# BOOK OF ABSTRACTS

# BENET 2021 10th BELGIAN NETWORK RESEARCH MEETING

November 18, 2021





# BENET 2021 10TH BELGIAN NETWORK RESEARCH MEETING

The 10th edition of the Belgian Network Research Meeting (BENet) is hosted by naXys (Namur Institute for Complex Systems) at the University of Namur on November 18, 2021. The webpage of the meeting is https://www.naxys.be/benet/. The purpose of this annual gathering is to foster communication among Belgian researchers employing the network paradigm on their work, regardless of the discipline. The scope of the meeting includes but is not restricted to social & organizational theory, economics & finance, social media & online activities, human communication & mobility, information diffusion & opinion dynamics, political networks & collective action, ecology, ethology, food webs, biology & bioinformatics, epidemiology, physics, mathematics & statistics, modeling and data analysis.

Previous editions were held in Ghent (Ghent University 2020, online event), Hasselt (UHasselt 2019), Ghent (UGent 2017), Louvain-la-Neuve (UCLouvain 2016), Namur (UNamur 2015), Brussels (ULB 2014), Leuven (IIS/KUL 2013), Antwerp (UA 2012), and Brussels (VUB 2011). To keep updated about future events and activities of the network, subscribe to the list http://listserv.vub.ac.be/mailman/listinfo/benet.

# Organizers

# Timoteo Carletti

Department of Mathematics, naXys, University of Namur, Belgium.

# Jérôme Daquin

Department of Mathematics, naXys, University of Namur, Belgium. School of Engineering & IT, University of New South Wales (UNSW), Canberra, Australia.

# Riccardo Muolo

Department of Mathematics, naXys, University of Namur, Belgium.

# Sponsor

The event is supported by naXys and the Department of Mathematics of the University de Namur.

# PROGRAM

## 9h10-9h30 Registration & Coffee

9h30-9h40 Welcome & Opening Remarks Anne-Sophie Libert (director of naXys) & Timoteo Carletti (chair organizer)

9h40-10h40 Session 1 - Chair Pietro Coletti (Hasselt Universiteit)

- Universal scaling of social interactions across animal species Luis Rocha (Ghent University)
- Node-edge relationship in ecological networks and their robustness to node removals Camille Carpentier (University of Namur)
- On the training of sparse and dense deep neural networks: less parameters, same performance Lorenzo Chicchi (Università di Firenze)

### 10h40-11h00 Coffee Break

11h00-11h50 Keynote 1 – Chair Timoteo Carletti (University Namur)

• Higher-order networks and their dynamics – Ginestra Bianconi (online, Queen Mary University of London)

11h50-12h10 Lightning Session – Chair Lorenzo Giambagli (University of Namur, Università di Firenze)

- Topological features of EEG and hypnotisability Maxime Lucas (ISI Foundation Torino)
- Lightning Round of Poster Presentations

12h10-13h40 Lunch & Poster Session

13h40-14h30 Keynote 2 – Chair Roma Siugzdaite (Ghent University, University of Cambridge)

• Signal processing on graphs and simplicial complexes – Michael Schaub (RWTH Aachen Universität)

14h30-15h30 Session 2 - Chair Luca Gallo (University of Namur, Università di Catania)

- Spectral Pruning of Fully Connected Layers: Ranking the Nodes Based on the Eigenvalues Lorenzo Giambagli (University of Namur, Università di Firenze)
- A Diffusion Approximation to the Competition-Induced Criticality Model Kleber Oliveira (University of Limerick)
- Dimension reduction of complex networks to address critical transitions on low dimensional manifolds Daniele Proverbio (University of Luxembourg, University of Exeter)

### 15h30-16h00 Coffee Break & Poster Session

16h00-17h00 Session 3 – Chair Danai Kafetzaki (KU Leuven)

- Connecting dots and pots: Integrating network science and pottery studies in archaeology Dries Daems (online, Middle East Technical University, KU Leuven)
- The impact of social contact networks on innovation and creation of new ideas Fatemeh Zarei (Ghent University)

• Beyond pairwise network similarity: exploring Mediation and Suppression between networks – Daniele Marinazzo (Ghent University)

17h00-17h50 Keynote 3 – Chair Riccardo Muolo (University of Namur)

• Network inference via process motifs for lagged correlation in linear stochastic processes – Alice Schwarze (University of Washington)

