The Fifth Conference on Information Theory and Complex Systems
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BOOK OF ABSTRACTS

Editors: Velimir Ilić and Miomir Stanković

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THEMATIC FIELDS

Information theory

Information transmission

Complex networks

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Stochastic processes

Intelligent systems

Bioinformatics

Mathematical physics

Content

Complexity research in the humanities – recent examples

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[1]Keywords

humanities; complexity; data processing; interdisciplinarity

Summary

Over the years, complexity research has become increasingly interdisciplinary [1]. In addition to natural sciences such as physics and biology and social sciences such as economy, the possibilities of complexity are being recognized in some unexpected fields [2].

The impression is that nowadays there are no more scientific disciplines in which numerical computation is not applied. Complexity has been used in humanities as well. The use of complexity in humanities can be shown by reviewing the volume No. 21 of *Complexity* journal for 2016. We have chosen to present here four articles from fields which have highly humanistic character such as music, history, culture and art.

Humanities are based on critical thought and understanding of human creativity in all its complexity, but using the numerical computation isn't their characteristic. On a line which represents the frequency of using data processing methods, humanities would be placed on the opposite side of natural, as well as social sciences.

The first example that we present is an article in the field of music. By measuring composer style's comprehensiveness it is concluded that Mozart's works have the highest complexity score [3]. The complexity score was determinated for 321 composers from the set of almost 10,000 classical themes.

The second article is in the field of history. It is about investigating a transmission of violence and instability in Imperial Rome throughout the time by using a time series of reign length of 82 Roman emperors, half of whom died unnaturally [4]. The author used two tests. The first one involved autocorrelation (the tendency of nearby points to correlate), which was performed using the Breusch-Watson test. The second one involved the Hurst exponent (presence of "memory" over time) which was obtained by using the Rescaled Range Analysis algorithm. The results indicate that reign length stability did not arise randomly, which could mean that succession-related violence in Roman Empire also came in time clusters.

The third example is an article about a model which considers cultural evolution to be a nonstationary stochastic process [5]. It is a modified Tangled Nature Model of biological evolution which uses interacting agents with a stochastic dynamics based on partial knowledge of their environment. This model could be used for cultural activity effected by a disruptive innovation (from the use of fire, The Stone Age, The Metal Age to the modern technologies such as personal computers and cell phones). To demonstrate the possibility of the model authors used data for automobile industry such as number of manufacturers from 1886 to 1981.

In the fourth article complexity has been applied in the analysis of Orthodox icons. It is an example of delicate problem in human creativity which has been studied, until now, only in the theory of art and theology of the icon. Processing the data of Orthodox iconography is equivalent to processing the top cultural achievements of The Middle Ages. The authors have recognized the existence of fractality and self-organization in the icons and the role of the observer in both [6].

By the mere fact that complexity has found its use within nearly all branches of science including humanities and by the increasing interdisciplinarity of complexity research, it actually becomes a framework for the science of the 21st century.

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Mitotic spindle as complex structure: relation between spindle size and energy distribution

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[1]Keywords

mitotic spindle; complex system; mechanical energy, mechanical model

Summary

A purpose of complex subcellular structure named mitotic spindle is to ensure equal division of genetic material during cell division process. Proper functioning of this structure is very important for physiological functioning of tissue and organs. Narrow and long mitotic spindle as well as wide and short are indicative for some mitotic spindle disorders [2, 5]. Cell size can also affect mitotic spindle size [1].
We came to an idea to make a simple biomechanical model of this complex structure [3]. The oscillatory behavior of this model is based on dynamics of coupled systems [4]. Each element in the model has its mechanical counterpart: microtubules are standard light visco-elastic elements, homologue chromosomes are mass particles that are interconnected with standard light massless elastic spring.
In this model, mitotic spindle is presented as a system of coupled oscillators [4] where one oscillatory pair consists of a centrosome, a microtubule and a related chromosome and these are interconnected with their homologous pairs. Centrosomes are presented as mass particles that represent two rheonomic centers of oscillations.
The aim of this work was to study how different spindle size-spindle angle affects the energy of pairs of homologue chromosomes in the system of mitotic spindle during metaphase. The analyses were done through mechanical oscillatory model of mitotic spindle [3].
For numerical analysis we considered forced oscillations in linearized system for tree cases when mitotic spindle size-angle are: π/3, π/2 and 2π/3 (narrow, normal and wide respectively) when homologue chromosomes with heavier masses are located in the central zone of metaphase equatorial plane. Data for numerical analysis (chromosomal mass, rigidity of eukaryote metaphase chromosomes, rigidity for microtubules at 37° C, centrosome mass, centrosome amplitude oscillations, centrosome circular frequency) were taken from the literature.
Analytical expressions for potential and kinetic energy as well as for total mechanical energy of oscillating pair of homologues chromosomes are given.
According to the model total mechanical energy of oscillating pair of homologue chromosomes under forced regime of oscillations has oscillatory character. When chromosomes with heavier masses are position in the central zone of mitotic spindle total mechanical energy is lower in the central zone of mitotic spindle. Spindle size affects total mechanical energy of each homolog chromosome pair. Total mechanical energy for each homologue chromosome pair increases with mitotic spindle size-angle. This approach could be useful for understanding mitotic spindle size disorders.

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Bifurcation in the complex Bray-Liebhafsky oscillatory reaction as a function of the hydrogen-peroxide concentration

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[1]Keywords

non-linear dynamics; Bray–Liebhafsky reaction; oscillations; bifurcation; complex networks

Summary

The investigation of complex nonlinear reaction systems with feedback, when they are far from thermodynamic equilibrium, has become one of the most active areas in chemical dynamics, primarily, due to the richness of dynamic states which can be found [1], as well as their importance in medicine, biological and social science [2,3]. In mentioned scientific fields, there are systems which are always in various periodic and aperiodic oscillatory dynamic states and the transition from one to other dynamic states can be of vital importance for their existence. Therefore, it is necessary to examine qualitative changes in the dynamics (bifurcations) and the parameter values at which they occur (bifurcation points). It is clear that mentioned dynamical systems in living organisms are very complex and any simplification, such as oscillatory chemical reactions are more appropriate models for the analysis of bifurcations. Thus, here we used Bray-Liebhafsky (BL) oscillatory reaction [4] as appropriate model-system for bifurcation analysis. The Bray-Liebhafsky reaction is the catalytic decomposition of hydrogen peroxide into water and oxygen in the presence of iodate and hydrogen ions [4,5], which exhibits very complex dynamics states as stable steady state, regular and mixed mode oscillations, chaos and intermittent behavior [6]. As a control parameter, for theoretical and experimental investigation the inflow concentration of hydrogen-peroxide was used.

