

*Higher-Order Connectivity and Correlations
in
Complex Systems*

Workshop @ Complexity Science Hub

1th Edition



November 25–26, 2019, Complexity Science Hub, Vienna, Austria

BOOK OF ABSTRACTS

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Supported by: Complexity Science Hub Vienna

Web: <https://www.csh.ac.at/event/higher-order-connectivity-correlations-complex-systems/>

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WS on Higher-Order Connectivity and Correlations in Complex Systems

Program Overview

Session Chairs

Mon 9:00-12:00 Stefan Thurner; Mon 13:15-14:30 Matjaz Perc; Mon 15:00-17:00 Alvaro Corral;
 Tue 9:00-12:00 Bosiljka Tadic; Tue 13:15-14:30 Matteo Marsili; Tue 15:00-17:00 Andrea Rapisarda;

Time	Mon	Time	Tue
9:00-10:00	OPENING	9:00-9:45	Petri
10:00-10:45	Baudot	9:45-10:15	Andjelkovic
10:45-11:15	Hanel	10:15-11:00	Bianconi
11:15-12:00	Marsili	11:00-11:30	Mitrovic Dankulov
12:00-13:15	LUNCH	11:30-12:00	Rapisarda
13:15-14:00	Arenas	12:00-13:15	LUNCH
14:00-14:30	Boguna	13:15-14:00	Kuehn
14:30-15:00	COFFEE	14:00-14:30	Jafari
15:00-15:30	Prochazka	14:30-15:00	COFFEE
15:30-16:00	Garcia	15:00-15:30	Diem
16:00-16:30	Perc	15:30-16:30	Battiston Bertagnoli Tadic
16:30-17:00	Corral: Discussion	16:30-17:00	Closing

Topological Entropy Measure of the Architecture of Simplicial Complexes

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Abstract. In recent years, the use of geometrical characterizations of complexity opened new horizons in the analysis of complex systems. In this context, new approaches are developed based on the tools of the algebraic topology and the mathematical structure of simplicial complexes, which made possible the analysis of higher-order connectivity and the related hidden structures in various complex systems. Some illustrative examples include the studies of simplicial complexes in the geometrical representations of time series [1,2], modelling cooperative self-assembly in nanoscience [3], and interpreting brain imaging data [4,5,6] and social dynamics [7,8]. The construction of simplicial complexes from a dataset represents the main point of the methodology for reconstruction of the relations in the dynamical system. There are different methods for building simplicial complexes from an observed dataset, e.g., the clique complex or the neighbourhood complex. The obtained simplicial complexes capture the relevant topological properties of the relations within the dataset. Here, we introduce a topological entropy measure based on the local structure of simplicial complexes. Using the model of aggregated simplexes of different orders, introduced in [3], we show how the topological entropy describes the coordination between vertices at different topology levels, i.e., the orders of interaction.

For describing the extended surrounding of vertices in both mathematical graph and simplicial complex, we introduced the Node's Q-vector [1]

$$Q^i = \{Q_{q_{max}}^i, Q_{q_{max}-1}^i, Q_{q_{max}-2}^i, \dots, Q_1^i, Q_0^i\},$$

where Q_q^i identifies the number of different simplexes of the order q in which the vertex i participates (an example is illustrated in Fig.1). Hence, the *vertex topological dimension* $dim Q^i = \sum_{q=0}^{q_{max}} Q_q^i$ represents the number of all simplexes to which the vertex i participates, or the vertex topological strength. Then the entropy of a topological level q is defined by [1]

$$S_Q(q) = - \frac{\sum_i p_q^i \log p_q^i}{\log M_q}$$

where $p_q^i = \frac{Q_q^i}{\sum_i Q_q^i}$ is the vertex occupation probability of the q level. The sum runs over all vertices and $M_q = \sum_i (1 - \delta_{Q_q^i, 0})$ is the number of vertices with a nonzero entry at the level q in the entire graph. In this context, the entropy measures the degree of cooperation among vertices. The vertices that comprise an isolated clique result in a higher entropy than the vertices that share different cliques at a particular level, which causes a decrease in the entropy. We also compute the number of all simplexes and faces f_q along the topology levels.

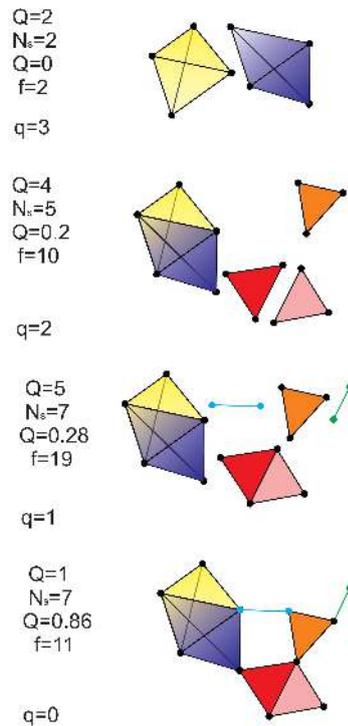


FIG . Example of a simplicial complex and its structure on different q -levels

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Higher-order interactions in complex networks of phase oscillators promote abrupt synchronization switching

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Abstract. Synchronization dynamics of network-coupled oscillators represents an important area of research in nonlinear science and complex networks [1, 2]. Applications where synchronization plays a critical role in a system's functionality include cardiac rhythms [3], power grid dynamics [4], and proper cell circuit behavior [5]. The interplay between structure and dynamics in such systems gives rise to novel nonlinear phenomena like switch-like abrupt transitions to synchronization [6, 7, 8] and cluster states [9, 10]. Recent work in physics and neuroscience have specifically highlighted the importance of higher-order interactions between dynamical units, i.e., three- and four-way interactions in addition to pair-wise interactions, and their role in shaping collective behavior [11, 12, 13, 14, 15, 16, 17, 18]. Here we show that higher-order interactions between coupled phase oscillators, encoded microscopically in a simplicial complex [19], give rise to added nonlinearity in the macroscopic system dynamics that induces abrupt synchronization transitions via hysteresis and bistability of synchronized and incoherent states. Moreover, these higher-order interactions can stabilize strongly synchronized states even when the pairwise coupling is repulsive. These findings reveal a self-organized phenomenon that may be responsible for the rapid switching to synchronization in many biological systems, without the need of particular correlation mechanisms between the oscillators and the topological structure.

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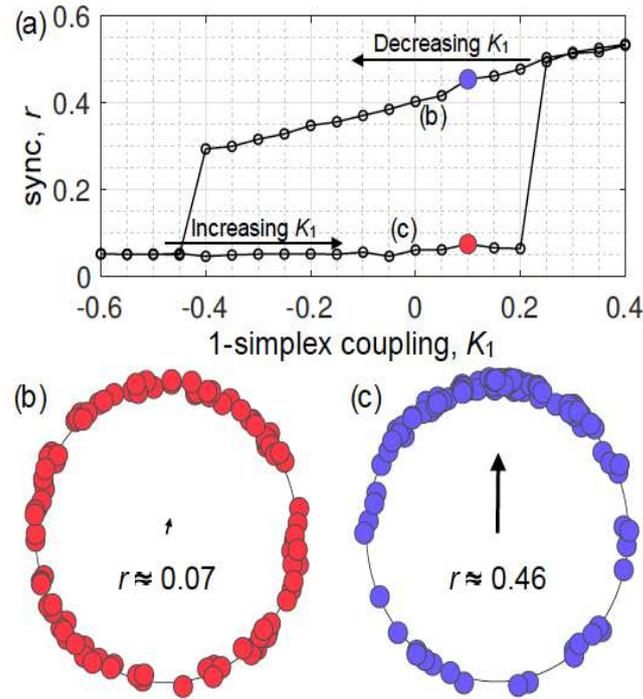


FIG. Abrupt synchronization in simplicial complexes: Macaque brain dataset. (a) The synchronization profile describing the macroscopic system state by the order parameter r as a function of 1-simplex coupling K_1 for higher-order coupling strengths $K_2=1.6$ and $K_3=1.1$. Results are obtained by adiabatically increasing K_1 from -0.6 to 0.4, then subsequently decreasing K_1 from 0.4 back to -0.6. This protocol reveals a hysteresis loop with abrupt synchronization and desynchronization transitions at $K_1^{\text{sync}} = 0.25$ and $K_1^{\text{desync}} = -0.4$ with a bistable region of incoherence and synchronization in between. Incoherent and synchronized states at $K_1 = 0.1$ are illustrated in panels (b) and (c), respectively.

