and mimics segregation-like patterns similar to the Schelling model. Additionally, we introduce a global noisy signal that emulates media influence-both informative and misleading-which modulates perceived risk across the entire population. We conduct extensive simulations and parametric sweeps to analyze how heterogeneity in behavior and different mobility schemes impact key epidemic indicators such as peak infection size, epidemic duration, and total number of cases. Results reveal that the coupling between local behavior and global signals induces rich dynamical regimes, including critical thresholds and phase transitions in epidemic outcomes. We identify regions in parameter space where small changes in mobility or perception rules lead to abrupt changes in disease spread. This work highlights the importance of considering both spatial constraints and adaptive human behavior when modeling epidemic processes. Our framework offers insights for the design of effective public health interventions and communication strategies during outbreaks, especially under uncertainty or misinformation. We also outline how this modeling approach can be extended to metapopulation networks, allowing for the exploration of epidemic dynamics across interconnected subpopulations with heterogeneous risk profiles and mobility links.

Theory and Applications of Pursuit-Evasion Games

Mehdi Salimi

Mathematics Department, Kwantlen Polytechnic University, Surrey, BC, Canada.

Pursuit-evasion differential games model the strategic interactions between opposing agentspursuers and evaders-within a dynamic framework governed by differential equations. This
presentation explores the development of effective pursuer strategies under geometric and integral
constraints, emphasizing the role of admissible domains that define feasible operational regions for
the players. A particular focus is given to parallel strategies, an approach where multiple pursuers
coordinate to improve capture efficiency. By refining the theoretical framework and addressing
complex constraints, this work advances both the understanding and practical applicability of
pursuit-evasion dynamics in constrained environments.

Thursday morning - PA08 (Room 8)

Electronic implementation of simplicial complexes

<u>VP Vera-Ávila</u>, RR Rivera-Durón, Miguel S Soriano-Garcia, R Sevilla-Escoboza, Javier M Buldú.

We design an experimental implementation of a simplicial complex, a complex network structure with higher-order interactions between nodes. Using a set of three Rössler-like (analog) electronic circuits under a chaotic dynamical regime, we demonstrate how the synchronization basin is enhanced by introducing higher-order interactions between the triplet of nodes, as suggested in recent theoretical works. The experiments prove that, when the coupling is introduced through the adequate variable, the synchronization area is increased. The combination of pairwise (i.e., node-to-node) with high-order (i.e., triplet) coupling is analyzed by modifying the corresponding coupling strengths σ_1 , and σ_2 . Importantly, we detail the procedure for reproducing the experimental setup and provide all datasets generated in the laboratory, in order to allow other researchers to further investigate the properties of complex networks with higher-order interactions.

Generación y transmisión no trivial de información en redes de mapas logísticos diseñados electrónicamente

Caracé Gutiérrez¹, Cecilia Cabeza¹, Nicolás Rubido².

- (1) Universidad de la República, Uruguay.
- (2) University of Aberdeen, United Kingdom.

En este trabajo, realizamos un análisis crítico de la información generada y transmitida en una implementación electrónica de mapas logísticos acoplados difusivamente. Nuestra implementación permite modificar la configuración de acoplamiento (es decir, la red) y ajustar con precisión la intensidad de acoplamiento y los parámetros del mapa, pero presenta un mínimo ruido electrónico y una heterogeneidad de parámetros mÃηnima, lo que genera comportamientos colectivos que difieren de las simulaciones numéricas. En particular, nos centramos en el análisis de dos regímenes dinámicos y su dependencia con la configuración de acoplamiento: uno donde se alcanza un máximo de información generada y transmitida (correspondiente a la sincronización de órbitas caóticas) y otro donde la información se genera pero (prácticamente) no se transmite (correspondiente al caos espacio-temporal). Utilizamos la entropía de Shannon para cuantificar la generación de información y la información mutua para cuantificar su transmisión. Para caracterizar los dos regímenes dinámicos, introducimos una entropía conjunta condicional que utiliza ambas magnitudes (entropía e información mutua) y analizamos sus valores para 60 configuraciones de acoplamiento diferentes que involucran 6 y 12 mapas acoplados. Observamos que el 90% de las configuraciones presentan sincronización caótica y el 92% caos espaciotemporal, que surge antes del régimen sincrónico caótico que requiere fuertes intensidades de acoplamiento. Nuestros resultados también destacan las configuraciones de acoplamiento que maximizan la entropía conjunta condicional en estos regímenes sin requerir un sistema densamente acoplado, lo cual tiene implicaciones prácticas (ya que introducir acoplamientos entre unidades puede ser costoso). En general, nuestro trabajo contribuye a comprender la relevancia de la estructura de red en la generación y transmisión de información en sistemas complejos.

Educational Inequities and Social Mobility in Colombia: Insights from Network-Based Analysis

Federico Úsuga Agudelo¹, Sol Mery Álvarez¹, Isabel C Hoyos² (2), Boris A Rodríguez³.

- (1) Observatorio Institucional Dirección de Planeación y Desarrollo Institucional, Universidad de Antioquia, Colombia.
- (2) Grupo de Física Teórica y Computacional, Facultad de Ciencias Básicas y Tecnologías, Universidad del Quindío, Colombia.
- (3) Grupo de Fundamentos y Enseñanza de la Física y los Sistemas Dinámicos, Facultad de Ciencias Exactas y Naturales, Universidad de Antioquia, Colombia.

This study examines structural inequalities in the Colombian education system using a methodology that combines statistical inference with complex network analysis on different spatial scales. For each one of these scales, we use 35 socio-economic, biological, and academic performance state variables as nodes in a graph, linked by conditional statistical dependencies using a Gaussian-Ising-Potts graphical interaction model, and validated through multiple correspondence analysis. Network centrality measures identify key factors perpetuating inequality, including socioeconomic stratum, school type (public or private), academic calendar (A or B), location (urban or rural), home internet access, and ethnic minority status. Our results reveal that Colombia's upper secondary education system reproduces broader social inequities. However, a gap analysis shows that public universities, such as the Universidad de Antioquia, play a significant role in reducing these barriers, acting as engines of social mobility. This work contributes to understanding the structural challenges limiting access to high-quality public higher education and highlights dynamics that could undermine the value of this critical public good.

Thursday afternoon - PA09 (Room 7)

Bridging nodes and their impact on epidemic activation mechanisms

J. C. M. Silva¹, D. H. Silva², W. Cota¹, S. C. Ferreira^{1,3}.

- (1) Universidade Federal de Viçosa, Brazil.
 - (2) Universidade de São Paulo, Brazil.
- (3) National Institute of Science and Technology for Complex Systems, Rio de Janeiro, Brazil.

Spreading processes on complex networks are often shaped not only by direct interactions among hubs, but also by indirect pathways involving low-degree nodes. Nodes that bridge key components in a network play an important role in maintaining its structure and supporting communication, and can be seen as secondary ties, indirect but impacting connections. Longrange mutual activation of hubs is a triggering mechanism, often involving the mutual activation of hubs mediated by paths made of low-degree nodes. Although common in networks, the role of these nodes when connecting hubs in epidemic activation has not been thoroughly explored. In this work, we investigate the role of secondary ties by adding degree-2 nodes that connect preferentially to hubs, using as backbone a power-law (PL) degree distribution network generated by the configuration model. Our results reveal that, in the absence of direct links among hubs, bridging nodes can mediate a feedback interaction that alters the localization and activation mechanisms of recurrent epidemic processes. This suggests that secondary ties can affect the spreading dynamics. In particular, under waning immunity – where hubs are not able to mutually infect each other through long-range interactions and a finite epidemic threshold with collective activation emerges – the presence of bridging nodes leads to a localized activation with a vanishing threshold.

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Threshold-Based Behavior and Epidemic Dynamics on Interacting Networks

Felipe Maresca^{1,2,3}, Hector Romero^{1,2}, Federico Vázquez³

- (1) Laboratorio de Genómica Evolutiva Facultad de Ciencias, Universidad de la República, Uruguay.
- (2) Centro Interdisciplinario de Ciencia de Datos y Aprendizaje Automático, Universidad de la Rep'ublica, Uruguay.
 - (3) Instituto de Cálculo, Universidad de Buenos Aires CONICET, Argentina.

The COVID-19 pandemic has highlighted the need to understand and anticipate the spread of infectious diseases, particularly the interaction between disease transmission and human behavior in response to it. Among the measures to contain an epidemic is social isolation. The decision to isolate or not involves individuals making a choice that can be influenced by social dynamics, where a person's decision is affected by those around them-resembling a contagion process. Most models used to study the temporal evolution and trends of epidemic outbreaks have overlooked human behavior. The multilayer network approach has enabled a deeper exploration of the interaction between these two dynamics. However, studies to date have mostly used simple contagion models to represent changes in social behavior, which we know does not accurately reflect reality. Our work intends to address this blind spot in the theoretical framework by using complex contagion models-also known as multiple-contact or social reinforcement models-to better capture the dynamics of isolation versus non-isolation. To do this, we use SIR models for the disease dynamics, interacting with threshold models for decision-making dynamics, where an agent changes their stance if the fraction of interacting agents holding the opposite stance exceeds a certain threshold. Depending on the parameters of these models, we see changes in the disease dynamics, affecting the final size of the epidemic, the behavioural dynamics and the peak of infected individuals. Unlike classical SIR models on networks, we observe a non-monotonous effect of infectivity on the final size of the epidemic, as the interplay between behaviour and disease transmission creates complex patterns.