Time series were obtained by numerical simulation of the model of ODEs for the Bray--Liebhafsky oscillatory reaction under isothermal CSTR conditions (see ref. [7]). The MATLAB program package was used. The system of the ordinary differential equations (Eq. 1) was integrated using the ode15s algorithm with variable step. In all simulations relative and absolute error tolerance values were $3\cdot10^{-14}$ and $1\cdot10^{-20}$, respectively. By changing the control parameter, i.e. the inflow hydrogen-peroxide concentrations, we obtained various dynamics states: stable steady states, simple quasi-sinusoidal oscillations and relaxation oscillations. All states are shown on the bifurcation diagram (Figure 1)

$$\begin{aligned}
\frac{d[H_2O_2]}{dt} &= -r_5 - r_6 - r_7 - r_8 + r_9 - r_{10} \\
\frac{d[I^-]}{dt} &= -r_1 + r_{-1} - r_2 - r_4 + r_{-4} + r_5 - r_{11} \\
\frac{d[HIO]}{dt} &= r_1 - r_{-1} + 2r_3 - 2r_{-3} - r_4 + r_{-4} - r_5 + r_6 - r_{12} \\
\frac{d[HIO_2]}{dt} &= r_1 + r_{-4} - r_2 + r_6 - r_7 + r_8 + r_{-4} - r_{13} \\
\frac{d[I_2O]}{dt} &= r_2 - r_3 + r_{-3} - r_6 - r_{14} \\
\frac{d[I_2]}{dt} &= r_4 - r_{-4} - r_{15}
\end{aligned} \qquad (1)$$

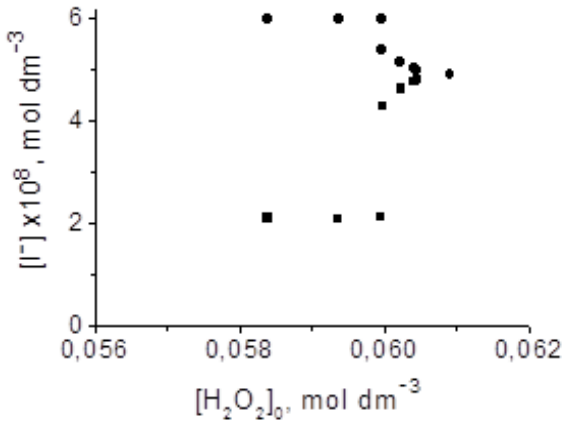

Figure 1. Theoretically obtained bifurcation diagram as a function of hydrogen-peroxide inflow concentration

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Experiments were carried out in a continuously fed well-stirred tank reactor (CSTR) at constant temperature of 45 ^{o}C. In order to maintain constant temperature of the system, a glass CSTR vessel was wrapped in a water recirculation jacket connected to a thermostat. For homogenization of the reaction mixture, a magnetic stirrer with a stirring speed of σ = 900 rpm was used. Amounts of species in the reactor were controlled by two peristaltic pumps. Three of the channels of the first peristaltic pump were used to deliver the reactants (KIO_3, H_2SO_4 and H_2O_2). One channel of the second pump was used to maintain constant volume (22.2 mL) of the reaction mixture. Every experiment was performed in the following procedure with different concentration of hydrogen-peroxide (inflow concentration of hydrogen-peroxide was varied in the range from $[H_2O_2]_0$ = 0.0560 to $[H_2O_2]_0$ = 0.0610 M). First, thermostated and protected from light, the reaction vessel was filled with the reactants at the flow rate of 0.431 mL/min. Concentrations of stock solutions were calculated so that their concentrations in reactor were: $[KIO_3]_0$ = 0.059 M and $[H_2SO_4]_0$ = 0.055M. After 34 min the flow rate was set to 0.052 mL/min and the other pump for removing the surplus volume of the reaction mixture was turned on. Experimentally obtained dynamic states of the BL system were recorder in the form of the potential-time evolution. Namely, in our paper potentiometric method was used for experimental recording of the dynamic states of the BL system. For that purpose, we used double-junction Ag/AgCl as a reference, I^- ion selective electrode as a working electrode and an electrochemical device (PCMultilabEH4 16-bit ADC) coupled with a personal computer for data recording.

The bifurcation obtained from numerical simulations (Figure 1) is compared with preliminary experimental results. The stable steady state (Figure 2a), low-amplitude oscillations (Figure 2b) and high-amplitude oscillations (Figure 2c) are also experimentally obtained in investigated concentration range of hydrogen-peroxide inflow.

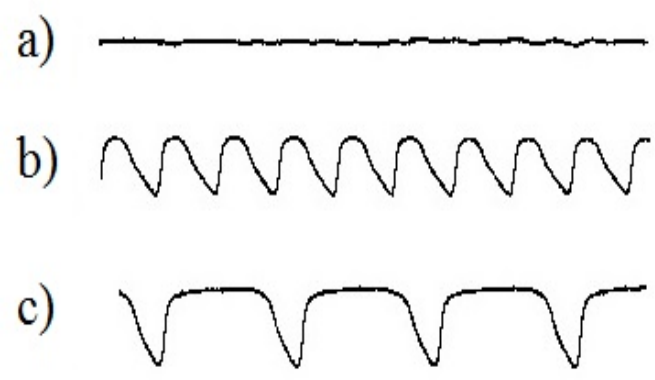

Figure 2. Experimentally obtained different dynamical states of the Bray-Liebhafsky system, under following conditions: σ= 900 RPM, j_0 = 0.007 min^{-1}, T = 45 ^{o}C, $[KIO_3]_0$ = 0.059 M, $[H_2SO_4]_0$ = 0.055 M, and hydrogen-peroxide concentrations were a) 0.0610 M, b) 0.0590 M and c) 0.0560 M.

It should be noticed that with hydrogen-peroxide concentration increases, oscillations amplitude decreases and at the concentration of hydrogen-peroxide 0.0610 M, Bray-Liebhafsky system exhibits stable steady state.

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Algebraicity of the co-domain lattice and related results on fuzzy set equations and inequations

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Keywords

fuzzy set; fuzzy relation; algebraic lattice; maximal solution; transitive closure.

Summary

Fuzzy set equations and inequations and the problems connected to them were dealt with in numerous papers, some of which consider the extremal problems: the existence of the greatest or the least solution to fuzzy set equations or inequations [3], while others deal with the more general problems of the existence of a maximal or a minimal solution [1, 6, 7].