# 17h50-18h00 Closing Remarks

### Posters

- Phase transition induced by non-linear random walks on lattices Jean-François de Kemmeter (University of Namur)
- Maximum Entropy applied on Twitter disinformation datasets Bart de Clerck (Royal Military Academy, Ghent University)
- Convolutional Neural Networks for image analysis Valentin Delchevalrie (University of Namur)
- Selecting controlled nodes to reduce network synchronization Martin Moriamé (University of Namur)
- Finite propagation enhances Turing patterns in reaction-diffusion networked systems Riccardo Muolo (University of Namur)
- Lack of practical identifiability may hamper reliable predictions in COVID-19 epidemic models Luca Gallo (University of Namur, Università di Catania)
- Geometrical description of the argument of weak values of general observables in therms of SU(N) generators Lorena Ballesteros Ferraz (University of Namur)
- Effects of local interactions in epidemis outbreaks in networks of structured populations Cédric Simal (University of Namur)
- WAL-SAT (WALlonia Space Awareness Technology): network theory and machine learning approach for space traffic management Matteo Romano (University of Namur)

# **KEYNOTES SPEAKERS**

#### Higher-order networks and their dynamics, by Ginestra Bianconi<sup>1</sup>

<sup>1</sup> School of Mathematical Sciences, Queen Mary, University of London, London, United Kingdom

Higher-order networks [1] describe the many-body interactions of a large variety of complex systems, ranging from the brain to collaboration networks and social contact networks. Simplicial complexes are generalized network structures which allow us to capture the combinatorial properties, the topology and the geometry of higher-order networks. In this talk we will show that simplicial complexes provide a very general mathematical framework to reveal how higher-order dynamics including synchronization and epidemic spreading depends on simplicial network topology. We will show that higher-order synchronization describing the dynamics of topological signals defined on links, triangles and higher-dimensional simplices is explosive [2-3] and we will show that this rich dynamics can have an important role for understanding brain rhythms. We will also show how epidemic spreading on higher-order networks [4] can take into account for time-dependent contacts due to co-location in space and how this modelling can help us understand the spreading dynamics of airborne diseases.

### References

1. G. Bianconi, Higher-order networks: An introduction to simplicial complexes (Cambridge University Press, 2021)

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### Signal processing on graphs and simplicial complexes, by Michael Schaub<sup>1</sup>

<sup>1</sup> Department of Computer Science, RWTH Aachen University, Aachen, Germany

We are confronted with signals defined on the nodes of a graph in many applications. Think for instance of a sensor network measuring temperature; or a social network, in which each person (node) has an opinion about a specific issue. Graph signal processing (GSP) tries to device appropriate tools to process such data by generalizing classical methods from signal processing of time-series and images – such as smoothing, filtering and interpolation – to signals defined on graphs. Typically, this involves leveraging the structure of the graph as encoded in the spectral properties of the graph Laplacian. In other applications such as traffic network analysis, however, the signals of interest are naturally defined on the edges of a graph, rather than on the nodes. After a very brief recap of the central ideas of GSP, we examine why the standard tools from GSP may not be suitable for the analysis of such edge signals. More specifically, we discuss how the underlying notion of a 'smooth signal' inherited from (the typically considered variants of) the graph Laplacian are not suitable when dealing with edge signals that encode flows. To overcome this limitation we devise signal processing tools based on the Hodge-Laplacian and the associated discrete Hodge Theory for simplicial (and cellular) complexes. We discuss applications of these ideas for signal smoothing, semi-supervised and active learning for edge-flows on discrete (or discretized) spaces.

# Network inference via process motifs for lagged correlation in linear stochastic processes, by Alice Schwarze<sup>1</sup>

<sup>1</sup> Department of Biology, University of Washington, Washington, United States

Many existing methods for causal inference from time-series data require (1) stationary or de-

trended input data, which can make it difficult to infer networks from observations of dynamical systems with slow mean-reversion, and (2) a trade-off between scalability and accuracy, which can make it difficult to infer large networks. We demonstrate that for time-series data of a linear stochastic system with slow mean-reversion, commonly used pairwise edge-likelihood measures (PELMs) including Granger causality, transfer entropy, and convergent crossmapping do not lead to a much higher accuracy of inferred networks than lagged correlation. Using process motifs for a linear stochastic process, we derive two new PELMs that aim to improve the inference accuracy of lagged correlation by correcting lagged correlation for confounding factors and reverse causation. For linear stochastic systems, our proposed PELMs are fast, accurate, and easy-to-implement methods for network inference with a clear theoretical underpinning. They provide a promising alternative to commonly used inference methods, such as Granger causality, vector- autoregression, and sparse inverse covariance estimation.