Visibility graph signatures for criticality in spreading phenomena on networks

<u>Juliane T. Moraes</u>¹, Silvio C. Ferreira^{1,2}.

- (1) Departamento de Física, Universidade Federal de Viçosa, Brazil.
- (2) National Institute of Science and Technology for Complex Systems, Brazil.

Criticality can be understood as a state of a large system of interacting agents lingering at the edge between order and disorder, in which nontrivial emerging phenomena are ubiquitous. Formerly born in the realm of phase transitions in condensed matter physics at the thermodynamic equilibrium, critically has been expanded to a broad set of non-equilibrium and natural systems. Strong evidence indicates that criticality also plays a central role in biological systems as, for example, neuron firing dynamics on brain networks and animal collective motion. In this talk, we examine critical time series of the order parameter in spreading dynamics undergoing active-to-inactive phase transitions on heterogeneous networks. Different activation mechanisms near the critical point are investigated. Using the visibility graph (VG) method, we find that a disassortative degree correlation in the VG signals criticality, while assortative correlation indicates off-critical dynamics. This VG signature is confirmed for collective activation phenomena, as observed in homogeneous networks. Similarly, for localized activation driven by a densely connected hub set, identified via maximum k-core decomposition, the VG method reliably detects critical time series. However, when activation is driven by sparsely distributed hubs, criticality is obscured and only discernible in very large systems. In cases of strong structural localization due to rare regions, the VG exhibits an assortative degree correlation, characteristic of off-critical series. Thus, while macroscopic time series effectively indicate criticality in collective or maximum k-core activation, spatial localization can delay these signatures or, in extreme cases, produce false for negatives time series criticality.

Complex Networks for the Dynamic Study of Classical and Quantum Oscillators

Juan José Estrada, Isabel Hoyos, Edgar Arturo Gomez.

Grupo de Física Computacional, Unversidad del Quindío, Colombia.

In this work, we study the dynamics of three oscillators: the harmonic oscillator, the Duffing oscillator, and the Kuramoto oscillator. We examine the classical and quantum regimes of each system by representing their evolution as a complex network. In the classical case, time series are generated by numerically solving the Hamiltonian equations of motion, while in the quantum case, we solve the Schrödinger equation using a coherent quantum state with minimal uncertainty as the initial condition-this state exhibits a Gaussian distribution in phase space. From the Hamiltonian formalism, representative time series for both classical and quantum systems are obtained and mapped into networks where nodes correspond to ranked segments of the time series, using an entropy-optimized window size. Temporal evolution determines the connections between nodes. The harmonic oscillator is represented by a regular lattice with two possible degrees of connectivity, k = 2 ($p_2 = 0.29$) and k = 3 ($p_3 = 0.71$). The classical and quantum regimes for the Duffing oscillator are represented by scale-free networks with degree exponents $\gamma = 2.06$ and $\gamma = 2.08$, respectively. In the Kuramoto oscillator, a quasiregular lattice topology with the presence of hubs is observed. For the nonlinear Duffing and Kuramoto oscillators, we observe the emergence of a larger number of nodes in the quantum regime compared to the classical one, indicating a higher complexity in the way the system explores phase space.

Thursday afternoon - PA10 (Room 8)

Leveraging Protein Embeddings and Network Theory for Drug Repurposing

<u>Ariel Chernomoretz</u>^{1,2,3}, Gonzalo Giordano^{3,4}, Nicolas Yanovsky^{3,4}.

- (1) Depto de Física FCEN, Universidad de Buenos Aires, Argentina.
 - (2) INFINA (UBA/CONICET), Argentina.
 - (3) Fundacion Instituto Leloir, Argentina.
- (4) Inst. Inv. Bioquímicas de Buenos Aires (CONICET), Argentina.

The biopharmaceutical industry increasingly relies on computational approaches in drug development due to the high costs of bringing new drugs to market. In this context, in silico identification of new therapeutic uses for existing drugs, known as drug repurposing, has gained significant attention. This approach offers substantial advantages by reducing costs, mitigating risks, and shortening development timelines. This work introduces a novel drug repurposing framework that combines network theory with state-of-the-art computational techniques. We utilize Large Language Models (LLMs), originally developed for natural language processing, adapted here for analyzing protein sequences. Using this approach, we mapped and characterized the binding-site landscape of over 3,000 pharmacologically relevant ligands and more than 180,000 putative pockets from protein complexes, derived from 6,619 crystallographic records in the Protein Data Bank. Our results demonstrate how the embedding space can expand predictive capabilities, offering new avenues for drug repurposing.

Examining the Influence of ENSO on the Hydroclimatology of Colombia's Inter-Andean Region through Complex Network Analysis

Santiago Castaño Moreno, Isabel Hoyos.

Universidad del Quindío, Grupo de Física Teórica y Computacional, Colombia.

This study examines the influence of tropical Pacific interannual variability on Colombia's hydroclimatology using complex networks in the period 1950-2024. The El Niño-Southern Oscillation (ENSO) is one of the main sources of climate variability in the region and has been shown to affect local precipitation in a heterogeneous manner. However, the regional hydroclimatological response depends on the ENSO phase, persistence, and intensity. We use the Niño 3.4 sea surface temperature anomaly time series to represent the ENSO phenomenon, while regional hydroclimatological variability is summarized by a time series of seasonal streamflow anomalies measured at the outflow of the Cauca-Magdalena river system. This observation point is key, as it reflects the integration of hydroclimatological processes across Colombia's inter-Andean region. Each time series is mapped to a graph, where each node corresponds to a temporal window whose data are ranked, defining a characteristic ordinal structure for each node. The optimal window size is determined through an entropic criterion, which sets the maximum number of nodes to represent the time series. Nodes are connected if they occur successively in the time series. Common connections between both networks reveal similar topological structures, which can be interpreted as evidence of shared dynamical evolution and serve as a measure of teleconnection strength. Both networks are classified as small-world. The Niño 3.4 network accounts for 178 links, while the streamflow anomaly network contains 195 links. We find that 98.31% of the Niño 3.4 network connections are also present in the streamflow network, representing 89.74% of the connections in the latter. The strong structural correspondence between the two networks highlights the value of the topological approach as an alternative tool for studying climatic teleconnections.

A distributed reconnection model for complex networks

Jorge Muñoz-García, Magalí Lopez-Chavira, <u>Daniela Aguirre-Guerrero</u>, Ricardo Marcelín-Jiménez.

Universidad Autónoma Metropolitana, México.

This research introduces a distributed reconnection model for complex networks that integrates spatial constraints related to cost and connection limits. The model begins with a planar network embedded in Euclidean space, where nodes maintain both fixed and dynamic links. Each node locally explores its neighborhood using the greedy routing algorithm Compass Routing and adjusts its dynamic connections based on Euclidean distance, interpreted as the cost of reconnection. The main objective is for nodes to strike a balance between the cost of establishing new connections and the benefit of accessing distant regions of the network. This local decision-making process fosters cooperative behavior, leading to emergent global properties such as hierarchical connection structures, high clustering, formation of local communities, and increased robustness to random failures and targeted attacks. To evaluate the model, we conducted a structural analysis of the generated networks, focusing on metrics such as network entropy, average path length, diameter, clustering coefficient, modularity, and robustness. Results show that the network's emergent properties are highly sensitive to both the routing strategy employed and the imposed spatial constraints. Specifically, networks generated under this model exhibited shorter average paths, high clustering, and strong community structure while maintaining robustness.

Multiple regime switching models: theory and applications

Gabriel Brida¹, Gaston Cayssials¹, Silvia London², Martín Puchet Anyul³

- (1) Grupo de Investigación en Dinámica Económica, Departamento Métodos Cuantitativos FCEA, UdelaR, Uruguay.
 - (2) Departamento de Economía, Universidad Nacional del Sur, Argentina.
 - (3) Facultad de Economía, Universidad Nacional Autónoma de México, México.

The notion of dynamic regime is increasingly employed across disciplines such as Economics, Sociology, and Ecology to understand, manage, and anticipate the behavior of complex systems. A diverse set of mathematical models has emerged to describe regime dynamics in systems that, despite appearing unrelated, share structural characteristics. These similarities suggest that multi-regime systems can be represented through meta-models-models of models-capable of capturing generalized patterns of systemic behavior. When endogenous variables respond in comparable ways under different exogenous pressures and across scales, it becomes possible to formulate unified rules, codified behaviors, and transferable analytical frameworks. This article offers a conceptual review of the key definitions and theoretical foundations of dynamic regimes and regime switching. It also examines the mathematical structure underlying many of the most common models used to represent these phenomena. Particular attention is given to the conceptual relevance of dynamic regimes in environmental economics, ecological economics, and tourism economics. In these fields, regime-based thinking supports the analysis of system transformations, resilience, feedback effects, and path dependence. It also contributes to the development of strategies for managing transitions, anticipating tipping points, and designing policies in the face of uncertainty and nonlinearity. By emphasizing the cross-disciplinary applicability of regime theory, we highlight its potential to improve the understanding and governance of socio-environmental and socio-economic systems undergoing structural change.