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Cohomological characterization of Information and Higher Order Statistical Structures - Machine Learning and Statistical Physic Aspects

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Abstract. We establish methods that quantify the statistical interactions structure within a given data set using the characterization of information theory in cohomology by finite methods and provide their expression in term of statistical physic and machine learning.

In a first part, we will have a look at the formalism of Information Cohomology obtained with Bennequin and extended by Vigneaux to Tsallis entropies [1,2]. It considers random variables as partitions of atomic probabilities and the associated poset given by their lattice. The basic cohomology is settled by the Hochschild coboundary, with a left action corresponding to information conditioning. The first degree cocycle is the entropy chain rule, allowing to derive the functional equation of information and hence to characterize entropy uniquely as the first group of the cohomology. (minus) Odd multivariate mutual informations (MI, I_{2k+1}) appears as even degrees coboundary, and the introduction of a second trivial or symmetric action coboundary gives even MI (I_{2k}) in the odd degrees. If time permits, I will try also to present how this setting fits nicely into a topos giving a constructive and multivalued probabilistic logic, and how related results came out surprisingly from motiv studies in the work of Catelineau, Gangl et al., leading to the conjecture that higher groups are polylogarithmic forms à la Aomoto.

In a second part, we will have a look at the application of this formalism to real data, here genetic expression, and its interpretation in terms of statistical physic and machine learning [3,4,5,6]. Mutual statistical independence is equivalent to the vanishing of all k -MI ($I_k=0$), leading to the conclusion that the I_k define refined measures of statistical dependencies and that the cohomology quantifies the obstruction to statistical factorization. I_k generalize correlation coefficient to non-linear relations. We develop the computationally tractable subcase of on the simplicial (Boolean) sub-lattice, represented by entropy H_k and information I_k landscapes. The marginal I_1 component defines a self-internal energy functional U_k , and $(-1)^k I_k$, $k>1$ define the contribution of the k -body interactions to the free energy functional G_k given by the KL-divergence between marginals and the joined variable (the "total correlation"). The set of information paths in simplicial structure is in bijection with the symmetric group and random processes and provides a trivial topological expression of the 2nd law of thermodynamic. The slope of the I_k paths is (minus) the conditional mutual information. The local minima of I_k longest paths, a conditional mutual independence criterion, characterize a complex corresponding to the minima of free energy components. The application to genetic expression and cell-type classification recovers the known differential expressions and co-

regulations of genetic modules, giving a topological version of Waddington epigenetic landscapes that quantifies the epigenetic information storage and learning beyond pairwise-interactions. Negativity of information detects clusters of differential genetic expression analogously to first order transition to the condensed phase. The complex has a direct interpretation in terms of unsupervised and supervised deep learning where the neural network architecture is given by the chain complex. I give several examples of the application of information topology to standard recognition challenges in machine learning.

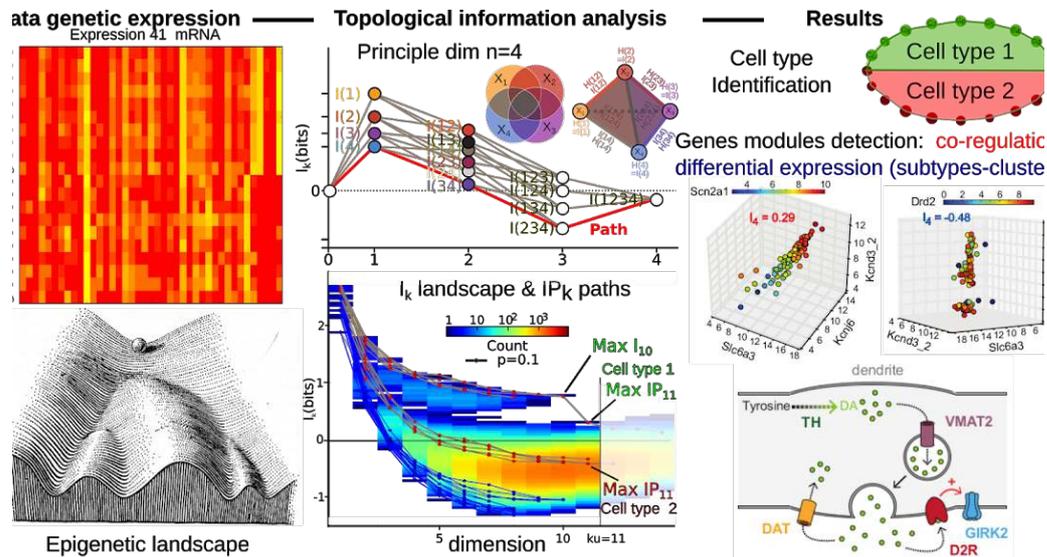


FIG . An example of unsupervised classification of cell types and genes modules with information topology (see [3,5] for details). The methods unravel biologically relevant subtypes as significant 10th order-dimension statistical interaction with a sample size of 41 genes and with few errors.

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Diffusion processes and the functional organization of complex networks

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Abstract. Complex networks provide a powerful tool for studying the behavior of real-world complex systems. Network science allows us to mathematically describe at an increasing level of detail the complexity of interactions between the units of a system, through multilayer networks, simplicial networks and hypergraphs. There is, therefore, an increasing interest in – and need for – the characterization of these networks at a fundamental level, through models and their (possibly latent) geometry. While models allow one to find the most suitable physical principles generating the observed networks, geometry allows us to probe the existence of a latent metric space to characterize the interplay between structure and function of a complex system. Our approach, based on diffusion processes, provides new insights both in the theoretical characterization of networks and in applications [1]. Mathematically, the propagator of the continuous time random walk is a time-varying function of the underlying network Laplacian, which encodes the topology of the network. The time parameter plays the role of a scale parameter, allowing for the analysis of networks from the micro-scale [2] structure (small diffusion times), to the meso- and macro-scale [3, 4]. This multiresolution method naturally accounts for higher-order interactions due to the interplay between structure and random search dynamics and can be used to characterize the importance of nodes in terms of median and contours, as well as their mesoscale organization.

In particular we will discuss applications to social networks (*Zachary's Karate Club*, *Network Scientists 2010*), biological networks (*connectomes of the Drosophila*, *Mouse and Macaque* and *the yeast proteome*), infrastructure networks (*international E-road network*).