# SPEAKERS

Universal scaling of social interactions across animal species, by Luis E C Rocha<sup>1,2</sup>

<sup>1</sup> Department of Economics, Ghent University, Ghent, Belgium

<sup>2</sup> Department of Physics and Astronomy, Ghent University, Ghent, Belgium

Social animals self-organise to create groups to increase protection against predators and productivity. One-to-one interactions are the building blocks of these emergent social structures and may correspond to friendship, grooming, communication, among other social relations. These structures should be robust to failures and provide efficient communication to compensate the costs of forming and maintaining the social contacts but the specific purpose of each social interaction regulates the evolution of the respective social networks. We collate 611 animal social networks and show that the number of social contacts E scales with group size N as a super-linear power-law  $E = CN^{\beta}$  for various species of animals, including humans, other mammals and non-mammals. We identify that the power-law exponent  $\beta$  varies according to the social function of the interactions as  $\beta = 1 + a/4$ , with  $a \approx 1, 2, 3, 4$ . By fitting a multi-layer model to our data, we observe that the cost to cross social groups also varies according to social function. Relatively low costs are observed for physical contact, grooming and group membership which lead to small groups with high and constant social clustering. Offline friendship has similar patterns while online friendship shows weak social structures. The intermediate case of spatial proximity (with  $\beta = 1.5$  and clustering dependency on network size quantitatively similar to friendship) suggests that proximity interactions may be as relevant for the spread of infectious diseases as for social processes like friendship.

#### References

Rocha LEC, Schoors K, Ryckebusch J, Smith M (2021), The scaling of social interactions across animals species. Scientific Reports 11:12584

On the training of sparse and dense deep neural networks: less parameters, same performance, by Lorenzo Chicchi<sup>1</sup>, Lorenzo Giambagli<sup>1</sup>, Lorenzo Buffoni<sup>1</sup>, Timoteo Carletti<sup>2</sup>, Marco Ciavarella<sup>1</sup>, and Duccio Fanelli<sup>1</sup>

<sup>1</sup> Dipartimento di Fisica e Astronomia, Università di Firenze, INFN and CSDC, Firenze, Italy

<sup>2</sup> naXys, University of Namur, Namur, Belgium

Learning from data via deep neural networks [1-4] is becoming popular in an ever-increasing number of applications [5–8]. Deep neural networks can be trained in reciprocal space, by acting on the eigenvalues and eigenvectors of suitable transfer operators in direct space [9]. Adjusting the eigenvalues, while freezing the eigenvectors, yields a substantial compression of the parameter space. This latter scales by definition with the number of computing neurons. The classification scores, as measured by the displayed accuracy, are however inferior to those attained when the learning is carried in direct space, for an identical architecture and by employing the full set of trainable parameters (with a quadratic dependence on the size of neighbor layers). In this paper, we propose a variant of the spectral learning method as appeared in Giambagli et al [9], which leverages on two sets of eigenvalues, for each mapping between adjacent layers. The eigenvalues act as veritable knobs which can be freely tuned so as to (i) enhance, or alternatively silence, the contribution of the input nodes, (ii) modulate the excitability of the receiving nodes with a mechanism which we interpret as the artificial analogue of the homeostatic plasticity. The number of trainable parameters is still a linear function of the network size, but the performances of the trained device gets much closer to those obtained via conventional algorithms, these latter requiring however a considerably heavier computational cost. The residual gap between conventional and spectral trainings can be eventually filled by employing a suitable decomposition for the non trivial block of the eigenvectors matrix. Each spectral parameter reflects back on the whole set of inter-nodes weights, an attribute which we shall effectively exploit to yield sparse networks with stunning classification abilities, as compared to their

homologues trained with conventional means.

References

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# Node-edge relationship in ecological networks and their robustness to node removals, by Camille Carpentier<sup>1,2</sup>, Frederick De Laender<sup>1,2</sup>

<sup>1</sup> Department of Biology, ILEE, University of Namur, Namur, Belgium

<sup>2</sup> naXys, University of Namur, Namur, Belgium

For over 45 years, ecologists have tried to understand how the number of ecological interactions (edges) scales with the number of species (nodes) in ecological networks. While most studies consider the edge-node relationship to be universal, it appears that this relationship can be described as a network-specific property. This network-specific approach of the edge-node relationship is based on degree distribution and allows identification of a single parameter b that describes how the number of edges changes when nodes are removed in a network. Because of this, b also allows formal expression of the network's robustness facing node removals. This expression is the same for errors (random removals) and attacks (removal of the most-connected nodes) and depends on and on the shape of the degree distribution of the particular network. Because this expression is based on the adjacency matrix only, it provides a null model to understand how other network properties (e.g. edges direction, sign, and weight) impact ecosystem resistance to species loss, elucidating the relationship between network structure and its robustness to node removal.