Friday morning - PA11 (Room 7)

Exploration mechanisms intrinsic to semantic networks and the nuanced appraisal of lexical repetition occurrences

Karen Nataly Gonzales¹, G. Espinosa-Otalora¹, Joaquin Goñi², F. Naranjo-M¹.

(1) Universidad Pedagógica y Tecnológica de Colombia, Colombia.

(2) CONN plexity lab, School of Industrial and Weldon School of Biomedical Engineering, Purdue University.

Semantic memory is responsible for storing knowledge of concepts or meanings in the long term. Based on the semantic network from the study by Goñi et al. (2011), we study the efficiency and performance of the network using the switching random walker model for different transition biases between nodes. Diffusion in the network is described by Markov chains, a process that allows the calculation of descriptive random variables such as average first-pass time and entropy rate. The MFPT and the entropy rate are very useful measures because they provide information about how reachable a node is on average from any other node, and the rate at which information can spread through the network. In addition, we designed a fluency test simulation model based on the changing random walker (SRW) where the relationship between short-term memory (STM), the number of repetitions and the flexibility of change is analyzed. STM was found to play an important role in verbal fluency performance, at least as it relates to verbal fluency tests.

Ultrafast Doppler and functional ultrasound of the brain: a novel research platform in Uruguay for studying functional networks and brain connectivity

Maximiliano Anzibar Fialho^{1,2}, Juan Barolin¹, Mariana Martínez Barreiro³, Lucia Vázquez Alberdi³, Victoria Sorriba⁴, Juan Pablo Damián^{5,6}, Maria Vittoria Di Tomaso⁷, Jérôme Baranger⁸, Mickael Tanter⁸, Miguel Calero⁹, Gonzalo Garay¹, Carlos Negreira¹, Nicolás Rubido¹⁰, Alejandra Kun^{3,11}, Javier Brum¹.

- (1) Laboratorio de Acústica Ultrasonora, Instituto de Física, Facultad de Ciencias, Universidad de la República, Uruguay.
 - (2) Física No Lineal, Instituto de Física de Facultad de Ciencias, Universidad de la República, Uruguay.
 - (3) Laboratorio de Biología Celular del Sistema Nervioso Periférico, Departamento de Proteínas y Ácidos Nucleicos, Instituto de Investigaciones Biológicas Clemente Estable, Uruguay.
 - (4) Unidad de imagenología, Departamento de Clínicas y Hospital Veterinario, Facultad de Veterinaria, Universidad de la República, Uruguay.
- (5) Departamento de Biociencias Veterinarias, Facultad de Veterinaria, Universidad de la República, Uruguay.
 - (6) Núcleo de Bienestar Animal, Facultad de Veterinaria, Universidad de la República, Uruguay.
 - (7) Departamento de Genética, Instituto de Investigaciones Biológicas Clemente Estable, Uruguay.
- (8) Institute Physics for Medicine Paris, Inserm U1273, ESPCI Paris, CNRS UMR 8063, PSL University, France.
 - (9) Chronic Disease Programme (UFIEC), and CIBERNED, Instituto de Salud Carlos III, Spain.
 - (10) Institute for Complex Systems and Mathematical Biology, University of Aberdeen, King's College, UK.
 - (11) Sección Bioquímica, Facultad de Ciencias, Universidad de la República, Uruguay.

With the development of ultrafast ultrasound imaging-capable of acquiring thousands of frames per second-the sensitivity of ultrasound to detect slow blood flow has increased by two orders of magnitude compared to the previous decade. This advancement enables the visualization of blood flow changes in small brain arterioles, which led to the introduction of ultrasound as a fully functional neuroimaging modality. Similar to functional MRI and functional optical imaging, functional ultrasound (fUS) leverages neurovascular coupling to indirectly monitor neuronal activity through ultrasound Doppler signals. fUS inherits the well-known advantages of ultrasound imaging: it is safe, rapid, and capable of imaging deep tissue with high spatiotemporal resolution $(100\mu m, 100ms)$. As a result, fUS has been successfully employed to map the activity of specific brain regions across various cognitive states in rodents, primates, and humans, establishing itself as a powerful tool for investigating brain dynamics and connectivity. The aim of this work is to review the major developments in ultrafast Doppler and fUS imaging, and to highlight their most

recent applications, with special emphasis on the contributions of our group in Uruguay studying the neurodegenerative disease of Charcot-Marie-Tooth. Specifically, in the work of Anzibar et al., using fUS and functional connectivity analysis, we demonstrated that TrJ mice-an animal model of Charcot-Marie-Tooth disease-exhibit significantly diminished neurovascular responses and altered brain connectivity compared to wild-type controls. These findings suggest a central nervous system involvement that could shift our understanding of the Charcot-Marie-Tooth disease.

Graph Contrastive Learning for Connectome Classification

Martín Schmidt¹, Sara Silva¹, Federico Larroca¹, Gonzalo Mateos², Pablo Musé¹.

- (1) Facultad de Ingeniería, Universidad de la República, Uruguay.
- (2) Dept. of Electrical and Computer Engineering, University of Rochester, USA.

With recent advancements in non-invasive techniques for measuring brain activity, such as magnetic resonance imaging (MRI), the study of structural and functional brain networks through graph signal processing (GSP) has gained notable prominence. GSP stands as a key tool in unraveling the interplay between the brain's function and structure, enabling the analysis of graphs defined by the connections between regions of interestâÅTreferred to as connectomes in this context. Our work represents a further step in this direction by exploring supervised contrastive learning methods within the realm of graph representation learning. The main objective of this approach is to generate subject-level (i.e., graph-level) vector representations that bring together subjects sharing the same label while separating those with different labels. These connectome embeddings are derived from a graph neural network Encoder-Decoder architecture, which jointly considers structural and functional connectivity. By leveraging data augmentation techniques, the proposed framework achieves state-of-the-art performance in a gender classification task using Human Connectome Project data. More broadly, our connectome-centric methodological advances support the promising prospect of using GSP to discover more about brain function, with potential impact to understanding heterogeneity in the neurodegeneration for precision medicine and diagnosis.

Friday morning - PA12 (Room 8)

Dinámica Poblacional del Gato Doméstico en Entornos Urbanos desde el enfoque de Sistemas Complejos

Rodrigo Perusquía Cortés¹, Pablo Padilla Longoria².

- (1) Posgrado en Ciencias Matemáticas, Universidad Nacional Autónoma de México, México.
 - (2) IIMAS, Universidad Nacional Autónoma de México, México.

El estudio del crecimiento de la población de gatos domésticos en entornos urbanos se ha vuelto un tema relevante en diferentes naciones. Si bien los gatos representan una amenaza para la biodiversidad debido a que son depredadores de diversos tipos de especies (e.g. aves, reptiles, peces, insectos, mamíferos), el poco cuidado que se les da en la sociedad ha conllevado a la creación de leves que los protegen, reconociendo la importancia de su rol como animal de compañía. El diseño e implementación de métodos de control efectivos y éticos se ha convertido en una necesidad. No obstante, un paso previo para llevar a cabo dichas acciones consiste en estudiar y entender la dinámica poblacional de la especie. Uno de los posibles enfoques para abordar este tema es a través de los sistemas complejos. En este trabajo, desde el enfoque de la teoría de redes, se construye una red dinámica que se basa en las características biológicas de los gatos y en sus interacciones intraespecíficas e interespecíficas. El modelo propuesto pone particular interés en el sistema reproductivo de la especie, sumado a la contribución de la sociedad en el crecimiento de la población. Debido a la variabilidad de diversos factores que rigen la dinámica poblacional de los gatos, en el sistema se considera una combinación de parámetros deterministas con parámetros estocásticos, con el fin de obtener resultados que se apeguen a la realidad. Adicionalmente, para probar la confiabilidad del modelo, se realiza un estudio de sensibilidad de parámetros difíciles de estimar. Los resultados muestran que la población alcanza un equilibrio periódico, a causa de la reproducción natural de los gatos y los factores sociales. AsÂη, una polÂηtica efectiva de control de la especie debe incluir también una regulación social.

Decreasing the spectral radius by removal of a node

Andres Angel², <u>German Combariza</u>¹, Camilo Perez², Arley Torre¹.

- (1) Universidad Externado de Colombia, Colombia.
 - (2) Universidad de los Andes, Colombia.

We find bounds and approximations to the change of the spectral radius of a graph when a node is removed. We characterize the graphs for which some of these approximations are exact.