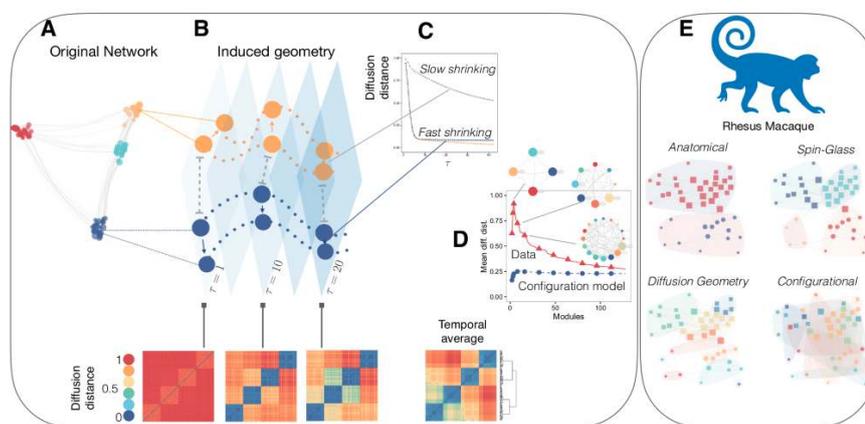


FIG . Functional organization of complex networks using the latent geometry induced by diffusion distance. (A) Euclidean embedding of a network with four clusters,

corresponding to the latent diffusion geometry with $\tau = 1$. (B–C) In the diffusion space, two nodes from the same functional cluster are – and keep – closer across time (τ) than nodes belonging to different clusters. The community structure is clearly visible in the block structure of the diffusion-distance matrices corresponding to the times. (D) The functional modules maximizing the average diffusion distance define the mesoscale structure which favors the overall information exchange and the significance of this structure can be quantified by comparing against the result obtained from a configuration model preserving the degree distribution of the original data while destroying other correlations. (E) Diffusion geometry analysis of the anatomical connectivity (335 visual, 85 sensorimotor and 43 heteromodal) from 30 visual cortical areas and 15 sensorimotor areas in the Macaque monkey. Clusters identified by structural analysis of the connectome using the spin-glass approach are different, as the anatomical organization and the mesoscale organization obtained from the configuration model.

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Emergent hyperbolic network geometry and dynamics

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Abstract. Simplicial complexes are ideal structure to investigate the interplay between network topology, geometry and dynamics. Here we propose a non-equilibrium model of growing simplicial complexes called Network Geometry with Flavor (NGF) [1] as a novel framework for emergent geometry. The model NGF generate networks with hyperbolic network geometry [2] starting from purely combinatorial rules that make no use of the underlying geometry of these structure. In this talk we will reveal the complexity of the NGFs and their non-trivial spectral properties [3]. Finally we will show how their spectral properties of the NGFs affects the synchronization dynamics defined on these structures [4,5]. These results shed light on novel experimental result on brain cultures showing that 3D scaffolds favor higher level of synchronization in neuronal cultures compared to 2D slices [6].

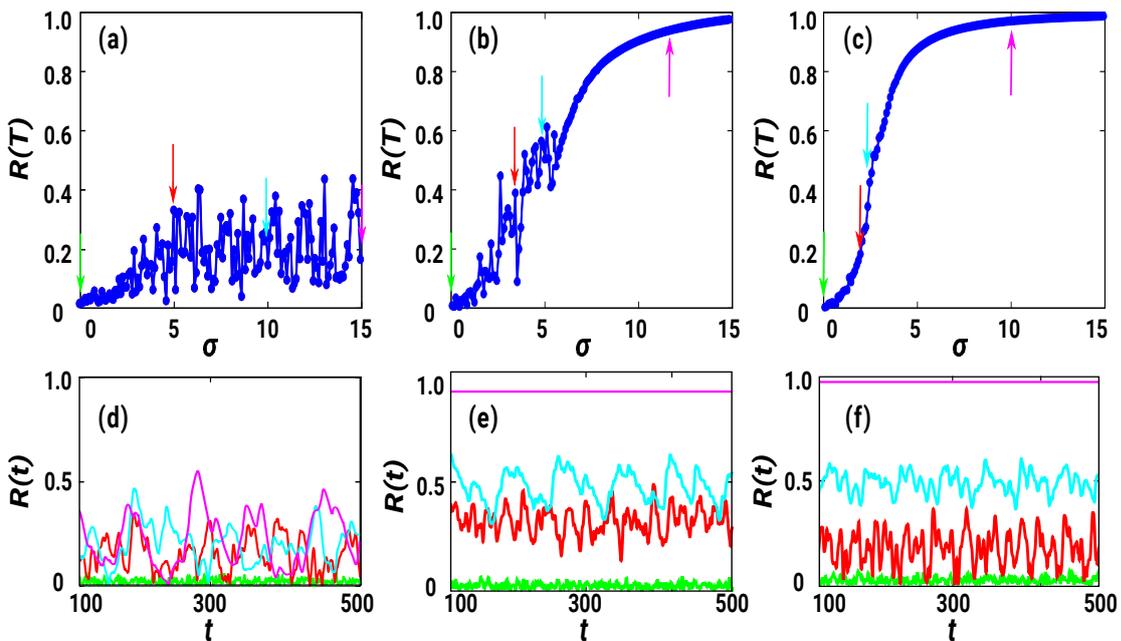


FIG . Synchronization order parameter $R(T)$ of the Kuramoto model as a function of the coupling constant s defined on the simplicial complex model Network Geometry with Flavor of dimension $D=1$ (panel a), $D=2$ (panel b), and $D=3$ (panel c). Time series of the order parameter $R(t)$ for $D=1$ (panel d), $D=2$ (panel e) and $D=3$ (panel f). Figure from [3].

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Small worlds and clustering in spatial networks. A maximum entropy approach to geometric random graphs

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Abstract

The main hypothesis of network geometry states that the architecture of real complex networks has a geometric origin [1,2,3]. The nodes of the complex network can be characterized by their positions in an underlying metric space so that the observable network topology—abstracting their patterns of interactions—is then a reflection of distances in this space. This simple idea led to the development of a very general framework able to explain the most ubiquitous topological properties of real networks [1, 2], namely, degree heterogeneity, the small-world property, and high levels of clustering. Network geometry is also able to explain in a very natural way other non-trivial properties, like self-similarity [1] and community structure [4,5,6], their navigability properties [7, 8, 9], and is the basis for the definition of a renormalization group in complex networks [10].

These results are all based on the class of models introduced in [1] which is isomorphic to a class of geometric random graphs models in hyperbolic geometry [2]. However, the particular form of the connection probability assumed in these models is not derived from first principles and, thus, the question remains as if other specific forms for the connectivity law could lead to similar results. Here [11] we show that the maximally random class of geometric models able to generate ensembles of graphs that are simultaneously sparse, small-world, heterogeneous, clustered, and without degree-degree correlations is the model introduced in [1, 2], which is thus to be considered as the fundamental null model for sparse, small-world, heterogeneous, and clustered real complex networks.

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Financial Contagion Risk on Multi-Layer Networks

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Abstract.

Systemic risk in financial networks has been extensively investigated for different types of contractual networks. Examples are interbank loan networks, derivative exposure networks, equity cross holding networks or exposure networks arising from asset crossholdings of agents. More recently the paradigm of multi-layer networks has been used to model systemic risk for multiple financial networks jointly. [1] aggregated different direct exposure networks and showed that looking at single layers in isolation can underestimate systemic risk drastically. [2] take a different approach using extensions of classical centrality measures, like eigenvector centrality or page rank to multiplex networks. However, these algorithms cannot provide a monetary quantification of banks systemic riskiness in case of defaults. DebtRank, which aggregates the losses occurring in asset valuation cascades does not suffer this problem, but is only defined on a single layer [3,4].