Those problems vary on the lattice we take as the co-domain lattice. The studied cases include: [0,1] interval lattice [6], the residuated lattice [4], as well as the more general complete lattice [5]. Apart from the residuated lattice, the algebraic lattice is also a special case of the complete lattice. The algebraicity of the co-domain lattice implies the algebraicity of the lattice of fuzzy subsets of a crisp set, as well as the existence of a maximal solution to some fuzzy set and fuzzy relational equations and inequations. The key condition we use to prove the latter is so called "meet-continuity" of the elements of an algebraic lattice. Without it, a maximal solution may not exist, as it is proven by an example. A maximal solution to some fuzzy set and fuzzy relational inequations may not be a solution to the related equation, unless an additional condition be fulfilled.

The existence of the least solutions to some fuzzy set and fuzzy relational equations over a complete lattice may easily be proved. These solutions may be constructed in at most countably many steps in this more special case of an algebraic lattice. A version of a general algorithm for computing the transitive closure [2] works also in this case of fuzzy relations over an algebraic lattice.

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Kraus operators for a pair of interacting qubits: a case study

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Keywords

microscopic model; quantum entanglement; Kraus decomposition

Summary

The Kraus form of the completely positive dynamical maps is appealing from the mathematical and the point of the diverse applications of the open quantum systems theory.

The "integral", i.e. so-called, Kraus form [1] of a completely positive dynamical map for an open quantum system [2, 3] is appealing for the mathematical reasons. Mathematical existence of the Kraus form for such processes is guaranteed by the Kraus theorem, universally [1-3]. On the other hand, a Kraus-form (KF) may be regarded as a solution to a differential master equation (ME) for the open system's statistical operator (density matrix); a case when no ME exists for the process can be found e.g. in Refs. [4,5].

The Kraus operators are often constructed due to some physical assumptions or understanding of the underlying physical processes [6]. Nevertheless, such derivations may not provide the full physical (e.g. microscopic) details [7]. One way to obtain a proper KF for the open system's dynamics is derivation from the related master equation for the process [7,8]–if such an ME exists [4,5]. To this end, it is important to note: phenomenological derivations of MEs may also be unreliable–often there appear certain subtleties of both mathematical and physical nature as well as unexpected pitfalls [9,10].

Unfortunately, the Kraus operators are poorly known for the two-qubit processes. Having this in mind as well as the above-distinguished usefulness of KF, in this paper we derive the Kraus operators starting from a microscopically derived master equation for a pair of two-level systems (qubits). We are concerned with an ancilla qubit interacting with another qubit, which is subjected to a $\hat{S}_x$ spin-projection quantum measurement, while the strength of the interaction is arbitrary. Usefulness of the KF for the process is emphasized by application of our results in investigating the dynamics of entanglement in the qubits system. The obtained results are applied to calculate the dynamics of the initial entanglement in the qubits system. We obtain the loss of the correlations in the finite time interval; the stronger the inter-qubit interaction, the longer lasting entanglement in the system.

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On the concept of local time in quantum mechanics

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[1]Keywords

Quantum dynamics; quantum local time; mixed quantum states; quantum linear entropy

Summary

Recently, a novel concept of "local time" (LT) in quantum theory has been proposed [1-3]. This new paradigm removes the concept of the universal time as the foundational concept of quantum theory. Local Time for every approximately isolated quantum system is introduced as an emergent, classical hidden parameter, whose measurement is prohibited due to the so-called no-cloning theorem [4,5]. As a consequence, even an (at least approximately) isolated system's state is "mixed", thus exhibiting behavior that is typical for the so-called open quantum systems [6,7] as well as the lack of information regarding the system's (local) time. As a quantitative measure of this ignorance, we utilize the so-called linear entropy [5] that points out a (non-sharp) separation between the micro- and macro-scopic quantum systems. We find that, the larger the system, the larger is the maximum value of the linear entropy, i.e. the larger the ignorance about the macroscopic system's local time. Hence a basis for the macroscopic-systems irreversible dynamics even on the level of the single quantum systems, that requires a separate and careful analysis. Another research direction regards a possible relation between the LT kind of irreversibility and the alternative structures of composite quantum systems [8,9]. Both open topics are in progress.

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Dynamical identity of the Brouwer continuum

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[1]Keywords

Brouwer continuum; dynamical identity; time operator; Ford circles; wavelet domain hidden Markov model

Summary

The intuitionism developed by Dutch mathematician and philosopher Luitzen Egbertus Jan Brouwer is a philosophy of mathematics that considers it through realization of increasingly complex features [1]. In opposition to idealism of the formal logic, he indicates a dynamical identity of mathematical concepts, similar to that of the Jungian psychology [2]. In the current paper, the author elaborates Brouwer`s conception of the continuum in terms of the time operator formalism introduced by Ilya Prigogine [3].

Prigogine relates temporality of the fundamental physical theories to the measurement problem that requires the departure from classical causal laws. Exactly the same subject occurs in the very constructive definition of continuum. It is about the Euclidean algorithm corresponding to commensuration of the magnitudes, that results in a continued fraction expansion.

A hierarchical diagram established in order to give a temporal significance to the measurement process is named the *Ford circles*. The diagram represents an element of the continuum in the form of a vertical line whose intersections with circles correspond to its Diophantine approximations. Lochs` theorem [4] links the process to the decimal representation stating that, on average, each successive step tends to determine a decimal digit of the element.

The Ford circles imply an extraordinary arithmetic operation termed *mediant* ($\oplus$), relating tangent members of the diagram. The algebraic structure it generates is isomorphic to the arithmetic mean due to a mapping designated by ?, such that $?(x \oplus y) = \frac{?(x)+?(y)}{2}$. It is Minkowski`s question mark function [5] transmuting representation of the continuum from the continued fraction to the binary one.

So conceived, the continuum hierarchy is related to a binary tree structure with elements corresponding to paths in the tree from its root downward. In Brouwer`s terms, it is the *space of choice sequences* whereby each choice corresponds to a binary digit of the element. In that regard, the dynamics of the structure is related to the Rényi mapping (R) that generates binary digits through its successive applications [6].

The evolutionary operator induced by the underlying dynamics takes the form $Uf(x) = f(Rx)$. Applied to a mother wavelet function ψ, it generates a wavelet basis of the continual signal space up to a constant factor $\psi_{j,k}(x) = \psi(2^i x - k)$, wherein j designates the hierarchical scale and k the position of a basis element. The time operator in the basis is determined by $T\psi_{j,k} = j \cdot \psi_{j,k}$, having eigenvalues that correspond to the hierarchical scale of a basis element. In such a hierarchy, the choice is expressed through uncertainty relations $[T,U] = U$ realized between the evolutionary and the time operator.

The dynamical identity represents self-similarity of the binary tree structure indicating a fractal geometry of the Brouwer continuum. It is reflected in the statistics of wavelet coefficients forming the hidden Markov model of the continual signal space [7]. The insight potentiates a theoretical foundation of the model that has not been done so far.