Graph based models for anomaly detection in multivariate time series

Federico Bello^{1,2}, Gonzalo Chiarlone^{1,3}, Gaston García¹, Marcelo Fiori¹, Federico Larroca¹.

- (1) Facultad de Ingeniería, Universidad de la República, Uruguay.
 - (2) Tryolabs
 - (3) Pento

Time Series Anomaly Detection (TSAD) has been a subject of study for the past century, and its wide range of applications, from fraud detection to healthcare, highlights its significant importance. The rise of deep learning (DL) has led to numerous efforts to apply it to TSAD. In parallel, Graph Neural Networks (GNNs) have emerged as powerful tools for learning on graph-structured data. Their ability to capture complex relationships makes them a natural fit for modeling timeseries interdependencies. This work explores the application of GNNs to TSAD by representing multivariate time series systems as feature-enriched graphs. We assess models on two datasets, one where the underlying system structure can be naturally represented as a graph and one which does not, analyzing not only anomaly detection performance but also dataset characteristics, comparing GNN-based and non-GNN models, and experimenting with graph topologies and threshold selection. The findings suggest that GNNs offer promising results when an underlying graph structure exists, but yield less promising results when no such structure is present. To perform this analysis, particular attention is given to the evaluation metrics commonly used in TSAD. We show that many of these metrics, while widely adopted, present significant flaws. This work emphasizes the importance of using multiple, well-understood metrics and supports the development of more informative evaluation strategies, showing that a more graphical analysis is key for a thorough and interpretable evaluation of model performance. To support these findings and facilitate future research, we introduce GraGOD, an open-source, well-documented repository designed for reproducing all aspects of this work. To the best of our knowledge, no other open-source project currently offers such a comprehensive analysis of datasets, metrics and model predictions in this specific context. GraGOD's utility and extensibility was also validated using an additional industrial dataset provided by the Uruguayan Power Company (UTE).

Posters Sessions

Mathematical model for Aedes aegypti populations in temperate climates incorporating adaptive mechanisms

Lucas Alonso¹, Hernán Solari^{1,2}, Juan Aparicio³.

- (1) Departamento de Física, FCEN-UBA, Argentina.
- (2) Instituto de Física de Buenos Aires (IFIBA), UBA-CONICET, Argentina.
- (3) Instituto de Investigaciones en Energía No Convencional (INENCO), UNSa-CONICET, Argentina.

Aedes aegypti mosquitoes can survive winter in temperate regions in the form of eggs. In South America, the annual 15°C isotherm has traditionally been considered a reliable criterion for delimiting the species' survival range. However, recent studies suggest that Ae. aegypti has established itself in colder areas of Buenos Aires Province, Argentina-specifically, in southern locations below the 14.5°C isotherm. The reasons for this southward expansion remain unclear. Two main hypotheses have been proposed: climate change and adaptive development. The past decade has been warmer and drier than previous ones. While increasing temperatures may facilitate the mosquito's expansion, decreased rainfall could hinder it. In 2019, Ae. aegypti populations collected in Buenos Aires Province were found to exhibit a diapause mechanism: females lay eggs capable of withstanding prolonged periods of inactivity when day length falls below 12 hours. This strategy may allow eggs to survive winter conditions in temperate climates by delaying hatching. In this study, we address the following questions: Can these biological factors explain the observed expansion of Ae. aegypti? How far south can the species potentially spread? To explore this, we use the latest version of a detailed stochastic and spatial population model for Ae. aegypti that incorporates climate data and food availability dynamics. We incorporate the diapause mechanism into the model and perform simulations for several cities across Buenos Aires Province.

Exploring Transfer Learning in Hybrid Classical-Quantum Neural Networks

Lucas Burdman, Leonidas Facundo Caram.

Laboratory of Networks and Mobile Systems, Department of Electronics, FIUBA, Argentina.

Based on the proposal by Mari et al. (2020), this work explores hybrid classical-quantum architectures for supervised transfer learning, combining pre-trained classical models with variational quantum circuits (VQC) optimized in the NISQ era. Experiments were conducted with different pre-trained neural network architectures, datasets, and hyperparameter configurations, evaluating the performance of hybrid models against classical approaches. The results, validated on simulators and real quantum hardware, provide evidence of the feasibility of integrating quantum components into machine learning pipelines using current quantum hardware.

Two basic element's behaviour belonging to a quantum network which distributes entanglement

Leonidas Facundo Caram & Claudia M. Sarris

Universidad de Buenos Aires, Facultad de Ingeniería, Laboratorio de Redes y Sistemas Móviles (LSRyM), Argentina.

The objective of this work is to describe the basic operation of two elements of a quantum network (quantum nodes) which are necessary to perform the entanglement swapping procedure. These two elements are: the repeater node and the source emitting entangled photons.

Barriers in Cities: A Case Study of the Sarmiento Railway Line in Buenos Aires, Argentina, and Access to Schools

Manuel Graña¹, Paula Mascías², Inés Caridi^{1,3}

- (1) Instituto de Cálculo, FCEN-UBA, Argentina.
- (2) Facultad Latinoamericana de Ciencias Sociales, FLACSO, Argentina.

(3) CONICET, Argentina

Physical or perceived barriers-whether natural (e.g. rivers) or human-made (e.g. avenues or highways)-can significantly shape urban segregation by limiting access to essential services and opportunities, such as schooling. In this study, we assess whether the Sarmiento railway—which bisects Buenos Aires along a north-south axis-acts as an effective barrier for primary-school pupils. Using an open smart-card dataset capturing 15 million public-transport trips made in a single one day across Argentina, we reconstructed 5425 trajectories of students attending primary schools in the Metropolitan Area of Buenos Aires. For each infrastructure (e.g. the railway) we compute the Barrier Score (BS), following the approach proposed in [1], which compares the observed number of origin-destination crossings with those expected under a null model that preserves trip distances and spatial distribution while randomizing endpoints. The Sarmiento railway exhibits a Barrier Score indicative of a strong barrier effect, substantially greater than that of a major avenue or another suburban railway. A directional breakdown reveals a marked asymmetry: the north-to-south direction acts as a stronger barrier than the south-to-north. This pattern reflects Buenos Aires' socioeconomic gradient—wealthier northern districts versus poorer southern ones—and suggests that the railway reinforces existing inequalities in school accessibility. This open, high-granularity transport data highlights spatial barriers that may hinder equitable access to schools. Beyond schooling, the same framework can interrogate other mobility-related dimensions of urban segregation-such as access to health care, employment, or leisure-offering a versatile, evidence-based tool for urban planners and policymakers addressing mobility barriers that contribute to inequalities in cities. A key negative aspect of urban segregation is the homogenization of urban space, where certain groups become spatially isolated and have limited opportunities to interact with others [2,3]. Physical or perceived urban barriers further contribute to this homogeneization.

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Dispersed sparking vs. epidemic wave in the spatiotemporal spread of a vector-borne disease in a bilayer model

L. Claro, A. Pomi.

Sección Biofísica y Biología de Sistemas, Facultad de Ciencias, Universidad de la República, Uruguay.

Since its inception, network science has been widely applied to epidemiology. In particular, recent data support the importance of network-based human mobility in capturing the observed spatiotemporal spread of an epidemic. Given the large number of insect-borne diseases and the growing risk of pandemics, the importance of having good models of epidemic spread cannot be underestimated. In this work, we present a bilayer network to model the spatiotemporal spread of an epidemic transmitted by a vector, which we identify with a mosquito to establish ideas. Our model presents a first layer for human movements, which couples a discrete spatial model with a small-world network, and a second layer with a regular grid for the mobility of insect vectors. Each vertex of the network, comparable to a city, is provided with a SIR-based model, and the flows between the vertices were modeled according to a gravitational law. In the dynamics of the model, two limiting behaviors can be observed: a spreading wave propagation of the epidemic from the initial seeding site until it occupies the entire spatial layer vs. a succession of discrete sparks of random appearance, both converging to a final stationary state, with the extinction of the epidemic. Similar patterns have been observed during the recent COVID-19 pandemic. In some regions, a two-phase spread was even observed: an initial phase with the emergence of dispersed hotspots, followed by a diffusional progression through contiguity. Here, we present our model and characterize the two limiting behaviors, determining their dependence on the mobility of the two species and on other model parameters.

Distributed Quantum Computing over Quantum Internet

Leandro Delgado, José Canelón, Claudia M. Sarris, L. Facundo Caram

The fast advancement of quantum networking technologies demands the development of a robust, scalable, and intelligent control plane capable of managing the challenges posed by quantum communication. Unlike classical networks, quantum networks require the coordination of entanglement distribution, quantum memory management, and error correction mechanisms, all under strict temporal constraints. This paper explores the design and implementation of a control plane customized for the Quantum Internet, emphasizing its integration with distributed quantum computing frameworks.