Thus, we suggest to extend the valuation shock transmission mechanism of DebtRank into the multilayer framework when considering networks layers, which cannot be aggregated by summation. We establish such an extension of DebtRank by incorporating the funding liquidity contagion layer into the algorithm. Thus, this allows us to quantify the costs for the financial system in case of bank defaults in a more complete way. It also allows us to simulate different combinations of funding liquidity shocks and valuation shocks jointly. Since, valuation and funding liquidity cascades are interacting on most bi-layer network specifications we expect higher systemic risk impacts of bank defaults, than if the two contagion mechanisms are modelled separately. In a related study [5] modelled these contagion channels as supraadjacency matrix in order to analyse network stability properties for small simultaneous macro shocks.

Considering multiple networks simultaneously can change the structure of higher order connection of agents. In financial transaction networks this means that second and higher order risks agents are facing when creating a link, can look dramatically different in comparison to a single layer perspective. The multilayer extension of DebtRank can take such higher order connections arising from different layers into account.

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Complex privacy and resilience in online social networks

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Abstract. The networked nature of our digital society generates new phenomena that did not exist before online communication became widespread. The combination of behavioral data traces from different platforms can pose both risks and opportunities. In this talk I will present an example of each: the threat of complex privacy and the opportunity to understand social resilience.

Online social networks exist in application ecosystems that allow them to access data from other services, for example gathering contact lists through mobile phone applications. Such data access might allow social networking sites to create shadow profiles with information about non-users that has been inferred from information shared by the users of the social network. This possibility motivates the shadow profile hypothesis: the data shared by the users of an online service predicts personal information of non-users of the service [1]. I will present the state of the art of empirical evidence on the possibility to infer location [2], sexual orientation, and marital status [3] based on information that users share in combination with their contact lists including non-users. These estimates are based on simple heuristics that give lower bounds on the predictability of private information based on links between users, but better-informed estimates can use higher order structures to test how the identification of social circles can worsen these privacy threats.

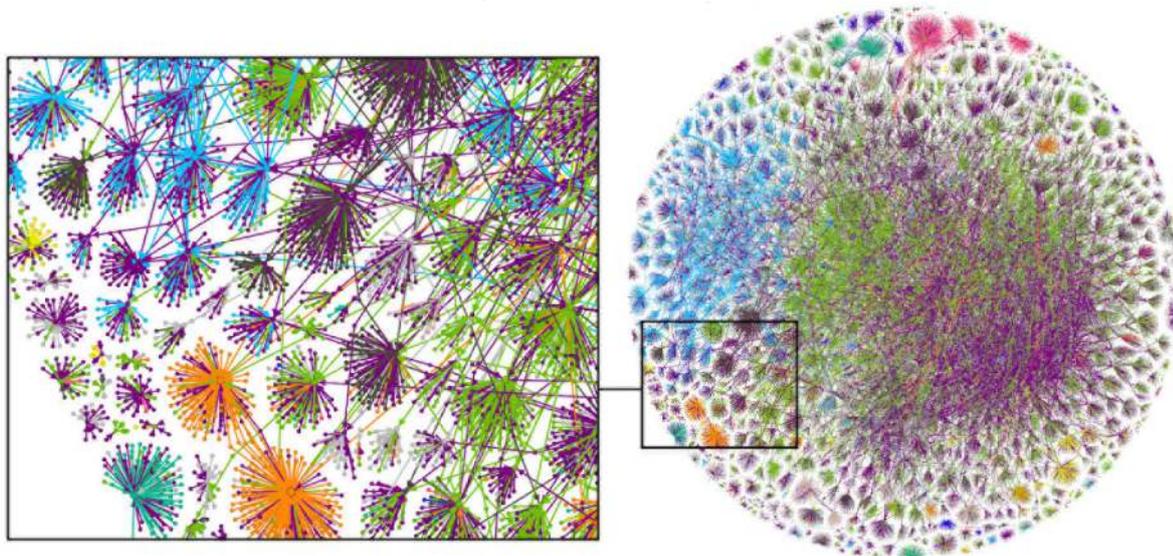


FIG. Ego network of locations of Twitter users including only alters that joined Twitter before the ego user, with nodes colored according to the country as a way to illustrate locations. A clear country assortativity pattern can be observed and exploited to infer the location of non-users.

Beyond auditing privacy issues, online social network data can be useful to understand more fundamental social dynamics. The structure of social networks, in combination with models of user decisions, can serve as an empirical basis to understand when online social networks collapse [4]. Furthermore, the behavioral traces of emotions in social networks reveal how a society responds to an external threat and how a social resilience process activates in reaction to a terrorist attack [5]. So far, all these approaches ignored the relevant role of social circles in creating identities and reinforcing social ties [6], a feature that could be analyzed by looking into higher order structures in the network.

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The emergence of structure - Correlations, Entropy Rate & Entropic Decision Rules

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Abstract.

The inference of structure within data using higher order correlations is a taunting challenge, especially when it comes to the question how the quantity of available data is related to the depth higher orders of correlations can be captured in the first place. The challenge may be complicated even more by the fact that typically, we only have limited prior knowledge about the dynamical class the underlying process of interest belongs to. For particular situations, such as the analysis of time series (for instance written texts in a body of literature) it is in fact basic information theory that provides us with formidable tools to adaptively zoom into the correlation landscape, which we subsume under *minimal description length* methodology. At its basis this methodology uses entropy based decision rules on expanding the alphabet of the process description language.



FIG. Simple cartoon for minimal description length procedure.

Following this path allows us to discuss fundamental connections between minimal description length methodology, maximum entropy principles and the emergence of generalized entropy functionals from Boltzmann type of entropies.

Interestingly, entropy functionals may not only be useful in predicting maximal configuration and deriving thermodynamic like relations for complex processes, e.g. [1,2], but with a slightly

different theoretical underpinning for classifying scaling properties of phase-space growth [3,4]. Finally we explore the possibility to let data “choose” the metric of its information geometry self-consistently, [5].

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Higher Order Interaction in Social Balance Dynamics

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Abstract. Every one of us has an experience that our relationships are not independent from each other. If we know a friend of my friend is a bad person maybe we will change my relationship with him/her. The original idea to adjust such relations is the structural balance theory proposed by Heider [1] and his key point: “We adjust our relationship based on reducing the psychological stress”. In 2005, Antal, Krapivsky, and Redner inspired to introduce the mathematical model of balance theory. Signed networks with both positive and negative links are used to indicate the relationships between nodes, such as friendship-like and animosity-dislike. In this model, the link between the nodes i and j is represented by S_{ij} , where $S_{ij} = \{\pm 1\}$ is the sign of the edge between nodes i and j , and it encodes the relationship (friend or enemy) between them. Balance theory is used to describe the attitudes of individuals to reduce tension among each other and measure social balance in a given signed network. The Hamiltonian of structural balance theory is $H = \frac{-1}{\binom{N}{3}} \sum_{ijk} S_{ij} S_{jk} S_{ki}$; where N is the size of network. This Hamiltonian leads a general tendency to a global structural balance, based on the updating of links status. A study on the dynamics of such sign networks can be traced back to Antal et al. [2]. They proposed a model based on the evolution of links, $\frac{dS_{ki}}{dt} = \sum_j S_{ij} S_{jk}$, which could describe how an imbalanced network attains a balanced state. To describe the dynamics mechanism of the structural balance, we explain the update rules devoted to evolving networks. At each update event, we randomly select a link and switch its sign to increase the total number of balanced triads. After each update step, some of the imbalanced triads become balance.