On the training of sparse and dense deep neural networks: less parameters, same performance, by Lorenzo Chicchi<sup>1</sup>, Lorenzo Giambagli<sup>1</sup>, Lorenzo Buffoni<sup>1</sup>, Timoteo Carletti<sup>2</sup>, Marco Ciavarella<sup>1</sup>, Duccio Fanelli<sup>1</sup>

<sup>1</sup> Dipartimento di Fisica e Astronomia, Università di Firenze, INFN and CSDC, Firenze, Italy

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Learning from data via deep neural networks [1-4] is becoming popular in an ever- increasing number of applications [5–8]. Deep neural networks can be trained in recip- rocal space, by acting on the eigenvalues and eigenvectors of suitable transfer operators in direct space [9]. Adjusting the eigenvalues, while freezing the eigenvectors, yields a substantial compression of the parameter space. This latter scales by definition with the number of computing neurons. The classification scores, as measured by the displayed accuracy, are however inferior to those attained when the learning is carried in direct space, for an identical architecture and by employing the full set of trainable param- eters (with a quadratic dependence on the size of neighbor layers). In this paper, we propose a variant of the spectral learning method as appeared in Giambagli et al [9], which leverages on two sets of eigenvalues, for each mapping between adjacent layers. The eigenvalues act as veritable knobs which can be freely tuned so as to (i) enhance, or alternatively silence, the contribution of the input nodes, (ii) modulate the excitability of the receiving nodes with a mechanism which we interpret as the artificial analogue of the homeostatic plasticity. The number of trainable parameters is still a linear function of the network size, but the performances of the trained device gets much closer to those obtained via conventional algorithms, these latter requiring however a consid- erably heavier computational cost. The residual gap between conventional and spectral trainings can be eventually filled by employing a suitable decomposition for the non trivial block of the eigenvectors matrix. Each spectral parameter reflects back on the whole set of inter-nodes weights, an attribute which we shall effectively exploit to yield sparse networks with stunning classification abilities, as compared to their homologues trained with conventional means.

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# Topological features of EEG and hypnotisability, by Maxime Lucas<sup>1</sup>

<sup>1</sup> ISI Foundation, Turin, Italy

Electroencephalography (EEG) is a very commonly used neuroimaging technique. Yet, EEG data are affected by arbitrary choices such as a reference site during the experiment and pre-processing steps before the data can be analysed. Hence, it is important to find analyses and quantities that are as independent as possible of those choices. Recent results from our group show that the topological structure of state spaces reconstructed via embedding of the EEG data have such property of independence, in addition to being subject-specific. We apply this method and investigate the topological structure of embedded spaces of EEG recordings in experiments studying hypnotic states and the differences between lowly and highly hypnotisable subjects. We will present preliminary results of this ongoing work.

# Spectral Pruning of Fully Connected Layers: Ranking the Nodes Based on the Eigenvalues,

by Lorenzo Buffoni<sup>3</sup>, Enrico Civitelli<sup>2</sup>, Lorenzo Giambagli<sup>1,4</sup>, Lorenzo Chicchi<sup>1</sup>, and Duccio Fanelli<sup>1</sup>

<sup>1</sup> Università degli Studi di Firenze, Dipartimento di Fisica, Sesto Fiorentino, Italy

 $^2$ Università degli Studi di Firenze, Dipartimento di Ingegneria dell'informazione, Firenze, Italy

 $^{3}$ Instituto de Telecomunicaco<br/>es, University of Lisbon, Lisbon, Portugal

<sup>4</sup> naXys, University of Namur, Namur, Belgium

In standard neural network training one seeks to optimize the weights that link pairs of neu-rons belonging to adjacent layers of the selected architecture. Alternatively, the learning can be carried out in reciprocal space: the spectral attributes of the transfer operators that underlie information handling across layers define the actual target of the optimization. This procedure, first introduced in [1] and further refined in [2], enables a substantial compression of the space of trainable parameters. The spectral method leverages on a limited subset of key parameters which impact on the whole set of weights in direct space. This work is meant to show that the spectral learning technology provides an efficient analysis tool for the trained network. More specifically, we prove that the eigenvalues do provide a reliable ranking of the nodes, in terms of their associated contribution to the overall performance of the trained network. Working along these lines, we empirically show that the absolute value of the trained eigenvalues consti- tute an excellent marker of the node significance in carrying out the assigned discrimination task. This observation can be effectively exploited in two ways: (i) Downstream of training, to filter the nodes in terms of their relative importance and prune the unessential units so as to yield a more compact model, with almost identical classification abilities. (ii) Upstream of the training, to find the smallest network to efficiently carrying out the classification task. The efficacy of the aforementioned procedures, at first heuristically proven, has been tested using feedforeward neural network and employing several activation functions and datasets.