Model of Opinion polarization in multidimensional spaces

- <u>F. Di Ciocco</u>¹, H. Pérez-Martínez^{2,3}, D. Soriano-Paños^{2,4}, J. Gómez-Gardeñez^{2,3}, P. Balenzuela¹, L. M. Floría^{2,3}.
 - (1) SoPhy Lab, Department of Physics, FCEyN, UBA.
- (2) GOTHAM lab, Institute for Biocomputation and Physics of Complex Systems (BIFI), University of Zaragoza, Spain.
 - (3) Department of Condensed Matter Physics, University of Zaragoza, Spain.
 - (4) Institute Gubelkian of Science (IGC), Portugal.

Polarization is a phenomenon present in many societies, manifested by the emergence of groups with extreme opinions. This phenomenon, often studied in relation to controversial topics such as abortion, actions toward foreigners, or gender policies, can hinder democratic decision-making by producing pendulum-like social contexts that swing from one extreme to the other. An additional issue is that polarization on certain topics often contains an ideological component that links people's opinions across various issues, such that these extreme opinion groups share positions on a diverse set of topics. For this reason, the study of this phenomenon requires a multidimensional approach, that is, one involving multiple topics simultaneously, in which not only the emergence of polarization is studied, but also ideological states. In this paper, we study a model of interaction between agents in a complex network that generates polarization states and ideological states, and we compare these generated states with survey data on controversial political questions.

Modelo topológico basado en la Estructura Weaire-Phelan para descentralización y sincronización en redes de neuronas

Alessandro Escobar-Banda¹, Luciano Stucchi²

- ((1) Universidad Andina del Cusco, Perú.
 - (2) Universidad del Pacifico, Perú.

Las redes neuronales modifican sus conexiones, generando nuevas o reorganizando las existentes, lo que influye en el procesamiento de información en el cerebro. Para modelar estos mecanismos, se emplean estructuras como las redes Newman-Watts (NW) y Watts-Strogatz (WS), utilizadas para simular la plasticidad neuronal y la eficiencia en la transmisión de señales. Esta investigación analiza una versión modificada de los poliedros constituyentes de la Estructura Weaire-Phelan como topología, en la que se incorporan nodos centrales y conexiones hacia el centro de cada polígono. Este diseño busca optimizar la distribución de nodos y conectividad neuronal, permitiendo una representación más precisa de la sincronización sináptica, inspirada en principios de estructuras naturales como panales de abejas y sistemas celulares. Para evaluar el impacto de esta topología, se implementó el modelo de Izhikevich y se analizó la sincronización neuronal en comparación con estructuras tradicionales, incluyendo teselaciones, redes aleatorias, WS y NW, considerando la dinámica específica de cada caso. Los resultados indican que la presencia de una distribución uniforme en los nodos favorece la estabilidad sináptica, la resiliencia de la red ante perturbaciones y la consistencia en la transmisión de señales, lo que sugiere que la topología de la red desempeña un papel fundamental en el equilibrio funcional de las redes neuronales artificiales. Además, el análisis mediante métricas de redes complejas-eficiencia, propiedades de Small-World y centralidad-muestra que este diseño conserva valores cercanos a los modelos tradicionales, pero con menor varianza, lo que sugiere una conectividad más uniforme en la red. Este enfoque contribuye a la comprensión de la relación entre arquitectura de red y actividad neuronal, proporcionando un marco para la extrapolación de modelos hacia configuraciones más complejas en simulaciones de procesamiento de información y descentralización en sistemas biológicos y computacionales.

Coexistence of multiple rumors in complex networks

Thainá Ferreira Silva¹, Silvio da Costa Ferreira Junior^{1,2}.

(1) Departamento de Física, Universidade Federal de Viçosa, Brazil.

(2) National Institute of Science and Technology for Complex Systems, Brazil.

The spread of rumors is a social phenomenon that significantly influences collective behavior, from information dissemination on social media to opinion formation and the emergence of social movements. Rumors can amplify misinformation and impact both public and private decisions. Traditional models of rumor spread typically consider a single rumor or include a forgetting mechanism to mimic the effects of multiple rumors. These limitations reduce their applicability to real-world scenarios where multiple rumors coexist and interact. In this work, we propose a framework to study the simultaneous spread of multiple rumors in complex networks. Each rumor evolves according to standard rules, while new rumors are spontaneously created at a small rate. We investigate how many rumors an individual can spread and how interactions among distinct rumors emerge by adjusting the spreading rate based on how many rumors an individual already knows. This formulation allows for either collaborative or competitive effects on rumor propagation. To assess the behavior of these models, we performed simulations on random regular networks. In the absence of interactions, the proposed model reaches an active steady state without oscillations, in contrast to models with a forgetting mechanism. Although new rumors are constantly introduced into the system, the total number of coexisting active rumors saturates at a characteristic timescale that is independent of the rumor creation rate. The per capita number of spread rumors increases monotonically with the maximum number of rumors M that an individual can spread, but it quickly saturates as M increases. In the case of collaborative rumors, we observe that the time required to reach the steady state increases as the interaction strength grows, and oscillatory behavior emerges. Future work will extend the analysis to different network topologies and explore alternative interaction mechanisms between rumors.

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Characterizing the political gatekeeping in the context of Argentina's 2019 Elections

L. L. Garcia^{1,2}, P. Balenzuela^{1,2}

- (1) Departamento de Física, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Argentina.
 - $\hbox{$(2)$ Instituto de F\'sica Interdisciplinaria y Aplicada (INFINA), CONICET Universidad de Buenos Aires, } \\ Argentina.$

Gatekeeping refers to the process by which actors such as media outlets, editors, influencers, or algorithms filter and prioritize information, shaping what reaches the public. With the rise of social media, traditional gatekeeping structures have weakened: any user can become a source of information, and journalists now participate in these platforms, blurring the boundaries between professional and public agendas. Most studies on social media when analyzing news consumption typically focus on posts belonging to a single hashtag used as a thematic axis (Bastos 2013, Aruguete 2022). This work proposes a broader methodology that considers multiple thematic axes, aiming to provide a more comprehensive view of the political landscape on social media X (former Twitter). Using the same X dataset as Zhou (2021), we analyzed tweets posted between March 1 and October 31, 2019. Tweets were collected via the Twitter Academic API using keywords related to local politicians and parties. Only tweets containing at least one hashtag were included. If a tweet also linked to a URL, it was retained only if the source was an Argentine media outlet, as verified through the ABYZ News Links directory. Our analysis explores how topics emerge, propagate, and are shared between users and media. We identify thematic gaps between public and media agendas and quantify the delay in topic transmission across them. This raises key questions: Can we detect gatekeeping effects through agenda gaps? Do certain topics originate in one agenda before impacting the other? How long does this influence take to manifest? By examining the timing and content of these interactions, this study contributes to understanding the evolving dynamics of information flow and agenda-setting in social media.

Mapping the Pocketome Landscape Using Complex Networks

Gonzalo Giordano^{1,2}, Nicolas Yanovsky^{1,2}, Ariel Chernomoretz^{1,3,4}.

- (1) Fundación Instituto Leloir, Argentina.
- (2) Inst. Inv. Bioquimicas de Buenos Aires (CONICET), Argentina.
- (3) Depto de Fisica FCEN, Universidad de Buenos Aires, Argentina.
 - (4) INFINA (UBA/CONICET), Argentina.

The pocketome refers to the full set of ligand-binding pockets across all known protein structures. These cavities play a central role in molecular recognition and drug binding, making their characterization a key step in rational drug discovery. While individual pockets have been extensively studied, a global, network-based view of pocket relationships remains underexplored. Using a Large Language Model, in this study we modeled the pocketome as a similarity network and investigated its structural properties through the lens of complex network theory. Our work focuses on characterizing cases where our network-based similarity suggests biologically meaningful relationships that are not captured by traditional sequence- or structure-based approaches. These cases may illuminate the strengths and limitations of current pocket characterization methods and reveal novel functional or evolutionary patterns.

Unbalances in the core-periphery structures of the World Trade Network: A perspective from Latin American Structuralism and Complexity Sciences

J.C. Higuera¹, <u>D. A. Heredia</u>¹, Gabriel Camacho-Cabrera², L. E. Higuera¹, Manu Barros¹, Guillermo Coronado³

- (1) Universidad Nacional de Colombia, Colombia.
- (2) Universidad Nacional de Costa Rica, Costa Rica.
- (3) Pontificia Universidad Católica del Perú, Perú.

Based on the place of countries in the Balance of Trade Power with respect to the rest of the world, center-peripheral structures were estimated, which are studied to expand the concept of structural imbalance beyond the Balance of Trade, including the diversity and weight of transacted products. Through this approach, postulates of Latin American Structuralism are empirically explored. The findings partially support their hypotheses, revealing that the center tends to export more diversified and lighter products than the periphery, suggesting greater product sophistication. However, contrary to their theoretical predictions, there is no evidence of a constant state of trade surplus in the center or deficit in the periphery.

Detección de sincronía en las dinámicas de comunidades biológicas.

Mariana Illarze^{1,2}, Matías Arim^{1,2}, Paola Bermolen^{2,3}, Agustín de León^{1,2}, Marcelo Fiori^{2,3}, Verónica Pinelli^{1,4}, Lucía Sosa-Panzera¹ (1), Ana Borthagaray^{1,2}.