Although the structural balance represents a state of the network with a lack of contentious situations, there are always tensions in real networks. To study such networks, we generalize the balance dynamics in nonzero temperatures and the weighted networks, and then we will apply it in some real data-sets. Balance theory has been applied in many fields, from social, economic, ecologic to political systems [3–8]. We will look through the “Gene Regulatory Network” of the cancerous and healthy cells. We will show how the imbalance state has an essential role in the cancerous network has less imbalance than the normal one. We will observe that the financial networks during crises have the same behavior similar to the cancerous cells.

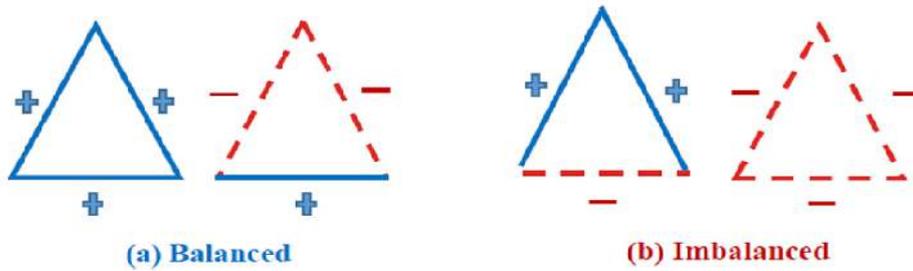


FIG . Different types of triads (a) balance states (b) imbalance states.

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Adaptive Networks and Higher-Order Structures

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Abstract. In this talk, we are going to discuss adaptive networks and their dynamics. We first introduce several adaptive network models [3,4,5] including adaptive versions of several classical interacting particle systems [1,2]. We start by presenting several results on an adaptive epidemic model with rewiring. We show how early-warning signs [6] can be transferred from individual and density-based measurements to broader classes of network measures [1]. Then we proceed to an adaptive voter model, where higher-order simplicies play a key role to model peer pressure. In this case, we show that the peer pressure accelerates the speed towards monolithic societies or towards fragmented societies [2].

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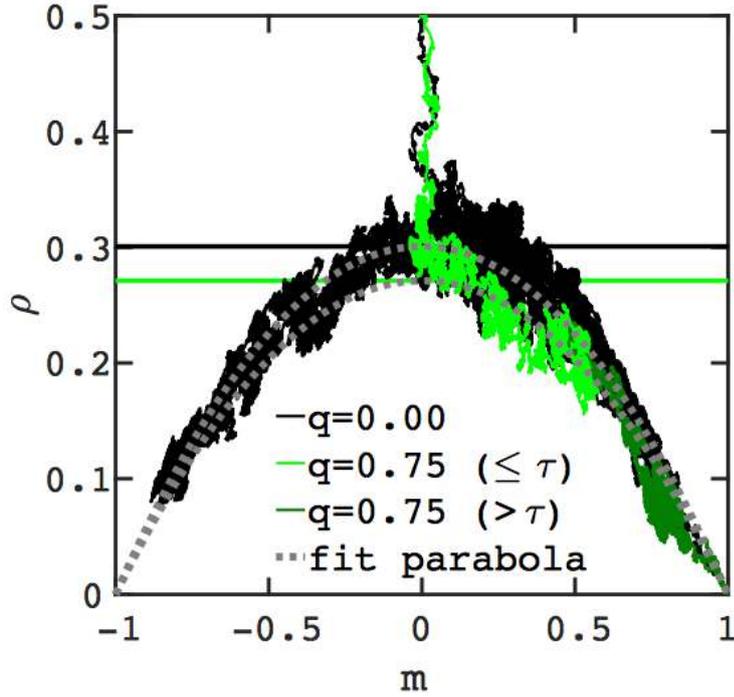


FIG. 1. We show two sample paths of the dynamics in the (m, ρ) -space at a rewiring probability of $p = 0.55$: The black path shows the scenario where peer-pressure is absent, i.e. $q = 0$. The light and dark green paths shows the scenario where the peer-pressure is at $q = 3/4$, respectively before the depletion of triangles at time τ and thereafter. The dot-dashed grey lines are best fits of the paths to the parameterized parabola $\rho = \xi_v(1 - m^2)$, respectively for $q = 0$ and $q = 0.75$

Optimal Learning Machines

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Abstract. I shall review recently proposed ideas on learning from high dimensional data, in a model free setting. I shall argue that, in the absence of prior information on the generative model, a quantitative estimate of the information content of a sample is given by the entropy of the frequency distribution, which we call *relevance*. Most informative samples, that have maximal relevance, exhibit statistical criticality. In particular, Zipf's law characterizes samples at the optimal trade-off between compression and relevance. This perspective also sheds light on the properties of learning machines. The analogous of the relevance for learning machines is the entropy of the distribution of energy levels. Machines which maximize this quantity -- that we call *optimal learning machines* -- feature a broad distribution of energy levels. We discuss the properties of optimal learning machines in a simple case, confirm their superior properties in a simple task, and discuss the perspectives that this approach opens on statistical and machine learning in general.

The content of this talk is drawn from Refs. [1,2,3,4].

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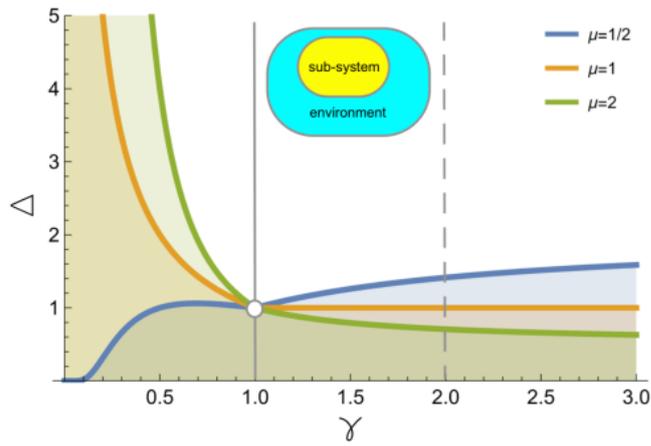


FIGURE 1. Phase diagram of the random optimisation problem pictorially described in the top center, as a function of the three main parameters, γ and Δ . Here γ controls the statistics of the objective function, with $\gamma = 2$ (dashed grey line) and $\gamma = 1$ (full grey line) that corresponds to the REM and to OLM, respectively. Δ quantifies the relative strength of the interactions in the sub-system with respect to those with the environment. Different lines correspond to different values of the ratio μ between the size of the environment and the size of the sub-system ($\mu = 1/2, 1$ and 2 , from top to bottom for $\gamma > 1$). The shaded regions below the lines correspond to the disordered (weak interaction) phase, in the three cases. The phase transitions are continuous for $\gamma > 1$ and discontinuous for $\gamma < 1$. The point at $\gamma = \Delta = 1$ denotes the point where Zipf's law occurs, and is the only point where the (analogous of the) specific heat diverges.

Spectral Properties of Graphs with Aggregated Simplexes

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Abstract. Considering the impact of higher-order interactions in the cooperative self-assembly of nanoparticles, we have recently introduced a model [1,2] based on the aggregation of simplexes of different sizes. The addition of a formatted geometrical group to the growing network depends on the geometrical compatibility of the added form with the current structure and the chemical affinity towards the addition of the new particles (vertices). As it is shown in [1], by varying the size of the added simplexes and the chemical affinity parameter, we can grow a whole class of structures that differ in the architecture of simplicial complexes. An example is shown in Fig.1. The aggregates of simplicial in these structures also manifest in the underlying topological graph (1-skeleton of these simplicial complexes).