### References

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 On the training of sparse and dense deep neural networks: less parameters, same performance, L. Chicchi, L. Giambagli, L. Buffoni, T. Carletti, M. Ciavarella, D. Fanelli; arXiv preprint arXiv:2106.09021, (2021)

A Diffusion Approximation to the Competition-Induced Criticality Model, by Kleber A. Oliveira<sup>1</sup>, Samuel Unicomb<sup>1</sup>, James P. Gleeson<sup>1</sup>

<sup>1</sup> MACSI, Department of Mathematics and Statistics, University of Limerick, Limerick, Ireland

Online communication is happening at an unprecedented scale and we are not able to regulate it adequately due to, among other things, the lack of understanding of the underlying physical processes [1]. The Competition-Induced Criticality model is an attempt at describing how information diffuses in the short-term [2]. It assumes social media users carry a limited number of memes at a time on their screens and they may receive memes from those they are connected to. At each iteration, they may either retweet their current meme or create a new one and also override their neighbours' screens. In this work, we offer a novel formulation of a simplified version of this model through a divide-andconquer strategy of aggregating activations via Central Limit Theorem (CLT). We derive a stochastic differential equation that allows the simulation of meme trajectories independently, which means they can be computed in parallel and a very similar system configuration is reached much more quickly and less costly in terms of memory. Additionally, we work the case when the underlying network is scale-free (hence produced from a process to which degree variance is unbounded) by refactoring the derivation with stable distributions and the generalised CLT [3]. Approximating this dynamics with a diffusion process also enables numerical investigation of different aspects of meme behaviour harder to extract from the branching process formalism, such as the evolution of meme screen occupancy average and standard deviation.

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Berlin Heidelberg, 2006), 2nd ed.

# Dimension reduction of complex networks to address critical transitions on low- dimensional manifolds, by Daniele Proverbio<sup>1,2</sup>

<sup>1</sup> University of Luxembourg, Luxembourg Centre for Systems Biomedicine, Belvaux, Luxembourg
<sup>2</sup> University of Exeter, College of Engineering, Mathematics and Physical Sciences, Exeter, United Kingdom

Many natural and social systems exhibit abrupt and rapid regime shifts between alternative stable states. A growing body of literature – under the framework of Critical Transitions – is devoted to identifying generic early warning signals to alert for impending shifts in partially unknown systems [1]. Nonetheless, much attention has so far been paid to low dimensional systems, for which the center manifold theorem guarantees generic results around bifurcation normal forms [2]. In recognition that many natural systems are properly described as network systems, dimension reduction techniques are recently being investigated [3]. The biggest challenges are that, in many instances, only the network topology – partial or complete – is known; in addition, some regime shifts can yield such severe consequences – cellular mutation, ecological collapse, climate changes – that knowledge about their resilience is necessary a priori, without the possibility for empirical stability analysis. Hence, precise methods with small sets of assumptions are preferable. In this talk, I will revise issues and results around this topic and present the most recent suggestions tackling the dimension reduction problem. I will also discuss the significance of such studies for systems with partial models or poorly identifiable parameters, to foster discussions and ideas on this fascinating field.

References

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# Connecting dots and pots: Integrating network science and pottery studies in archaeology, by Dries $Daems^{1,2}$

<sup>1</sup> Middle East Technical University, Ankara, Turkey

<sup>2</sup> KU Leuven, Leuven, Belgium

Archaeology uses material traces to learn about life and society in the past. Pottery material, in particular, has been one of the staples of archaeological research for over a century. This long history has resulted in standardized approaches to pottery analysis, using morphological and other parameters to establish two main axes of structuration: 1) typological classification; and 2) chronology, often pursued in combination as typo-chronological frameworks. The abundance of pottery material, combined with standardized practices of documentation, makes it an ideal data source for the recent upsurge in computational approaches in archaeology. This talk highlights the combination of network science and pottery studies as a vibrant research domain in archaeology. I first review major applications of network science in pottery studies, before presenting two novel network-based approaches to pottery studies, each addressing the aforementioned main goals of pottery studies. First, the usage of morphological similarity networks for creating typological classifications, using a dataset from Late Bronze Age to Hellenistic pottery from Sagalassos (southwest Turkey). Second, the effects of time averaging on pottery chronologies using a dataset of Hellenistic and Roman tablewares from the Eastern Mediterranean. The aim of this paper is to show the potential of network approaches for archaeology in tandem with traditional artefact studies, bringing together data scientists and archaeologists. The end goal of this approach is to develop a disciplinary framework where archaeological and computational approaches mutually reinforce each other through their respective strengths of interpretability and tractability.