- (1) DEGA, Centro Universitario Regional del Este, UdelaR, Uruguay.
 - (2) CICADA, Espacio Interdisciplinario, UdelaR, Uruguay.
 - (3) IMERL, Facultad de Ingeniería, UdelaR, Uruguay.
- (4) Departamento de Sistemas Ambientales, Facultad de Agronomía, UdelaR, Uruguay.

La sincronía en dinámicas biológicas es un fenómeno clave para muchos procesos ecológicos, como las interacciones bióticas. En un contexto comunitario, la sincronía se refiere a cambios acoplados en variables como la abundancia, biomasa o riqueza de especies a lo largo del tiempo en comunidades geográficamente separadas. Este fenómeno se ha asociado directamente con la estabilidad de los sistemas ecológicos. Específicamente, la existencia de dinámicas acopladas entre comunidades podría reducir la estabilidad del sistema, ya que variaciones locales (ej.: en biomasa o riqueza) se propagan directamente a variaciones en la estructura y funcionamiento a escala ecosistémica. El acople ha sido explicado principalmente por el flujo de materia o información (por ejemplo, la dispersión de individuos) y por respuestas similares de diferentes comunidades a variaciones ambientales, el efecto Moran. En este trabajo proponemos un enfoque basado en herramientas de teoría de grafos para detectar conjuntos de comunidades biológicas con dinámicas acopladas en términos de biomasa y riqueza de especies. Para ello, analizamos 20 años de datos provenientes de una metacomunidad de plantas de charcos temporales. La red de asociaciones fue estimada mediante el método Graphical Lasso, que infiere correlaciones parciales entre pares de nodos, es decir, asociaciones condicionadas que permiten controlar efectos indirectos. Incorporamos variables ambientales como nodos en la red para representar la sincronía asociada al efecto Moran. A partir de la red estimada realizamos un análisis de modularidad, mediante el cual evaluamos la composición funcional, las condiciones locales y la distancia geográfica de las comunidades dentro de cada módulo. Este enfoque permitió identificar los principales determinantes de la sincronía en el sistema estudiado.

EEG-Based Complex Network and Spectral Analysis in Parkinson's Disease: DBS Effects Across Resting States

<u>Lijandy Jiménez Armas</u>¹, Constantino Méndez-Bértolo³, Florencia Sanmartino³, Raúl Rashid-López^{3,4}, Raúl Espinosa-Rosso^{3,4} (3,4), Diego M. Mateos^{1,2,5}, Javier J. González-Rosa³.

- (1) Instituto de Matemática Aplicada del Litoral (IMAL-CONICET-UNL), CCT CONICET, Argentina.
 - (2) Facultad de Ciencia y Tecnología, Universidad Autónoma de Entre Ríos (UADER), Argentina.
 - (3) Institute of Research and Biomedical Innovation of Cadiz (INiBICA), University of Cadiz, Spain.
 - (4) Department of Neurology, Puerta del Mar Hospital, Spain.
 - (5) Achucarro Basque Center For Neuroscience, Spain.

Parkinson's disease (PD) is a progressive neurodegenerative disorder marked by the degeneration of dopamine-producing neurons, leading to characteristic motor symptoms, such as tremor, rigidity, and bradykinesia. While pharmacological therapies provide symptomatic relief, their effectiveness often declines over time. Deep Brain Stimulation (DBS) has emerged as a highly effective surgical treatment for advanced PD, significantly improving motor symptoms. However, the underlying effects of DBS on brain network, dynamics and connectivity patterns remain incompletely understood. In this study, we analyzed EEG recordings from PD patients with implanted DBS systems under stimulation ON and OFF conditions, and compared them to a healthy control group. Resting-state data were collected under both eyes open (EO) and eyes closed (EC) conditions. Functional brain connectivity was assessed using complex network measures, including link density, clustering coefficient, and global efficiency. Additionally, we examined the spectral properties of the connectivity graphs through Laplacian eigenvalue metrics such as algebraic connectivity, von Neumann entropy, and spectral complexity. Our findings show that, in the EC condition, PD patients with DBS OFF exhibit significant disruptions in beta and low/high gamma frequency bands. Under DBS ON, these measures shift toward control-like values. A similar pattern was observed in the EO condition, particularly in the alpha and gamma bands. These results suggest that PD induces frequency-specific alterations in resting-state brain networks, which can be partially mitigated through DBS, promoting a reorganization of connectivity dynamics toward more normative patterns.

Genomic data visualization using graphs and Fermat distance

Micaela Long¹, María Inés Fariello¹ (1), LucÃŋa Spangenberg²

(1) Facultad de Ingeniería, UdelaR, Uruguay. (2) Institut Pasteur de Montevideo, Uruguay

One of the challenges in population genetics data analysis is high dimensionality. Dimensionality reduction via principal components analysis (PCA) is commonly used for genetic data visualization and is usually used to make inference on population structure in combination with other methods. However, PCA focuses on capturing global linear relationships in the data, and as local variation is often found on higher principal components, a two-dimensional plot does not always capture all the relevant genetic variation. Non-linear methods such as t-distributed Stochastic Neighbor Embedding (t-SNE) and Uniform Manifold Approximation and Projection (UMAP) have become very popular as visualization and dimensionality reduction tools. Although these algorithms emphasize local patterns and complex relationships, they usually fail at preserving global structure, because distances between clusters are not always meaningful and visualizations are usually difficult to interpret. In this work we develop a method based on graphs for genomic data visualization. Specifically, we construct a graph where nodes are individuals and edges represent genetic similarity between them. We use Fermat distance as a measure of similarity, a weighted geodesic distance that takes into account both geometry and density of the data. Then, to obtain a graph embedding in a vector space we use node2vec, an autoencoder that learns low-dimensional vector representations for nodes based on random walks in the graph, following the idea that paths in a graph can be treated like sentences in a corpus. The construction of the graph based on Fermat distance enables the visualization of population structure by preserving both local and global patterns, reflecting geographical gradients and evolutionary history. This method shows some improvements compared to others, especially in representing populations with small sample sizes and effectively visualizing admixed individuals.

Identifying Core Genes of the Vector-Parasite-Human Tripartite Network by Analyzing Protein-Protein Interactions in Chagas Disease

<u>Francisco Javier Mendoza Proaño</u>^{1,3}, Shirley Michell Salcan Castillo¹, Marco Andrés Viteri Yanez², Moises Ruben Gualapuro Gualapuro^{1,4}.

- (1) Universidad Regional Amazónica Ikiam, Ecuador.
- (2) Biomolecules Discovery Group, Universidad Regional Amazónica Ikiam, Ecuador.
- (3) Centro Nacional de Acuicultura e Investigaciones Marinas, Escuela Superior Politécnica del Litoral, Ecuador.
 - (4) Department of Computational Biology, University of Kansas, USA

Trypanosoma cruzi is the etiological cause of Chagas Disease (CD), one of the most critical diseases in Latin America and considered among the 13 neglected tropical diseases worldwide. In recent years, the availability and quality of proteomic and transcriptomic data for vectors, parasites, and host in CD have improved substantially. These data are input for Protein-Protein Interaction (PPI) networks analysis, to shed light on the molecular mechanisms underlying hostpathogen interactions. In the Vector-Parasite-Human (VPH) system involved in CD, specific and complex interactions occur between proteins of the insect vector (Rhodnius prolixus), the parasite (T. cruzi), and the human host. Understanding these interactions is crucial for identifying key molecules involved in disease transmission, virulence, and pathogenesis. Therefore, this study aimed to explore the VPH system of CD through an automated analysis of PPI networks. Genes were collected from VEuPathDB (R. prolixus), TriTrypDB (T. cruzi), HostDB, and ChagasDB (Human). Gene ontology analysis was used to refine genes associated with the disease, while interactions were predicted using STRING-DB. A multilayer PPI network was constructed, and its topology was analyzed through connected components, centrality measures, and community detection algorithms. Out of 110711 initial genes, filtering and refinement yielded a final network of 1166 nodes and 65617 interactions. Key genes involved in host-pathogen interaction, virulence, and immune evasion were identified. In parasite, mucins and trans-sialidases like Q4D872, Q4CVU9, and Q4D8B3 mediate immune evasion. In humans, RHOA and AKT1 are central in immune response modulation. In vector, sulfotransferases such as T1HB80 play potential roles in parasite interaction. Due to their topological prominence and biological relevance, these genes emerged as core components of the tripartite PPI network and represent promising therapeutic targets for CD.

Implementation of the self-regulation model of Kuramoto oscillators in an in-silico neuronal culture.

Gustavo Espinosa Otalora, Fernando Naranjo Mayorga

Universidad Pedagógica y Tecnológica de Colombia, Colombia.