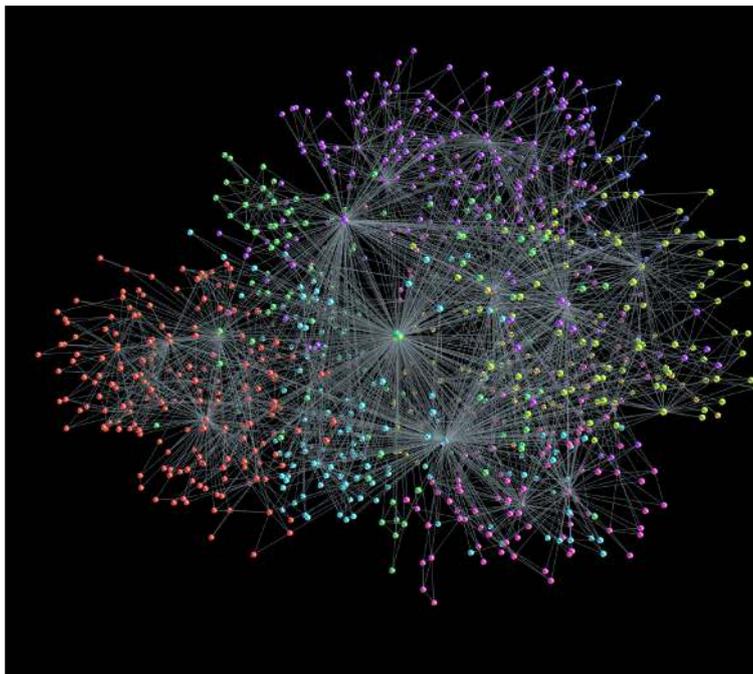


Fig1: A simplicial complex grown by aggregation of cliques of sizes from 3 to 6 vertices.

Here, we analyze the spectral properties of these graphs [3]. Specifically, we determine the eigenvalue spectra of the (normalized) Laplacian operator related to the adjacency matrices of these graphs, which describes the diffusion processes on them. Considering the aggregates of mono-disperse cliques, we demonstrate how the size of the elementary building blocks in conjunction with the chemical affinity between them affects the spectral dimension of the aggregates. In particular, we grow and describe the classes of structures that allow for the frustrated synchronization and transient random walk processes, in contrast to the structures compatible with non-transient random walks, in one limit, and the structures allowing the full synchronization, in the other. These findings demonstrate how the controlled aggregation of simplexes can lead to complex structures underlying specific dynamical properties, thus offering a deeper understanding of these dynamical processes in various complex networks with simplicial complexes inferred from the empirical data. See other related works in Refs. [4,5,6].

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Beauty in the visual arts through the eyes of physics

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Abstract. The 20th century is often referred to as the century of physics. From x-rays to the semiconductor industry, human societies today would indeed be very different were it not for the progress made in physics laboratories around the world [1,2]. What the past 100 years have been for science, the past millennium has been for the arts. From the late Byzantine and Islamic art to Renaissance, Realism and Pop art, the past 1000 years are packed with the most productive periods of our creative existence. The availability of digitized visual artworks

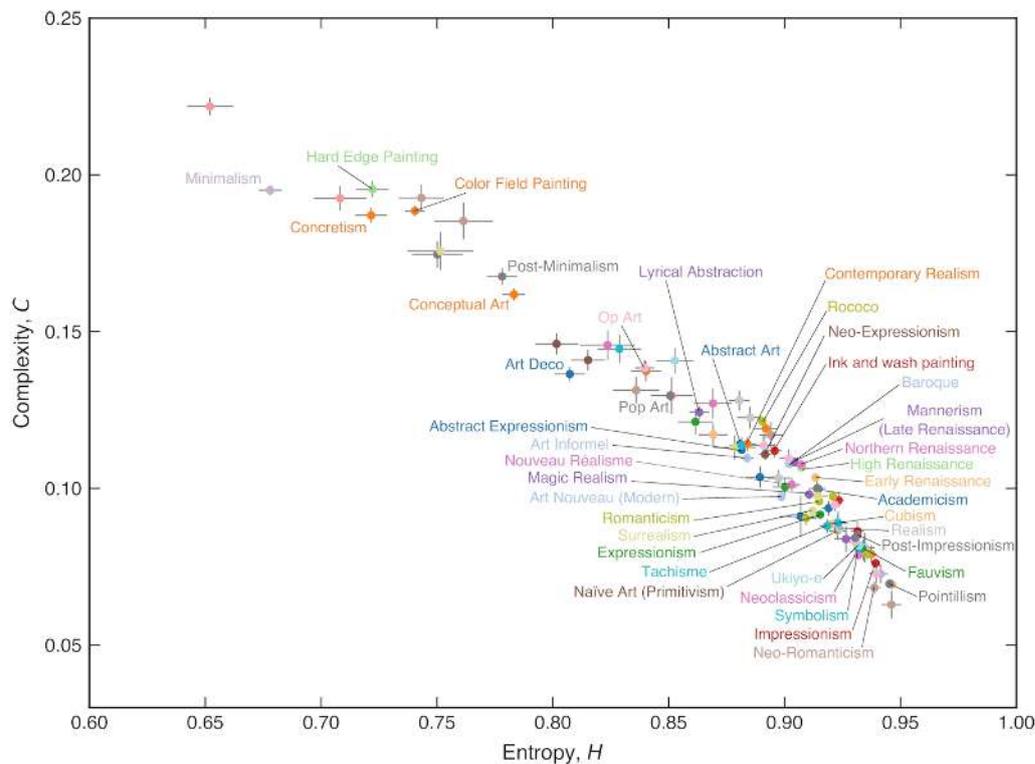


FIG 1. Different artistic styles on the complexity-entropy plane. The colorful dots represent the average values of H and C for each one of the 92 styles with more than 100 images in the dataset. Only 41 artistic styles with more than 500 images each are labeled for clarity.

allows us to perform large-scale quantitative analysis of the history of art. We have analyzed almost 140,000 visual artworks [3], the majority of which were paintings, by more than 2,300 artists created between the years 1031 and 2016. Based on the complexity and entropy of spatial patterns in the artworks, we were able to hierarchically categorize the artworks on a scale of order-disorder and simplicity-complexity, revealing a temporal evolution of the artworks that coincides with the main historical periods of art.

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The impact of higher order descriptions on structural analysis and dynamical processes

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Abstract. Topology, one of the oldest branches of mathematics, captures the concept of shape for spaces of arbitrary type and dimension. This allows to adopt some of its concepts to characterize and compare how complex systems evolve and restructure themselves. In the talk, I will introduce the most common topological techniques, persistent homology and Mapper, to illustrate what novel insights these new descriptive paradigms yield, and then provide a set of examples to motivate the importance and breadth of the results that can be obtained from a topological perspective.

Persistent homology studies the shape of topological spaces by producing progressively finer approximations using simplices, higher order analogues of links between nodes in a network. This procedure highlights the topological features in various dimensions (e.g. one-dimensional cycles, three dimensional cavities, etc.) that survive through the sequence of successive approximations and therefore characterize the shape of a dataset [1]. This allows to compare in a principled way generic spaces with different dimensions, number of points, etc. (Figure 1A). As an example, I will show how persistent homology can be used to study the shape of correlation spaces between brain regions from fMRI data and that functional, global homological and localized homological information can all be used to track the evolution of brain activity in time and to fingerprint individual subjects (Figure 1C). Then, I will show examples that psychedelic drugs alter the shape of the landscape of brain activity leading to a radical reorganization of the hierarchies of functional circuits [2]. Interestingly, a similar reorganization is observed also in the case of patients with bipolar syndrome that are treated with lithium medication, whose functional topology is pushed back toward the physiological configuration, and in simple imagery tasks [3].