The impact of social contact networks on innovation and creation of new ideas, by F. Zarei<sup>1,2</sup>, J. Ryckebusch<sup>2</sup>, K. Schoors<sup>1</sup>, L. E C Rocha<sup>1,2</sup>

<sup>1</sup> Department of Economics, Ghent University, Ghent, Belgium

<sup>2</sup> Department of Physics and Astronomy, Ghent University, Ghent, Belgium

Innovation is fundamental for development and creates a competitive advantage for societies and organizations. Innovation generates novel complex protocols, technologies, or ideas, and is rarely the result of individual capabilities. Most often, people combine complementary expertise and perspectives to innovate. Social networks structure play a key role because it defines how information flows and exchanged within people. Although the study of innovation includes the creation and diffusion of new ideas, most of the recent studies are only about the diffusion of ideas in a social network [1,2]. It has been shown that people focus social interactions within the same group, which creates holes in knowledge and in the information flow between groups, or simply, structural holes [3,4], and people connecting such groups are called brokers and believed to be at higher risk of having innovative ideas because of their potential to leverage knowledge from different groups. In this study, we analyze how the social network structure affects the creation of ideas from a dynamic perspective by designing an agent-based network model. The model studies mechanisms driving innovation through the simulation of human characteristics, social interactions, and innovation processes. We show innovation depends on both microscopic and macroscopic network structures. Increasing microscopic structural heterogeneity leads to high complexity levels for some individuals. Although heterogeneity causes some individuals to innovate more, decreases the average complexity level (which is a measure of the fraction of innovation) of the entire network. With a low macroscopic heterogeneity, useful network structures for the complexity level are reached.

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# Beyond pairwise network similarity: exploring Mediation and Suppression between networks, by Lucas Lacasa<sup>1</sup>, Sebastiano Stramaglia<sup>1</sup>, Daniele Marinazzo<sup>1</sup>

<sup>1</sup> Department of Data Analysis, Ghent University, Ghent, Belgium

Network similarity measures quantify how and when two networks are symmetrically related, including measures of statistical association such as pairwise distance or other correlation measures between networks or between the layers of a multiplex network, but neither can directly unveil whether there are hidden confounding network factors nor can they estimate when such correlation is underpinned by a causal relation. In this work we extend this pairwise conceptual framework to triplets of networks and quantify how and when a network is related to a second network directly or via the indirect mediation or interaction with a third network. Accordingly, we develop a simple and intuitive set-theoretic approach to quantify mediation and suppression between networks. We validate our theory with synthetic models and further apply it to triplets of real-world networks, unveiling mediation and suppression effects which emerge when considering different modes of interaction in online social networks and different routes of information processing in the nervous system.

# POSTERS

**Phase transition induced by non-linear random walks on lattices**, by Jean-François de Kemmeter<sup>1</sup>, Malbor Asllani<sup>2</sup>, Timoteo Carletti<sup>1</sup>

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Diffusion processes are among the most important stochastic processes with numerous applications through scientific disciplines. From the microscopic point of view, they describe the motion of individual (particles, molecules, cells, etc.) walkers which randomly hop from a spatial patch to another, usually interconnected through a network structure. In regular networks, the density distribution converges to a homogeneous asymptotic state. However, this scenario doesn't take into account the limiting carrying capacities of the nodes and the nonlinear interactions among walker sharing the same node, both phenomena being salient features of many real-life complex systems. Recently [1,2], a class of nonlinear random walks was introduced to model diffusion in a crowded environment. In the present work, we extend the latter approach by incorporating a proxy of agents' "social behavior": in addition to avoid crowded nodes, they also tend to "follow" each other. Interestingly, when taking place on top of a regular network, the homogeneous state becomes unstable when the density of agents decreases below a critical threshold. This symmetry breaking is described by a phase transition from a homogeneous state to an inhomogeneous one, the latter being characterized by the emergence of empty nodes. Interesting enough, the fraction of empty nodes follows a quantized pattern.

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## Maximum entropy networks applied on Twitter disinformation datasets, by Bart De Clerck<sup>1,2</sup>

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Identifying and detecting disinformation is a major challenge. Twitter provides datasets of disinformation campaigns through their information operations report. Each dataset contains information about the users that were identified as connected to a disinformation campaign. These datasets allow to create interaction networks. We compare the results of community detection using a classical network representation with a maximum entropy network model (using a directed bipartite interaction model). This approach is motivated by the possibility of suppressing noise - one-time or low-frequency interactions between users that can distort the discovered communities - in a more statistically sound way than simply ignoring all interactions below a certain threshold. We conclude that the latter method is useful to identify the most significant interactions in the disinformation network over multiple datasets. We also apply the method to a disinformation dataset related to COVID-19 which allows us to assess the repeatability of studies on disinformation datasets. We found that researchers who wish to conduct a comparative study or to reproduce previous results may run into problems due to data availability. Indeed, as social media platforms are ramping up the fight against disinformation, it is often impossible to retrieve data that was used in a study, even when researchers share the source of the data in accordance with a platform's terms of use.