In this work, we implement a regulatory model based on a network of Kuramoto oscillators in a neuronal culture. In this model, each neuron is represented as a Kuramoto oscillator, while glial cells act as inhibitory agents of the global synchronization of the neurons in the culture. The model is applied to two in-silico neuronal networks: one highly aggregated and another in which neurons are uniformly distributed. According to the simulation method used to generate the cultures, the resulting neuronal networks in both cases are directed. When a pair of neurons reaches a synchronization threshold, a connection is suspended. After each suspension, we adjust the synaptic weight -i.e., the coupling constant in the Kuramoto model - among the first neighbors of the affected neuron. Through this mechanism, we aim to observe dynamic patterns that reflect the activity of the network in conjunction with the glial cells, with the goal of developing new models that more accurately reflect the biological behavior observed in neuronal culture.

Beyond Pairwise Agentive Semiotics: A Higher-Order Interaction Model

Eduardo Mojica-Nava, NP Parra-Ortiz

Universidad Nacional de Colombia, UNAL, Colombia.

This work proposes a methodological framework to model meaning-making processes based on the principles of agentive semiotics, using tools from network science, particularly higher-order interaction models and complex networks. In agentive semiotics, the process of signification is not a static property of signs or objects, but an emergent activity produced when an agent enacts an agenda within a specific context. From this perspective, meaning is relational, situated, and dynamic. Traditional network models -based on pairwise relationships- are considered insufficient to describe the multi-agent nature of meaning emergence. Therefore, we propose the use of higher-order representations (such as simplicial complexes) to formally describe how agents, agendas, signs, and environments interact in the generation of meaning. These structures make it possible to model semiosis as a network of co-occurring intentional actions, rather than as a system of fixed associations between signs and objects. For instance, a hyperrelation can represent a group of agents interacting with the same sign while pursuing different agendas, whereas a simplicial complex can capture hierarchical layers of meaning construction over time or through lived experience. The proposed methodology is illustrated through examples involving simple interaction structures.

Causal Emergence in Complex Networks: A Multiscale Approach Using Markov Chains and Coarse-Graining

Jorge Luis Martín Quiroz-González

Pontificia Universidad Católica del Perú, Perú.

In many complex systems -such as living organisms, social dynamics, or critical infrastructurescollective behavior exhibits properties that are not reducible to the local rules of individual components. This phenomenon is known as emergence, and it occurs when global patterns arise from local interactions. A particular case is causal emergence, referring to situations where a macroscopic description of a system allows for more structured and accurate predictions than a detailed microscopic one. This concept has been formalized by Erik Hoel through the notion of Effective Information (EI), a metric that quantifies how specific and distinguishable the outcomes of different interventions are within a system.vv Building on this theoretical framework, we develop a computational approach to investigate causal emergence in complex networks. We implement Markov chain dynamics over synthetic network models (e.g., Barabási-Albert, stochastic block models), and apply hierarchical coarse-graining techniques to construct multiscale representations. The EI is measured at multiple levels to identify when a causal gain emerges as we move from the micro to the macro scale. Preliminary results show that certain topological and dynamical configurations -particularly those involving broken symmetries or cooperative interactions- favor the emergence of causal structure at the macro level. This framework is currently being extended toward empirical networks and simulations of real-world phenomena such as misinformation diffusion and biological self-organization. Our goal is to contribute conceptual and computational tools for detecting and quantifying emergent causal organization, opening new avenues for understanding multiscale structure in complex systems.

Una Nueva Medida para Caracterizar las Estructuras de Ciclos en Redes Complejas

<u>Kevin Nicolás Ramos Guasca</u>, María Elizabeth Mesa Pineda, Juan Camilo Higuera Calderón

Universidad Nacional de Colombia, Colombia

Este artículo propone una nueva medida llamada Enredamiento (R) para cuantificar el grado de acoplamiento entre ciclos irreducibles en redes complejas, definidos como aquellos ciclos simples que no pueden descomponerse en ciclos más pequeños. A diferencia de las métricas tradicionales basadas en caminos (como centralidad de grado, intermediación o cercanía), que suelen correlacionarse fuertemente entre sí, R captura información estructural independiente al medir el solapamiento de aristas entre ciclos, revelando nuevos patrones que no capturan las anteriores medidas. Utilizando redes de Watts-Strogatz, demostramos que R aumenta con la densidad y aleatoriedad de la red, pero se satura tras un umbral crítico, mostrando un comportamiento que contrasta con las medidas clásicas. Esta métrica ofrece una perspectiva innovadora para analizar sistemas donde los ciclos son funcionalmente relevantes (como redes biológicas o tecnológicas), proporcionando insights sobre robustez, modularidad y dinámicas emergentes aproximaciones alto. que otras pasan

Quantifying Emergent Behaviors in CA and ABM models Using Conditional Entropy

Sebastián Rodríguez Falcón¹, Luciano Stucchi².

- (1) Pontificia Universidad Católica del Perú, Perú.
 - (2) Universidad del Pacífico, Perú.

Los sistemas complejos están compuestos por numerosos componentes interconectados e interdependientes, y exhiben propiedades clave como la autoorganización, la adaptación y la emergencia: la formación espontánea de patrones estructurados sin control centralizado. Herramientas como la Modelación Basada en Agentes (ABM) y los Autómatas Celulares (CA) han demostrado que reglas simples pueden generar comportamientos globales complejos. En este contexto, Stephen Wolfram propuso una clasificación en cuatro tipos de comportamiento para los autómatas celulares: convergente, periódico, caótico y complejo. Sin embargo, comprender cómo surgen los fenómenos emergentes a partir de interacciones locales sigue siendo uno de los principales desafíos de la ciencia de la complejidad, debido a la falta de un marco formal y cuantitativo que permita caracterizar y diferenciar estos comportamientos de manera precisa. En este trabajo, proponemos un método para cuantificar las diferencias entre comportamientos de sistemas utilizando la entropía condicional de un sistema de autómatas celulares bidimensional. Para aplicar este método, presentamos un modelo de caminata aleatoria sesgada de múltiples agentes, controlado por dos parámetros binarios, capaz de reproducir los cuatro tipos de comportamiento identificados por Wolfram.

Boxeo y redes complejas: Estudio cuantitativo de las propiedades físicos de los estilos y estrategias de combate.

S. Rosas Mogollón, Rafael Hurtado

Departamento de Física, Universidad Nacional de Colombia - UNAL, Colombia.

Este estudio realiza un análisis cuantitativo de estilos de boxeo mediante redes complejas, con el objetivo de identificar patrones estratégicos a partir de datos de combates. Se construyeron ego redes multiplex para modelar interacciones ofensivas y defensivas, calculando métricas de entropía y fortaleza nodal que reflejan eficiencia en el gasto energético y efectividad de golpeo. Los resultados validan correlaciones entre las propiedades emergentes de las redes y los estilos cualitativos conocidos, demostrando que este enfoque puede cuantificar diferencias tácticas entre boxeadores. Además, el modelo muestra capacidad predictiva al anticipar resultados reales de combates. El trabajo establece las bases para un marco analítico innovador en el estudio de deportes de contacto, con potencial aplicaciones en scouting y preparación táctica.

Palabras clave: Boxeo, redes complejas, redes multiplex, entropía, métricas de desempeño, estilos de boxeo.

Geographical Network Analysis of Connectivity and Dengue Contagion Dynamics in Ecuador

Shirley Michell Salcan Castillo¹, Moises Gualapuro^{1,2}, Francisco Javier Mendoza Proaño^{1,3}.

- (1) Universidad Regional Amazónica Ikiam, Ecuador.
- (2) Department of Computational Biology, University of Kansas, USA.
- (3) Centro Nacional de Acuicultura e Investigaciones Marinas, Escuela Superior Politécnica del Litoral, Ecuador.

Dengue fever is a significant public health concern in Ecuador. The disease is endemic to the Coast, Amazonia, and the Andean foothills. Dengue prevalence is closely related to climatic patterns, socioeconomic conditions, vector control measures, and human mobility. Although statistical methods have been extensively employed to analyze incidence patterns in Ecuador, how the connectivity between cities affects these patterns is required. To fill this gap, we developed a network analysis for the propagation of dengue fever. Nodes are cities with a high prevalence of reported cases of dengue, the edges were assigned by terrestrial connectivity between neighboring cities, and the weights of the edges are the cross-correlation of cases between them over the geographical distance. After that, spontaneous infection, recovery, and loss of immunity were determined by Gillespie's Algorithm to identify the best link to the SIR epidemic model for dengue cases in Ecuador. The network analysis identified six strongly connected clusters, mainly in the coastal region, and the nodes with the highest number of links are also concentrated in this region. The centrality of proximity points to the coastal nodes as the main dispersers of dengue due to their geographic location, while the intermediation centrality highlights two nodes that connect the Coast and the Amazon, these belong to Quito and Archidona. On the other hand, the models that best represented the dispersion of dengue in Ecuador were combinations 34, 56, 51, 50, and 19, with the lowest error (RMSE) and high stability. In addition, the R_0 is between 6and 10, indicating that a city can infect 6 to 10 cities during its infectious period. These findings provide useful inputs for decision-making, epidemiological control, and surveillance strategies.