Mapper is instead a topological dimensionality reduction tool that focuses on extracting a low-dimensional simplicial complex backbones from high-dimensional datasets (Figure 1B). It has been used successfully in the past to extract insights in a range of different fields, ranging from cancer genomics to drug recommendations. Here as examples, I will show: i) how it is possible to use this type of topological information to build a topological genetic skeleton highlighting differences in structure and function of different genetic pathways within the brain[4] (Figure 1D); and ii) how Mapper can be used to build a topologically-informed map of a feature space hence improving and stream-lining the choices of important features for classification in that space [5].

I will then discuss recent advances in our understanding of the effects of higher order interactions on the evolution of dynamical processes, such as contagion and synchronization. In particular, I will introduce a higher-order model of social contagion in which a social system is represented by a simplicial complex and contagion can occur through interactions in groups of different sizes [6]. Numerical simulations of the model on both empirical and synthetic simplicial complexes highlight the emergence of novel phenomena such as a discontinuous

transition induced by higher-order interactions. I will show that the transition is discontinuous and that a bistable region appears where healthy and endemic states co-exist. These results are important because they may explain why critical masses are required to initiate social changes and contribute to the understanding of higher-order interactions in complex systems. Finally, I will briefly discuss the challenges of inferring such higher order interactions in cases where they are not explicit, e.g. starting from timeseries data.

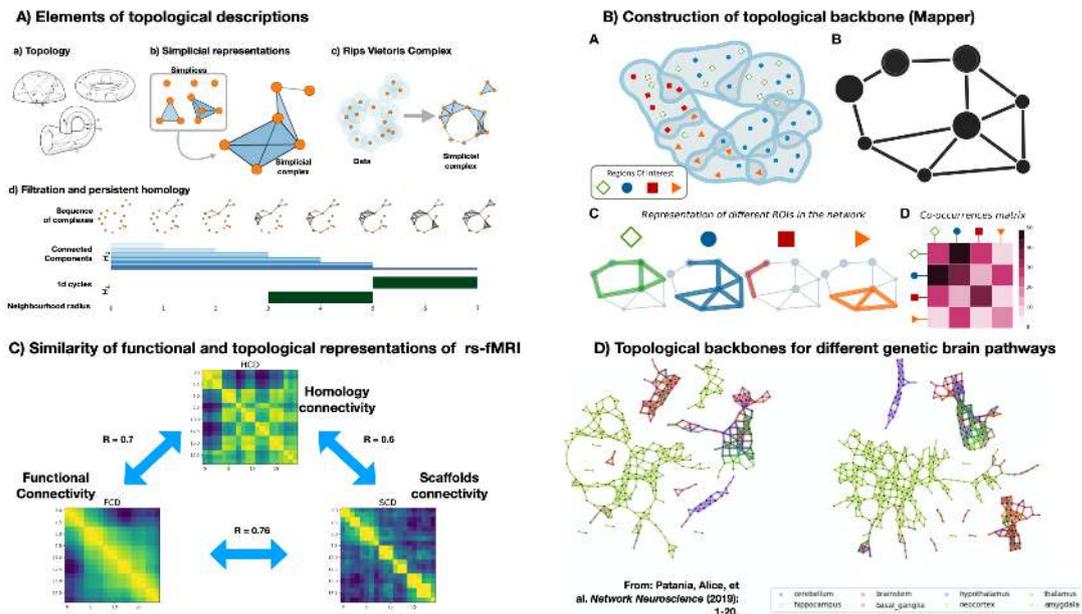


Figure 1. A) Elements of topological descriptions (simplices, construction from metrical space, filtration); B) Construction of Mapper; C) similarity between dynamical connectivities in vanilla functional connectivity, homological connectivities and their resulting scaffolds; D) examples of Mapper backbones extracted from gene expression markers specific to dopamine and GABA pathways in the human brain.

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Describing language shift over time and space

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Abstract. Language is something each of us is familiar with and uses daily. However, language as a complex system is constantly changing with words and constructions being introduced and disappearing. Sometimes, people even stop using one language and start using another instead. The latter phenomenon is called language shift and occurs for a number of reasons, e.g. migration, political pressure, societal attitudes towards a language or economic factors. In this talk, we will show how mathematical models based on models of physical diffusion can be used to find the factors contributing to language shift in a dataset.

Language shift occurs in many places all over the world, both historically and recent. The system we will present is the multinational historic state of Austria-Hungary and its successor states in today's Europe. Austria-Hungary with its many languages is well-documented and offers many language shift situations for case studies (fig. 1). Moreover, census data is available for the whole territory from 1880 on, meaning we have data with sufficient spatial and temporal resolution. These can be modelled mathematically as diffusion processes: the spreading use of a language in analogy to the spread of atoms [1].

We present a model based on cellular automata [2] to describe one language shift situation, the ongoing shift from Slovenian to German in Carinthia, Austria (fig. 2). Our model was able to identify interaction with people in the neighborhood as the most important factor for language maintenance whereas other factors such as bilingual schools and parish language have only a minor impact. We will also discuss the applicability of this model to other situations with different conditions, e.g. the shift from German to Hungarian in Southern Hungary with the different social and geographic circumstances.

As the basic model is very simple, it can be extended in a number of ways to account for the complex language shift process. For example, network techniques could be used to describe the connectivity between villages (actual communicative distance vs. Euclidean distance) and thus actual interaction networks and their higher order structures in more detail. Further possible avenues are the consideration of transport networks, the long-range influence of mass media, and migration patterns which are also likely to exhibit higher-order structures.

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FIG 1. Distribution of languages in Austria-Hungary around 1900, based on census results. Many language contact areas (interfaces between two languages) can be observed, and in most of these language shift took place. [map based on Wikimedia Commons, User: Andrein, public domain]

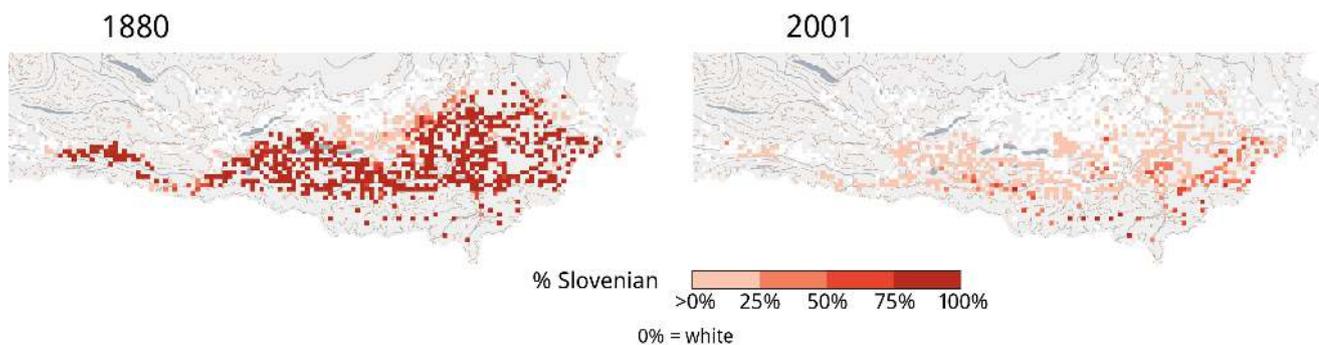


FIG 2. Percentage of Slovenian in Carinthia, Austria, in 1880 (top) and 2001 (bottom), based on census results. Between these two time points, the number of Slovenian speakers declined from approximately 85,000 to around 12,000.