# Convolutional Neural Networks for image analysis, by Valentin Delchevalerie<sup>1,2</sup>

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Convolutional Neural Networks (CNNs) are known as being among the most powerful tools for image analysis. One of the main reasons why CNNs are so much used in computer vision lies in the fact that they achieve translation invariance thanks to convolutions. Filters sweep the image locally and patterns can be recognized regardless of their absolute position in the image. However, some other important types of invariance are more difficult to obtain. It is for example the case for the rotational invariance, which is relevant for many applications. One could for example consider medical imaging where tissues, cells, tumors or other objects of interest have a local, arbitrary, orientation in the images. In this work, we present a new type of convolutional layer that takes advantage of Bessel functions, well known in physics, to build Bessel-CNNs (B-CNNs). In B-CNNs, Bessel functions are used to obtain a representation of the images that is more adapted to deal with rotations. Based on this representation, we propose a new way to build CNNs that are invariant to all the continuous set of possible rotation angles by design.

# Selecting controlled nodes to reduce network synchronization, by Martin Moriamé<sup>1</sup>, Timoteo Carletti<sup>1</sup>

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In the framework of dynamical interactions between entities, synchronization- desynchronization patterns are widely studied. For instance, brain activity can be seen as a succession of synchronized and desynchronized states linking certain cerebral regions. In some settings, too strongly synchronized states may induce issues like epilepsy seizures in the brain. A way to deal with it is to act on some nodes' dynamics to prevent synchonization and this control action often has to be minimally invasive ([1]). As the eciency of this kind of method strongly depends on the choice of controlled nodes, we here exa- mined how to optimally select them. To do so we applied the control method designed in [1] on coupled Kuramoto oscillators networks with scale-free and small-worlds topologies. We compared several node selection methods : ran- dom, degree-based and functionability-based ones. Functionability is a new centrality measure developed in [2] whose aim is to nd the nodes with the most inuence on the system's synchronized state when we apply a phase shift on them. We found that functionability- and degree-based selections provide better results than the random one on scale-free networks. However, we found bad results for functionability-based selection on small-world ones. This could be explained in part by the weak spreading of highest functionability nodes is such networks. Finally, degree-based selection seems to be the best way to choose controllers. To generalize our results in a further work, we would like to analyze other network topologies such as core-periphery networks that exhibits features of both small-world and scale-free topologies.

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# **Finite propagation enhances Turing patterns in reaction–diffusion networked systems**, by Timoteo Carletti<sup>1</sup>, Riccardo Muolo<sup>1</sup>

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Nature is pervaded by regular spatio-temporal patterns, signature of self-organized processes where order emerges from disorder [1]. Very often, the interaction among the coupled microscopic constituting units can be modeled by reaction-diffusion equations governing the time evolution of the concentrations on a complex network [2]. Spatially homogeneous equilibria of the reaction-diffusion system may undergo a symmetry breaking instability eventually driving the system towards a spatially heterogeneous solution, i.e., a pattern, as firstly explained by Alan Turing [3]. Nowadays applications of the Turing instability phenomenon go well beyond the original framework of the morphogenesis. It stands for a pillar to explain self-organization in Nature [4,5], being rooted on an elegant mechanism involving slow diffusing activators and fast diffusing inhibitors. The reaction-diffusion process at the basis of the Turing mechanism is characterized by an infinite fast propagation and thus it can accurately model the physical phenomenon only in cases of very large diffusivity. To overcome this issue Cattaneo proposed to modify the constitutive equation by allowing for a relaxation term (inertial time), eventually obtaining a modified diffusion equation responsible for a finite propagation velocity [6]. In this work [7] we extend the conditions for the onset of Turing instability for a reactiondiffusion system defined on top of a complex network and modified according to the Cattaneo recipe, eventually obtaining a hyperbolic reaction-diffusion system defined on top of a complex network. We analytically determine the conditions for the onset of the Turing instability and we show that the proposed framework strongly enlarges the parameters region for which Turing instability can emerge. Indeed, Turing instability can set up with a fast activator and slow inhibitor, in contrast with the classical case. The patterns arising solely due to the presence of the inertial times, we propose to call them inertia-driven patterns.