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Some Recent Results Concerning Conditional Rényi Entropy

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Keywords

Rényi entropy; conditional entropy, quasi-linear mean

Summary

Rényi entropy (RE) is a well known one parameter generalization of Shannon entropy. It has successfully been used in a number of different fields, such as statistical physics, quantum mechanics, communication theory and data processing [5], [3].

On the other hand, the generalization of conditional Shannon entropy to Rényi entropy case is not uniquely defined. Thus, different definitions of conditional Rényi entropy (CRE) has been proposed in the context of channel coding [1], secure communication [2], [6], [4] and multifractal analysis [5]. However, no one of the generalization satisfies a set of basic properties which are satisfied by the Shannon conditional entropy and there is no general agreement about the proper definition, so the choice of the definition depends on application purpose.

In this talk we first determine the set of properties which are satisfied by all of the previously established generalizations. After that we present α-β-γ CRE previously proposed by the authors [7] which can be represented as an quasi-linear average uncertainty about a random variable X if a random variable Y is given. The α-β-γ CRE contains previously defined conditional entropies as special cases that can be obtained by a proper choice of the parameters. Moreover, it satisfies all of the properties that are simultaneously satisfied by the previous definitions, so that it can successfully be used in aforementioned applications. Thus, the proposed CRE is positive, continuous, symmetric, permutation invariant, equal to Rényi entropy for independent X and Y, equal to zero for $X = Y$ and monotonic.

Possible directions for future research are also discussed.

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GNN models for solving matrix equations

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Keywords

Recurrent neural network; Generalized inverse; Dynamic equation; Matrix equation; Activation function.

Summary

There are two general approaches in finding solutions to the problem of solving linear matrix equations. The traditional approach includes a great set of direct or iterative numerical algorithms aimed to digital computers. Usually, traditional numerical algorithms are of serial-processing nature and may not be efficient enough for online or real-time simulations, which must guarantee response within specified time constraints. The second approach is different from a number of conventional numerical methods, and it is based on dynamic neural networks. The dynamical system approach is one of important, powerful and promising alternative for solving many kinds of matrix algebra problems because of its parallel distributed nature, possibility to ensure a response within a predefined timeframe and convenience of hardware implementation. As a consequence, numerous dynamic and analog solvers based on recurrent neural networks (RNN) have been developed and investigated recently.

We are concerned with the solution to the linear matrix equation $AXB = D$, $A \in \mathbb{R}^{m\times n}$, $B \in \mathbb{R}^{p\times q}$, $D \in \mathbb{R}^{m\times q}$, by means of a gradient based neural network (GNN) model, called $GNN(A, B, D)$. The nonlinearly activated $GNN(A, B, D)$ model is defined by the dynamic equation

$$\frac{\mathrm{d}V(t)}{\mathrm{d}t} = \dot{V}(t) = \gamma A^{\mathrm{T}}\mathcal{F}(D - AV(t)B)B^{\mathrm{T}}, \qquad (1)$$

wherein $V(t)$ is unknown matrix of activation state variables corresponding to the unknown matrix X, $t \in [0, +\infty)$ denotes the time and γ is a positive scaling constant which should be established as large as the hardware permits or selected appropriately for simulative and/or experimental purposes. The matrix-valued activation function $\mathcal{F}(E)$, $E = (e_{ij})$, is defined as $(f(e_{ij}))$, $i, j = 1, 2, \ldots, n$, where $f(\cdot)$ is a scalar-valued monotonically-increasing odd function.

Theorem 1. *Assume that real matrices $A \in \mathbb{R}^{m\times n}$, $B \in \mathbb{R}^{p\times q}$ and $D \in \mathbb{R}^{m\times q}$ satisfy*

$$AA^{(1)}DB^{(1)}B = D, \qquad (2)$$

for some inner inverses $A^{(1)}$ and $B^{(1)}$. If an odd and monotonically increasing function $f(\cdot)$ is used to define the array activation function $\mathcal{F}(\cdot)$, then the state matrix $V(t) \in \mathbb{R}^{n\times m}$ of the $GNN(A, B, D)$ model (1) *satisfies $AV(t)B \to D$ when $t \to +\infty$, for an arbitrary initial state matrix $V(0)$.*

Theorem 2. *Assume that the real matrices $A \in \mathbb{R}^{m\times n}$, $B \in \mathbb{R}^{p\times q}$ and $D \in \mathbb{R}^{m\times q}$ satisfy*

$$AA^{\dagger}DB^{\dagger}B = D. \qquad (3)$$

Then the unknown matrix $V(t)$ of the model $GNN(A, B, D)$ is convergent when $t \to +\infty$ and has the limiting value

$$\tilde{V}_{V(0)} = A^{\dagger}DB^{\dagger} + V(0) - A^{\dagger}AV(0)BB^{\dagger} \qquad (4)$$

for every initial matrix $V(0) \in \mathbb{R}^{n\times p}$.

The resulting matrix generated by $GNN(A, B, D)$ is defined by the choice of the initial state and coincides with the general solution

$$X = A^{\dagger}DB^{\dagger} + Y - A^{\dagger}AYBB^{\dagger}$$

of the matrix equation $AXB = D$, where the arbitrary matrix Y is replaced by the initial state matrix $V(0)$.

Several particular appearances of the matrix equation $AXB = D$ and their applications are considered.

(a) The $GNN(A, A, A)$ model generates the least squares solution of the matrix equation $AXA = A$, according to [5, Theorem 3.2].

(b) GNN models defined in [1, 2, 3, 5, 6] can be derived as modifications of some appearances of the $GNN(A, B, D)$ model. Conditions for the existence and representations of $\{2\}$-, $\{1\}$- and $\{1, 2\}$-inverses of complex matrices which satisfy certain conditions on ranges and/or null spaces are introduced in [4]. These representations involve solutions of certain matrix equations. The most general method is defined as follows. Solution $\tilde{V}_{V(0)}$ of the matrix equation

$$BV(t)CAB = B$$

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defined by the $GNN(AB, CAB, B)$ model

$$\dot{V}(t) = B^{\mathrm{T}}\mathcal{F}(B - BV(t)CAB)(CAB)^{\mathrm{T}} \tag{5}$$

gives $\tilde{V}_{V(0)} \in (CAB)\{1\}$. Then $X = B\tilde{V}_{V(0)}C$ gives various representations of outer inverses, according to Urguhart formula.

The implementation of introduced algorithms is defined on the set of real matrices and it is based on the Simulink implementation of the GNN models of the general form (1) for solving the involved matrix equations.