Quantum statistics in Network Geometry with Fractional Flavor

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Abstract. Quantum statistics have been shown to emerge to describe the statistical properties of growing networks when nodes are associated to a fitness value [1]. Recently it has been shown that quantum statistics emerge also in a growing simplicial complex model called Network Geometry with Flavor (NGF) which allows for the description of many-body interactions between the nodes [2,3]. This model depends on an external parameter called flavor that is responsible for the underlying topology of the simplicial complex. When the flavor takes the value $s=-1$ the d -dimensional simplicial complex is a manifold in which every $(d-1)$ -dimensional face can only have an incidence number $n_\alpha \in \{0, 1\}$. In this case the faces of the simplicial complex are naturally described by the Bose–Einstein, Boltzmann and Fermi–Dirac distribution depending on their dimension. In this paper we extend the study of NGF to fractional values of the flavor $s = -1/m$ in which every $(d-1)$ -dimensional face can only have incidence number $n_\alpha \in \{0,1,2,\dots,m\}$. We show that in this case the statistical properties of the faces of the simplicial complex are described by the Bose–Einstein or the Fermi–Dirac distribution only. Finally, we comment on the spectral properties of the networks constituting the underlying structure of the considered simplicial complexes [4].

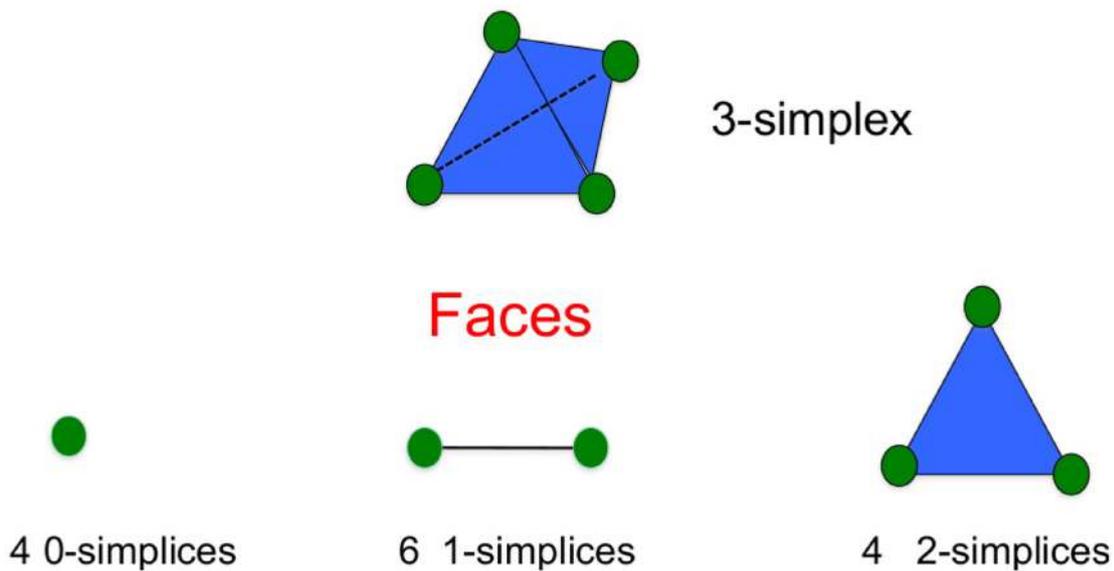


FIG .1 The faces of a $\delta = 3$ dimensional simplex (a tetrahedron) are shown and their relative number is indicated correspondingly.

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Structure of Simplicial Complexes in Human Connectomes

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Abstract. The whole-brain networks represent a specific type of network structures that can be inferred from experimental data. First, the brain's anatomical structure provides connections among different brain regions, whose size, position, and neurological functions are well known; while these connections develop over time and specific brain functioning. Furthermore, different computational modelling approaches are necessary to interpret the experimental data. Notably, the brain imaging data obtained in the laboratory by fMRI are processed to compute diffusion-tensor imaging followed by the tractography to identify the fibre tracts as potential connections between known brain regions. These are eventually mapped to the brain graph by tools that observe the full anatomical structure of the brain. These procedures depend on different parameters that can be varied. The brain networks that we study, cf. Fig., are generated at the Budapest connectome server [2] based on the data from the Human Connectome Project.

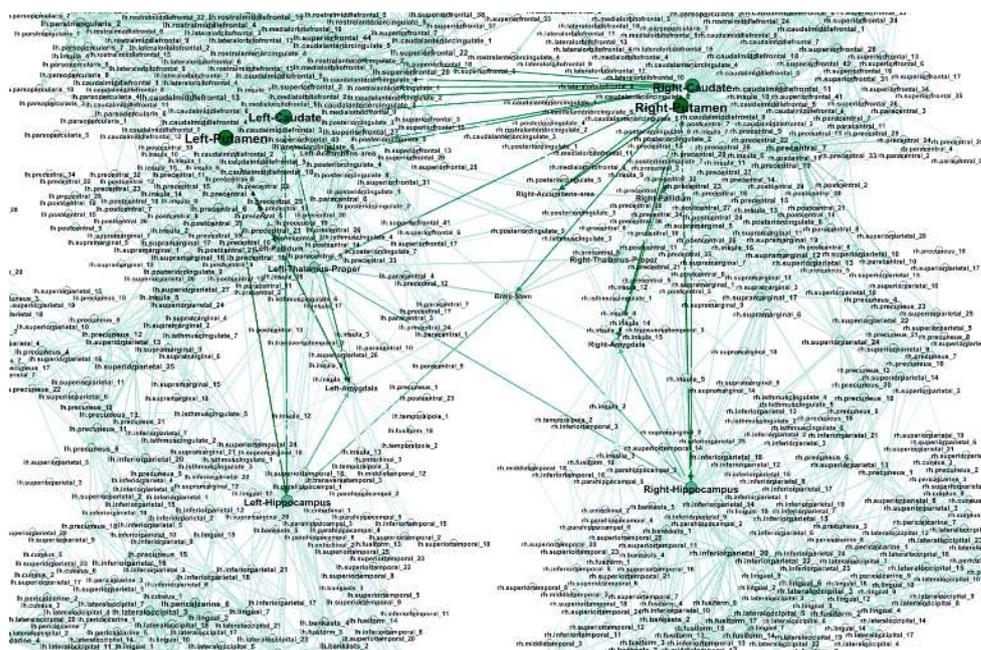


FIG . A segment of brain graph showing connections near large hubs in both hemispheres

By setting the appropriate parameters, we generate the following two types of networks. The consensus female connectome consists of edges that appear in all 100 female subjects, and the consensus male connectome contains the links that are common for 100 male individuals. We analyse the structure of simplicial complexes, which comprise the inner structure of the brain anatomical modules in both hemispheres [1]. Explicitly, by identifying simplexes of all orders and the ways that they are interconnected into complexes, we compute structure vectors to quantify their structure for both network types. It appears that these topology features, which embody higher-order connections in the brain, comprise the main difference between the female and male connectomes. Meanwhile, their topological graphs are self-similar and equally hyperbolic. Other related works of the authors include functional multi-brain networks from EEG data mapping [3,4] and entropy measure related to the structure of simplicial complexes in segments of the human connectomes [5].

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