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# Lack of practical identifiability may hamper reliable predictions in COVID-19 epidemic models, by Luca Gallo<sup>1,2,3</sup>, Mattia Frasca<sup>4,5</sup>, Vito Latora<sup>1,2,6,7</sup>, Giovanni Russo<sup>8</sup>

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Compartmental models are widely adopted to describe and predict the spreading of infectious diseases [1]. The unknown parameters of such models need to be estimated from the data. Furthermore, when some of the model variables are not empirically accessible, as in the case of asymptomatic carriers of COVID-19, they have to be obtained as an outcome of the model [2]. Here, we introduce a framework to quantify how the uncertainty in the data impacts the determination of the parameters and the evolution of the unmeasured variables of a given model. We illustrate how the method is able to characterize different regimes of identifiability [3,4], even in models with few compartments. Finally, we discuss how the lack of identifiability in a realistic model for COVID-19 may prevent reliable forecasting of the epidemic dynamics [4].

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# Geometrical description of the argument of weak values of general observables in terms of SU(N) generators, by L B. Ferraz<sup>1</sup>, D Lambert<sup>2</sup>, Y Caudano<sup>1</sup>

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Measurements play an important role in quantum mechanics. Amongst them, weak measurements have attracted much interest, for both theoretical and experimental reasons. Weak measurements are feasible when the interaction between a system and an ancilla is weak. After applying pre- and postselection (which is equivalent to imposing initial and final conditions to the system evolution), the ancilla wavefunction is shifted by an amount dependent on a quantity called the weak value, multiplied by the coupling constant. Weak values depend on the initial and final states of the system, as well as on the observable probed weakly. As weak values are complex and unbounded numbers, they give rise to many applications, especially related to metrology (due to their amplification power) and to probing foundational issues in quantum mechanics (due to the non-perturbative features of weak measurements). Usually, weak values are studied in terms of their real and imaginary parts. Nonetheless, to understand their geometrical properties (related to geometric phases), their study in terms of modulus and argument becomes crucial [1, 2]. In this work, we have studied the argument of the weak values of general observables in N-dimensional quantum systems. This argument describes the area of a geodesic triangle created by three vectors representing the preselected state, the observable and the post-selected state on a hypersphere. The area of this geodesic triangle characterizes the generalization of a solid angle. This scheme can be applied to measure 3D Stokes parameters in terms of Gell-Mann matrices. Our work extends significantly previous results that were limited to weak values of qubits observables and to projectors.

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# Effects of local interactions in epidemics outbreaks in networks of structured populations

, by C. Simal<sup>1,2</sup>, B. Siebert<sup>2</sup>, T. Carletti<sup>1</sup>, J. P. Gleeson<sup>2</sup>, M. Asllani<sup>3</sup>

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Spreading phenomena constitutes a class of processes that models applications that span from the diffusion of information to contagion diseases [1,2]. Depending on the spatial extension of the social interactions, mathematical modeling has been focused either on the role that the pairwise

interactions between individuals have on the overall dynamics or geometry of the spatial support where the agents move before they enter into contact. However, little is known about the effects that the local and global network structures simultaneously have on the dynamics outcomes, although the unequal interactions between these two parts might strongly affect the overall behavior. In this work, we introduce a mean-field model that explicitly considers the role that local interactions play in spreading models of structured populations [3]. Such a concatenated network model has been named a metaplex network [4]. Based on linear stability analysis, we show that the average degree of the local networks can capture their contribution in the global reaction-diffusion system and detect which of them drives the spreading of infection. Furthermore, we show that counterintuitively, the final size of the epidemic is not necessarily proportional to the global degree of the node that spreads the infection.

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# WAL-SAT (WALlonia Space Awareness Technology): network theory and machine learning approach for space traffic management, by Matteo Romano<sup>1</sup>, Jérôme Daquin<sup>1,2</sup>, Anne Lemaitre<sup>1</sup>, Timoteo Carletti<sup>1</sup>

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With more than 23,000 catalogued objects currently orbiting the Earth, space traffic is so dense in low-Earth orbit alone that hundreds of close approaches between catalogued space residents are notified to satellite operators per week, in possible collision scenarios. This situation is destined to worsen, due to the ever-more affordable exploitation of space and the growing population of defunct spacecraft and space debris, which threaten operational satellites and are becoming, to all effects, a new environmental problem. With a partnership between the naXys institute within the Department of Mathematics at the University of Namur and the industrial partner Aerospacelab, the WAL-SAT (WALlonia Space Awareness Technology) project is developing innovative approaches, techniques, and algorithms in the fields of space traffic management and space situational awareness. A software to better apprehend, manage, and advance space-traffic protocols will be prototyped, combining tools from dynamical system theory to accurately model the evolution of orbits and their uncertainties, network science to represent the topology of the population and obtain a global picture of the orbital collisional risk, and machine learning (ML) techniques to predict the temporal and long-term evolution of the network.