Sostenibilidad en red: Caso exitoso de cooperación multiescalar en monitoreo ambiental

Stephania Suarez Grajales, Juan Mauricio Castaño Rojas

Universidad Tecnológica de Pereira, Colombia

El Sistema de Alertas Tempranas y de Monitoreo Ambiental (SATMA) de Risaralda, operado por la Universidad Tecnológica de Pereira desde 2005, se presenta como un caso de éxito en la sostenibilidad de redes de monitoreo ambiental a través de la cooperación institucional. Su crecimiento de una a 103 estaciones en dos décadas fue impulsado por la colaboración continua de diversos actores (Gobernación, Aguas y Aguas, CARDER, Empresa de Energía, municipios), quienes contribuyeron con recursos técnicos y financieros, superando los 400,000 USD en los últimos tres a nos. La eficiente recopilación y difusión de información crucial a través de su web y app demuestran la efectividad de esta gobernanza multiescalar para la gestión de riesgos climáticos y el ordenamiento territorial. El SATMA constituye un modelo ejemplar de gestión ambiental descentralizada en que a partir de la interacción de agestes institucionales con intereses diferentes construyen un único sistema regional de de alertas tempranas y monitoreo ambiental. Esto tiene el potencial de replicabilidad en otros contextos de América Latina.

Analyzing Temporal Evolution of Time Series Using Information Theory Measures: Applications in Hydrology and Cryptocurrency Markets

<u>Micaela Suriano</u>^{1,2}, Leonidas Facundo Caram², Cesar Caiafa³, Hernán Daniel Merlino⁴, and Osvaldo Anibal Rosso^{5,6}.

- (1) Departamento de Hidráulica, Facultad de Ingeniería, Universidad de Buenos Aires, Argentina.
- (2) Laboratorio de Redes y Sistemas Móviles, Departamento de Electrónica, Facultad de Ingeniería, Universidad de Buenos Aires, Argentina.
 - (3) Instituto Argentino de Radioastronomía-CCT La Plata, CONICET/CIC-PBA/UNLP, Argentina.
 - (4) Grupo IngenIA, Facultad de Ingeniería, Universidad de Buenos Aires, Argentina.
 - (5) Instituto de Física (IFLP), Universidad Nacional de La Plata, CONICET, Argentina.
 - (6) Instituto de Física, Universidade Federal de Alagoas (UFAL), Brasil.

This work investigates the temporal evolution of time series using information measures such as the complexity-entropy causality plane (CECP) and the representation of the Shannon entropy and Fisher information measure (FIM). The main objective is to differentiate between various levels of randomness and chaos and use this information to support decision-making across diverse domains. The methodology was applied to two distinct types of time series. First, it was used on daily streamflow data from several rivers in Argentina. Results show that the daily discharge series could be approximately represented as noise with power spectrum frequency dependence, although the observed variances highlight the inherent challenges of modeling natural phenomena. Furthermore, the size of the basin plays a relevant role in modulating the process. Large basins exhibit lower entropy values and less noisy signals due to integration over larger spatial and temporal scales, while small and mountainous basins respond rapidly to precipitation events, resulting in higher entropy and lower complexity. These findings characterize the hydrological dynamics of Argentine rivers and provide valuable insights for improved hydrological modeling. Second, the methodology was applied to the daily closing price series of various cryptocurrencies. The results reveal that cryptocurrency series shorter than two years exhibit chaotic behavior, whereas those longer than two years tend to display stochastic dynamics resembling colored noise. Additionally, a Natural Language Processing (NLP) analysis of white papers identified key terms, enabling a clustering approach that yielded four distinct groups. However, no significant differences in time series dynamics were observed across these clusters, challenging the assumption that project narratives strongly influence market behavior. Together, these case studies illustrate

the broad applicability of information theory measures for analyzing complex time series from both natural and financial systems, providing a robust framework for distinguishing randomness, chaos, and noise characteristics in diverse contexts.

Análisis de Redes Sociales para la Caracterización de la Actuación Institucional del Sistema de Alertas Tempranas por Inundaciones en Risaralda, Colombia

Laura Vizcaino Herrera, Juan Mauricio Castaño Rojas

Facultad de Ciencias Ambientales, Universidad Tecnológica de Pereira, Colombia.

Esta investigación caracterizó la actuación institucional del Sistema de Alertas Tempranas (SAT) para inundaciones y avenidas torrenciales en siete municipios de Risaralda, Colombia (Pereira, Dosquebradas, Santa Rosa de Cabal, La Virginia, La Celia, Pueblo Rico y Mistrató). El objetivo fue analizar la capacidad de respuesta del sistema ante estos fenvmenos a través de la aplicación de métodos de análisis de redes sociales, concibiendo el SAT como un sistema socioecológico complejo. Siguiendo la metodología propuesta por Palacio (2015), se identificaron actores clave, variables atributivas y estructurales, ventanas temporales y propiedades de la red, integrando principios del análisis de redes sociales (Wasserman y Faust, 1994) y la teoría del actor-red (Callon, 1999). El procesamiento de datos, la visualización de grafos y el cálculo de métricas de red (densidad, grado y centralidad) se realizaron con el software Gephi. Los resultados revelaron la estructura de actores y relaciones que conforman el SAT de Risaralda, permitiendo analizar la complejidad de su sostenibilidad. Se identificaron tres subsistemas diferenciados por sus capacidades técnica, operativa y financiera en la gestión del riesgo de desastres. Este hallazgo subraya la importancia de una articulación diferenciada del SAT, considerando las particularidades de cada municipio dentro de una estrategia integral para la adaptación y el desarrollo sostenible en contextos urbanos.

Structurally-Informed Graph Networks for Predicting Drug-Target Interactions

Nicolas Yanovsky^{1,2}, Gonzalo Giordano^{1,2}, Ariel Chernomoretz^{1,3,4}.

- (1) Fundacion Instituto Leloir, Argentina.
- (2) Inst. Inv. Bioquimicas de Buenos Aires (CONICET), Argentina.
- (3) Depto de Fisica FCEN, Universidad de Buenos Aires, Argentina.
 - (4) INFINA (UBA/CONICET), Argentina.

Accurate prediction of drug-target interactions (DTIs) is essential for drug repositioning, design, and discovery. However, identifying DTIs through experiments or simulations is expensive and time-consuming. For this reason, there is growing interest in using Graph Neural Networks (GNNs) to predict DTIs efficiently. In this work, we apply GNNs to a heterogeneous chemogenomic network composed of two layers: one representing drugs and the other representing protein targets. Inter-layer edges represent known DTIs, while intra-layer edges reflect structural similarity-between compounds in the drug layer and between proteins in the target layer. We show that including structural similarity information in the network construction could improve DTI prediction performance. Additionally, we enrich the initial feature representations of targets with external data beyond the network's topology and assess its contribution to model accuracy. Finally, we analyze the predictions to identify potential biases related to node connectivity.

Cultura como dinámica de red: una simulación basada en agentes y la selección por consecuencias

Milene Paloma Zamalloa Bohorquez

Universidad Andina del Cusco, Facultad de Ciencias de la Salud, Escuela profesional de Psicología, Perú.

El proyecto propone una herramienta computacional para explorar cómo emergen, se mantienen o se extinguen prácticas culturales a partir del comportamiento individual, utilizando principios del análisis conductual. El modelo simula un sistema social artificial en NetLogo donde agentes (individuos) y unidades de conducta interactúan dentro de una red dirigida. Cada agente elige comportamientos en función de su historia de refuerzo. Las consecuencias –positivas, neutras o aversivas– modifican la probabilidad de futuras respuestas. A través de múltiples iteraciones, se observa cómo ciertos patrones conductuales comienzan a compartirse entre agentes, consolidándose como clústeres que representan prácticas culturales emergentes. El modelo permite experimentar con condiciones específicas de reforzamiento social para observar su impacto sobre la dinámica cultural de un sistema. Esto abre posibilidades para aplicaciones prácticas en el diseño de intervenciones conductuales en contextos comunitarios, educativos o institucionales, facilitando la identificación de condiciones que promuevan o inhiban ciertas prácticas a gran escala.

Caracterización de textos sobre la base de la densidad léxica

Cynthia Zhou, Alexandra Sanjinez, Úrsula Carrión, Walter Aliaga, Victor H. Ayma, Luciano Stucchi.

Universidad del Pacífico, Perú.

La estructura de un texto puede modelarse como un grafo, donde las palabras se representan como nodos y sus co-ocurrencias como aristas, lo que permite aplicar herramientas de teoría de redes al análisis lingüístico. Estudios previos han demostrado que métricas estructurales pueden revelar propiedades clave del discurso, como cohesión, complejidad y estilo. En este trabajo, proponemos una caracterización cuantitativa de textos periodísticos mediante grafos léxicos y analizamos la relación entre la densidad del grafo y el número de nodos, como un indicador de la complejidad léxica. Para ello, hemos recopilado noticias mediante técnicas de web scrapping, de diferentes fuentes y autores. El análisis nos revela patrones que permiten distinguir estilos de escritura y niveles de cohesión léxica, lo que permite proponerla como una herramienta útil para el estudio comparativo de textos en medios de comunicación.

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