The general computational pattern for commuting generalized inverses is based on the general representation $B(CAB)^{(1)}C$, where the matrices A, B, C satisfy certain conditions imposed in the proposed algorithms. It can be described in two main steps:
(1) Solve appropriate linear matrix equation $BVCAB = B$ with respect to V using the $GNN(B, CAB, B)$ model.
(2) Compute the matrix product BVC.

(c) An useful application of the $GNN(A, B, D)$ model is the $GNN(A, I_1, b)$ model

$$\dot{v}(t) = \gamma A^{\mathrm{T}}\mathcal{F}(b - Av(t)), \tag{6}$$

for solving linear equations $Ax = b$, where $A \in \mathbb{R}^{m\times n}$ is the coefficient matrix, $b \in \mathbb{R}^m$ is given and $x \in \mathbb{R}^n$ is an unknown vector.

The globally convergent $GNN(AA^{\mathrm{T}}, A^{\mathrm{T}}A, A)$ model can be exploited in computation of the Moore-Penrose inverse. That application is investigated theoretically and numerically.

Theorem 3. *Consider the* $GNN(AA^{\mathrm{T}}, A^{\mathrm{T}}A, A)$ *model*

$$\dot{V} = \gamma AA^{\mathrm{T}}\mathcal{F}\left(A - AA^{\mathrm{T}}V(t)A^{\mathrm{T}}A\right)A^{\mathrm{T}}A, \tag{7}$$

for solving the matrix equation $AA^{\mathrm{T}}VA^{\mathrm{T}}A = A$. *Let* $\tilde{V}_{V(0)}(t)$ *be a solution of the model* (7)*. Then the matrix* $X(t) = A^{\mathrm{T}}\tilde{V}_{V(0)}(t)A^{\mathrm{T}}$ *converges to the Moore-Penrose inverse* $A^{\dagger}$ *for every initial matrix* $V(0)$.

Example 1. *Consider the input matrices*

$$A = \begin{bmatrix} 0.2238 & 0.2551 & 0.6991 \\ 0.7513 & 0.5060 & 0.8909 \end{bmatrix},$$

$$B = \begin{bmatrix} 0.9593 & 0.2575 & 0.2435 \\ 0.5472 & 0.8407 & 0.9293 \\ 0.1386 & 0.2543 & 0.3500 \\ 0.1493 & 0.8143 & 0.1966 \end{bmatrix},$$

$$D = \begin{bmatrix} 0.2511 & 0.4733 & 0.8308 \\ 0.6160 & 0.3517 & 0.5853 \end{bmatrix}.$$

Since the condition $AA^{\dagger}DB^{\dagger}B = D$ *is satisfied, it is possible to use the* $GNN(A, B, D)$ *model* (1) *to compute the minimum norm least squares solution* $X = A^{\dagger}DB^{\dagger}$ *of the matrix equation* $AXB = D$. *The gain parameter of the model is chosen as* $\gamma = 10^5$, $V(0) = 0$ *and the activation function is* $f(x) = x$. *The least squares solution of* $AXB = D$ *in the time interval* $[0, 0.01]$ *are generated with the accuracy* 10^{-5}. *Elementwise trajectories of* $V(t)$ *corresponding to* `ode15s` *solver are shown in Figure 1.*

Figure 1: Elementwise convergence trajectories of $GNN(A, B, D)$ in Example 1.

The influence of the scaling parameter γ *on the convergence speed of the* $GNN(A, B, D)$ *model under various time intervals* $[0, \tau]$ *is presented in Table 1. These results confirm that smaller time intervals require greater values of* γ.

γ	$\|AV(t)B-D\|_F$	γ	$\|AV(t)B-D\|_F$
$[0, 10^{-5}]$		$[0, 10^{-1}]$	
10	1.3495	10	0.5040
10^3	1.2788	10^2	0.2954
10^6	0.2954	10^4	$1.2208e$–05
10^9	$3.4219e$–16	10^6	$2.8305e$–16

Table 1: The influence of the scaling parameter γ in the $GNN(A, B, D)$ model in Example 1.

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Error analysis of a kernel regression based on a randomized matrix approximation

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Keywords

Regression; Kernel method; randomized matrix approximation; Nystrom method; randomized SVD;

Summary

In this paper we investigated the predictive performance a randomized approximation of a kernel matrix applied to the regression problem and its application to a multi-view semi supervised regression. We assume that the input set contains n d-dimensional feature vectors.

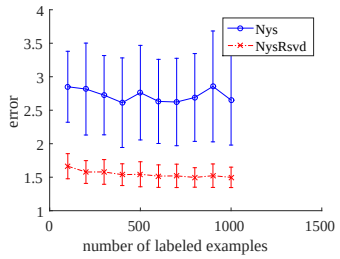
Kernel regression requires time complexity that is cubic in the number of data points which is too expensive for large data sets. A popular solution to this problem is the Nystrom method, where m (where $m \ll n$) columns of a kernel matrix are randomly selected and the entire matrix is approximated based on this columns. As a consequence of Nystrom method m-dimensional random feature vector is computed for each input vector. Finally, a linear regression is applied on a set of random feature vectors and time complexity of this algorithm is $O(nm^2 + m^3)$, as oposed to the time complexity of $O(n^3)$ of a kernel regression. Authors in [1] showed that expected error of an approximated kernel regression is similar to the error of a kernel regression.

Our idea is that using l (where $l > m$) randomly selected columns of a kernel matrix for a construction of m-dimensional random feature vectors while keeping time complexity linear in n will produce better results then using only m-columns. We propose to use the idea from [3], where Nystrom method is combined with randomized SVD, to construct random feature vectors. In the end linear regression is applied on random feature vectors and time complexity of this algorithm is $O(nl+l^2m+m^3)$ which means that we kept time complexity linear in n. Furthermore we proved in theorem (1) that expected error of approximated kernel regression based on a combination of Nystrom method and randomized SVD is similar to the error of unapproximated kernel regression.

Theorem 1. *Let $\lambda > 0$ and let $z \in \mathbb{R}^n$ and $K \in \mathbb{R}^{n\times n}$ be a vector of output observations and a kernel matrix derived from input data points respectively. Assume $d = n||diag(K(K + n\lambda I)^{-1})||_\infty$ and $R^2 = ||diag(K)||_\infty$. Define the estimate $z_K = (K + n\lambda I)^{-1}Kz$. Assume S is a uniform random subset of l indices in $\{1, 2, \ldots, n\}$ and consider L as approximate kernel matrix based on Nystrom method and randomized eigenvalue decomposition, with the approximate estimate $z_L = (L + n\lambda I)^{-1}Lz$. For every $\delta \in (0, 1)$ there is l_δ such that for every $l \geq l_\delta$*

$$\frac{1}{n}E[||z_L - z||^2] \leq (1 + 6\delta)\frac{1}{n}||z - z_K||^2$$

From multi-view learning assumption and theorem (1) follows that using more than one set of random feature vectors, derived sampling different sets of kernel matrix columns, will improve results. We apply our idea into the semi supervised regression algorithm from [2]. We empirically compared our **NysRsvd** algorithms with **Nys** algorithm from [2] . Because of the limited space we only show results on *elevators* data set. For error we chose the mean squared error (MSE) normalized by the variance of the test output, and we set $m = 10$.



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Sequential adaptiation of recurrent NARX neural network structure using derivative free bayesian filters

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[1]Keywords

Derivative free sequential estimation, NARX recurrent neural network, growing, pruning, Divided Difference Filter, Unscented Kalman Filter

Summary

The non-linear AutoRegressive with eXogenous inputs (NARX) recurrent neural network has adaptive feedbacks between the output and the hidden units. These feedback connection and possible input connections are implemented as FIR filters. It has been shown [1] that NARX RNN often outperforms the classical recurrent neural networks, like Elman or fully connected RNN, in tasks that involve long term dependencies for which the desired output depends on inputs presented at times far in the past.

In this work adaptation of recurrent NARX network parameters, state and structure is performed applying sequential Bayesian derivative filters: Divided Difference Filter (DDF) [3] and Unscented Kalman Filter (UKF) [2]. DDF is based on a derivative free polynomial approximation of nonlinear dynamic and observation equation using Stirling's interpolation formula which uses central divided differences. We will consider here only second order polynomial approximation. UKF is using the unscented transformation as a method for calculating the statistics of a random variable which undergoes a nonlinear transformation, based on the intuition that is easier to approximate a probability distribution than arbitrary function.

We are using the first and second order statistic, recursively recursively estimated by derivative free filters DDF and UKF, to derive criteria for growing and pruning of synaptic connections and hidden neurons in NARX recurrent neural networks. The test for adding new hidden neurons is based on the assumption that the innovations should be acceptable as zero mean and should have magnitude commensurate with the theoretical covariance as yielded by the filters.

During adaptation some connections or hidden neurons may become statistically insignificant and should be pruned. The well-known pruning method Optimal Brain Surgeon, ranks synaptic weights according to the saliency defined as the increase of the training error if the particular synaptic weight is eliminated. The weight with the smallest saliency is pruned. OBS was developed for the off-line trained networks with fixed training and test set. Here we will use first and second order statistics, recursively estimated by derivative free filters, to derive analogous criteria for on-line pruning. As a consequence of the weight pruning, we apply partitioned matrix inversion lemma to eliminate corresponding rows and columns in the Hessian of the cost function, which inverse is estimated as posterior covariance matrix.

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Optimal slicing in wireless 5G networks

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Keywords

mobile networks; slices mapping; concept

Summary

Today, fifth generation (5G) wireless technology hold a place among the biggest research areas within both industry and academia. The 5G networks support different services and applications, while requirements are diverse and often conflicting, so an optimization process is inevitable. The network slicing problem is combined optimization problem of placing network functions over a set of candidate locations and deciding their interconnections. For details and implementation, overview papers, keynote speeches, special issues and the latest books are presented through our references [1-5]. After presenting related work-background network slices are analyzed together with the offered advantages. To illustrate the benefit, we analyze cost savings in basic example of optimal mapping traditional services, video delivery and IoT slices onto simplified physical network [6,7].

The new generation of wireless technology will be in a position to support high bit rates, higher network capacity and lower operating costs as well as to reduce power consumption. New demands are imposed because of numerous users establish connections on human-to-human (H2H), machine-to-machine (M2M), vehicle-to-vehicle (V2V). The achievement of ambitious goals concerning 5G is aimed by a number of technology components, massive (large scale) multiple-input-multiple-output (MIMO), millimeter wave (mmWave), network densification, heterogeneous dense networks, heterogeneous cloud radio access networks, direct device-to-device (D2D) communications in the in-band and out-band, network slicing. Network slicing enables networks operators to allocate logical self-contained networks towards service providers [1-5,8].

The network slicing concept has been proposed as a mean for providing *better resource isolation and increased statistical multiplexing*. Next generation mobile network alliance (NGMNA) defines network slicing as *a concept for running multiple logical networks as independent business operations on a common physical infrastructure* [9]. Researchers can select the optimal Control/User Plane split, compose and allocate virtualized network functions VNFs as particular locations inside the core radio access network, depending on the service requirements.

5G network slicing enables a particular communication service exploiting the principles of software defined network (SDN) and network function virtualization (NFV). The goal is to fulfill the business and regulatory requirements [10,11]. By means of SDNs and NFV, operators can deliver automation, flexibility and programmability, allowing legacy functions to partitioned or migrated in data center environments, advancing virtual network architectures.

Here, network slices are defined as *end-to-end logical networks, mutual isolated, with independent control and management, which can be created on demand*. Basic network slicing problem is a constrained optimization problem ILP (integer linear program) [6]. In its simplest form this is a virtual network embedding-type of problem [7], in which researcher have to ***jointly*** decide: the optimal placement of VNFs at resource nodes, and the necessary link capacity reservations for their interconnection, under additive link and node capacity constraints so that the overall resource utilization cost is minimized.

We analyze an example of simplified **physical network** $G=(V,E,\beta,c)$ G and a **virtual network** H, where the virtual one is ***embeding*** or ***maping*** onto the physical network. Considered parameters, capacities and costs (β,c) of physical nodes $v \in V$ and links $e \in E$ are shown in Fig. 1. Depending on the application, costs may reflect congestion, preference in terms of operator agreements, load balancing, or real cost of operation.

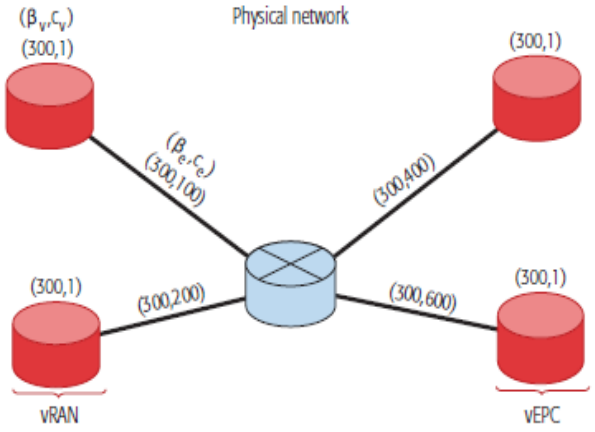
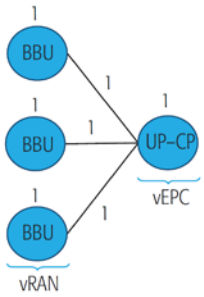


Fig. 1 A simple numerical example of physical network: capacities and costs of nodes and links in area of vRAN (virtual Radio Access Network) and vEPC (virtual Evolved Packet Core) [6].

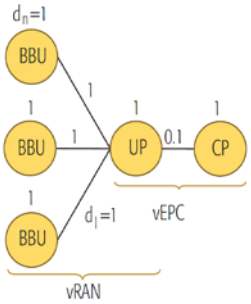
To quantify the benefit of network slicing, three types of slices are embedded onto the physical network by solving the network slicing optimization problem. The slice is defined by $H=(N,L,d,M)$ where (L,d) are links with capacity requirements as before, while the virtual nodes N represent VNFs. The location constraint sets M can be used to capture both the capabilities of physical nodes to run a specific VNF and the location requirements of the applications and users of the network. Different network functions can be embedded on either a virtual radio access network (vRAN) or virtual Evolved Packet Core (vEPC), or on both in the special case of UP for video services. The obtained network cost of utilized resources according to the optimal slicing is presented as follows.

1st Type of slice. Traditionally, cellular networks have been architected to support specific services (voice, messaging, and Internet access).



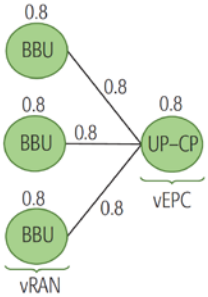
BBU (Baseband unit)
UP/CP are VNFs in Control/User Plane

2nd Type of slice. The enhanced mobile broadband (eMBB) requires a large bandwidth to support high data rate services. The video service has small bandwidth requirement between user plane and control plane functionality, due to edge caching, which ensures that video service is obtained directly at the edge for popular videos.



BBU (Baseband unit)
UP/CP are VNFs in Control/User Plane

3rd Type of slice. Internet of thing (IoT) serves a large number of static or dynamic machine type devices (sensors, monitors). IoT slices may rely on a simplified control plane and hence require a smaller bandwidth.



BBU (Baseband unit)
UP/CP are VNFs in Control/User Plane

The solution of mapping three services in simple physical wireless network is to find the feasible slice embedding with the least cost. Cost savings of up to 25 and 40 percent can be achieved in example of two possible traffic mixes (2:1:1, 1:2:2) of tradional, video and IoT services [6]. The important result is that slicing flexibility is better exploited under proper dimensioning of the network.

For real-life 5G wireless network scenarios, exact optimal ILP solution is impractical as they require huge computational and storage capabilities. Instead, heuristic approaches are developed to provide sub-optimal solutions with additional chalenges of end-to-end constraints, heterogeneous requirements, multitenancy and nonlinear resource utilization, and slice fairness.

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Positional analysis of multi-mode fuzzy networks

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Keywords

Fuzzy relational system; fuzzy relation inequality; fuzzy network, one-mode network, two-mode network, multi-mode network, positional analysis, blockmodeling

Summary

Social network analysis is a branch of sociology and mathematics which provides formal models and methods for the systematic study of social structures. Since social networks share many common properties with other types of networks, methods of social network analysis are applied to the analysis of networks in general, including many kinds of networks that arise in computer science, physics, biology, etc., such as the hyperlink structure on the Web, the electric grid, computer networks, information networks or various large-scale networks appearing in nature. In order to overcome the vagueness, which is unavoidable when discussing the relationships between individuals, it is quite natural to study social networks from the aspect of fuzzy set theory, i.e., to study *fuzzy networks*, what is being done in our research.

Positional analysis is a discipline of social network analysis whose main aim is to identify the position or role of actors in the network on the basis of relationships between them (cf. [8,15]). A key role in the positional analysis play regular equivalences, and in our approach to fuzzy social networks such equivalences are obtained as solutions of particular systems of fuzzy relation equations, called weakly linear (cf. [11,12]).

Social network analysis deals with different types of networks, which could be roughly classified as *one-mode*, *two-mode* and *multi-mode networks*. It mostly deals with the one-mode networks, and a wide variety of methods has been developed for handling the one-mode case. However, two-mode and multi-mode networks are also common. For instance, typical examples of two-mode networks include actor-by-event attendance, actor by group membership, actor by trait possession, actor by object possession, and many others (cf. [3, 10]). Positional analysis of two-mode networks was carried out in [18,21] by means of a direct method for computing the greatest pair of regular fuzzy equivalences based on the solving the so-called two-mode systems of fuzzy relation inequalities. The advantages of this method in relation to other methods used in positional analysis of two-mode networks are shown in [7].

The main subject of this talk are much more complex networks consisting of multiple sets of entities and ties inside and between some of them, which are called *multi-mode networks* (the name *multilevel network* was also used in the related literature). Examples of such networks which could be found in the literature include organization networks [24], networks of academic publications [22], network of the elite of cancer researchers in France [13, 14, 25–27], genetic regulatory (interaction) network [23], and many others. Ordinary (crisp) multi-mode networks have been intensively studied in the recent literature (cf., e.g., [13, 14, 16, 22, 25, 26]), and from the aspect of positional analysis and blockmodeling they have been studied in [27]. Here we present our recent results from [6, 17, 19] concerning multi-mode fuzzy networks. Namely, we have introduced the concepts of a *multi-mode fuzzy relational system*, and a *multi-mode fuzzy network*, as its natural interpretation, and position analysis has been reduced to the problem of solving particular systems of fuzzy relation inequalities and equations (shortly FRIE) determined by the given multi-mode fuzzy relational system. We provided algorithms for computing the greatest solutions of these systems of FRIE, which are n-tuples of fuzzy quasi-orders or fuzzy equivalences and play the crucial role in determining positions in the considered multi-mode fuzzy network. As a natural example we will discuss the network of employees, jobs and skills within some company.

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Topological counterpart for integration and differentiation in complex networks

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Keywords

complex networks; mesostructures; simplicial complex; integration/differentiation; (co)boundary operator

Summary

Complex networks are abundant with different substructures generated by aggregations of pairwise relations between nodes. Nevertheless, widely accepted definition and criteria for differentiation between integrated groups of nodes is still lacking. Commonly, such substructures are called communities [1], characterized as highly dense collections of nodes, and node's membership to a community depends on the applied community detection algorithm.

In the present work we are focusing on the hierarchical aggregation of substructures associated to simplicial complex, the so called clique complex [2], built from complex network by aggregating complete graphs, i.e., cliques. Although the definition of communities as collections of cliques is rather rigid, it provides us an unambiguous partition of complex network into substructures. Furthermore, since cliques are built by subcliques, the collections of cliques and subcliques build natural setting for examination of structural differentiation and integration of cliques, topologically resembled by the interplay between actions of boundary operator and its adjoint, respectively.

In a plain words, the action of boundary operator disintegrates a clique into subcliques, whereas the action of the adjoint boundary operator does the opposite. Vertices are integrating into links, and some of them are members of more than one link; links are integrating into triangles, and some of them are members of more than one triangle; and so on. Clearly, an isolated complete graph is a maximally integrated-minimally differentiated structure, on the other hand, the overlapping between cliques builds highly nontrivial structures.

The information about the actions of boundary operator and its adjoint is stored in the entries of the associated matrices, whereas the relationship between actions at different hierarchical levels is stored in the matrix entries of the combinatorial Laplacian [3]. The analysis of combinatorial Laplacian reveals the intrinsic structural subtleties resulting from the interplay between boundary operator and its adjoint, at different hierarchical levels. We have calculated the eigenvalues of combinatorial Laplacians for different artificial and real world networks, and the results display nontrivial mesoscopic structures which originate from the interplay between differentiation and integration of collections of nodes.

These findings are not of purely theoretical nature, but can find an applicability in various phenomena. For example, in neuroscience, the patterns involving three or more neurons are of paramount importance, and they cannot be described in terms of pair correlations, hence presenting natural higher order phenomena.

Furthermore, the outcome of this research promotes shifting the focus of algebraic topological research on complex networks from the interest in homology and its generators, geometrically represented as holes, to the higher-order structures embedded within the relations of collections of nodes.

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High-dimensional structure phenomenon in social brain

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Keywords

social neurology; complex network; simplicial complex; brain imaging;

Summary

Availability of large brain imaging datasets and mapping the data onto networks led to a big leap in the understanding of brain functions, which underly human behavior in various circumstances. In this context, research on the functional brain patterns related to information processing, learning, and social communications are of the increasing interest. However, the collection of such data requires innovative multiscan platforms, although measurement results are still sparse. Therefore, the multi-brain structures and connections underlying human social behavior remain mostly unexplored. In the recent work [3], we have analyzed the aggregate graph which maps EEG signals previously recorded in a social experiment with speakerlistener communications involving many individuals, as described in [2]. Using the methods from the algebraic topology of graphs, we developed a systematic methodology to analyze multi-brain networks. Specifically, the analysis comprises determination of the higher-order simplicial complexes [3, 1] created by entangled cliques of different orders, which represent typical structures of the mutually correlated EEG signals from different brains. Our results reveal that the corresponding topological quantifiers provide a sensitive measure for detecting the differences in the brain activity patterns and interbrain synchronization between speakers and listeners. This analysis have shown that the topology of higher-order complexes precisely quantifies the differences in the brain activation patterns between the participants during the social communication. Furthermore, the topology provides the accurate measure for the speaker-listener coordination and the speakers impact onto a group of listeners. Results also display super-brain phenomenon during spoken communications which comprises strong frontal-to-frontal and parietal-to-parietal synchronization in dyads.

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Structure and dynamics of event-driven social groups

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Keywords

complex networks, social groups, event-driven dynamics

Summary

A combination of methods and tools from complex networks theory, statistical physics and computer science has proven to be very successful approach for studying collective behavior in various social groups [2, 1, 5]. These techniques have enabled extensive studies of human activity patterns, social networks structure and dynamics, and thus provided a better understanding of mechanisms that underlie the emergence of collective behavior in online social groups. Here we demonstrate that similar approach can be used for studying and better understanding of principals behind the growth and evolution of offline event-driven communities. Although these groups have an important role in every society [7, 6], they have attracted less attention in past few decades mostly due to the lack of data. Their most significant feature is their event-driven dynamics, i.e., their members meet and build social connections during the events which are well localized in time and space. Recent research on several types of these groups [6, 7] have shown that dynamics of these groups is characterized with universal patterns of member's participations in group activities.

We demonstrate this universality by analyzing the data from two different types of social groups: series of scientific conferences [6], which are representatives of event-driven professional social groups, and four leisure groups from Meetup platform [7]. The conference dataset includes six different series of conferences from various fields of science [6]: American Physical Society March Meeting (APSMM), American Physical Society April Meeting, Society for Industrial and Applied Mathematics Annual Meetings, Neural Information Processing Systems Conference, International Conference on Supercomputing, and Annual International Conference on Research in Computational Molecular Biology. The Meetup dataset contains four large groups that belong to different categories and have different type of activit [7]: Geamclt group is made of foodie thrill-seekers, VegasHiker (LVHK) group consists of hikers, Pittsburgh-free people search for free social events, and TechLife Columbus a technology-related community. Both datasets contain the detailed information about the members of the social group and organized events (conferences or meetups depending on the type of social group), as well as the attendance list for each event. This enables us to study in details the participation patterns for each of the six conferences and four Meetup social groups by calculating the probability distribution of the total number of attended events, the number of successive participations and the length of pauses between each two attended events by a member. What is striking is that all these distributions exhibit truncated power-law behavior with the value of power-law exponent between 1 and 2. In order to better characterize this universal participation dynamics, we model a probability for a member to attend the next event at time $t+1$ with non-linear Polya urn process

$$g(z(t)) = \frac{z(t)^p}{1+z(t)^p}, \tag{1}$$

where $z(t) = \frac{x(t)}{y(t)+y_0}$ is the ratio between the number of attended events $x(t)$ by the event $t+1$ and number of missed events $y(t)$ increased with the parameter that quantifies the openness of the social groups toward new members y_0. The narrow range of the value of parameters p and y_0 for all six conference series and all four Meetup groups further confirms the universality of event-driven dynamics, and suggests that event-driven dynamics is strongly influenced by social factors, such as members association with the community and inclusiveness of social groups [6, 7].

The analysis of the evolution of ego-social networks of members of four Meetup groups further confirms these findings. We obtain these networks by mapping the data for each Meetup group onto a bipartite network of members and events, where the link between nodes i and j indicates the participation of member i in the event j.

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The social network between members of one Meetup group is obtained by projecting the appropriate bipartite network to members partition and filtering out the redundant links using the technique based on configuration model of random bipartite networks [3, 4]. We study the evolution of average local features of ego-networks, such as degree, strength, weighted and non-weighted clustering coefficient, with the number of attended events. Our results show that at the beginning of their engagement in the group activities members spend most of their effort on enlarging their social circle, while latter engagement is primarily associated with the strengthening of already existing ties and increase of the bonding social capital. Our analysis of importance of events shows that both big and small events have their role in the growth and evolution of event-driven social groups: big events are primarily important for the growth of social groups and incorporation of group members, while smaller events serve the purpose of strengthening of already existing ties.

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