

The Seventh Conference on Information Theory and Complex Systems  
TINKOS 2019

# BOOK OF ABSTRACTS



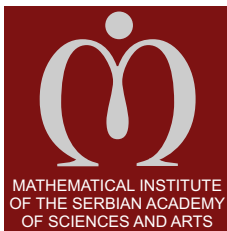
Belgrade, Serbia, October 15-16, 2019  
Mathematical Institute of the Serbian Academy of Sciences and Arts  
Institute of Physics Belgrade

The Seventh Conference on  
Information Theory and Complex Systems  
TINKOS 2019

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Editor: Velimir Ilić



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## TINKOS 2019 – CONFERENCE PROGRAM

<b>DAY 1 (15.10.2019.)</b>	
<b>09:30 - 10:00</b>	<b>REGISTRATION</b>
<b>10:00 – 10:20</b>	<b>OPENING</b> Velimir Ilić – Introduction to TINKOS 2019
<b>10:20 – 11:30</b>	<b>INFORMATION MEASURES</b>
10:20 - 10:50	Jan Korbel CLASSIFICATION OF GENERALIZED ENTROPIES AND APPLICATIONS TO COMPLEX SYSTEMS
10:50 - 11:10	Slavko Simić ON THE SYMMETRIZED S-DIVERGENCE
11:10 - 11:30	Zlata Tabachova, Petr Jizba RENYI ENTROPY TRANSFER IN DETERMINISTIC CHAOTIC SYSTEM
<b>11:30 – 11:50</b>	<b>Coffee Break</b>
<b>11:50 – 13:40</b>	<b>QUANTUM AND NONEQUILIBRIUM SYSTEMS</b>
11:50 - 12:20	Édgar Roldán MARTINGALE THEORY OF STOCHASTIC THERMODYNAMICS
12:20 - 12:50	Gonzalo Manzano Paule, Rosario Fazio, Édgar Roldán QUANTUM MARTINGALE THEORY AND ENTROPY PRODUCTION
12:50 - 13:20	Igor Petrović, Jasmina Jeknić-Dugić, Momir Arsenijević, Miroljub Dugić ON THE STABILITY OF THE QUANTUM BROWNIAN ROTATOR
13:20 - 13:50	Miroljub Dugić, Jasmina Jeknic-Dugić, Momir Arsenijević ‘DOES ‘THE OLD MAN’ PLAY DICE?’
<b>13:50 - 15:10</b>	<b>Lunch Break</b>
<b>15:10 – 16:30</b>	<b>SIGNAL COMPLEXITY</b>
15:10 - 15:40	Miloš Milovanović, Bojan M. Tomić A STOCHASTIC THEORY OF WAVELETS
15:40 - 16:00	Nicolleta Saulig COMPLEXITY ESTIMATION OF NONSTATIONARY SIGNALS BY MEANS OF THE RÉNYI ENTROPY
16:00 - 16:30	Jonatan Lerga LOCAL ENTROPY MEASURES WITH APPLICATIONS IN BIOMEDICINE
<b>16:30 – 16:50</b>	<b>Coffee Break</b>
<b>16:50 – 17:50</b>	<b>NONLINEAR DYNAMICS</b>
16:50 – 17:20	Vladimir Jaćimović GEOMETRY OF THE KURAMOTO MODEL AND ITS EXTENSIONS: TOWARDS THE THEORY OF COLLECTIVE MOTIONS ON MANIFOLDS
17:20 – 17:50	Igor Franović MACROSCOPIC DYNAMICS IN HETEROGENEOUS ASSEMBLIES OF EXCITABLE AND OSCILLATORY UNITS
<b>17:50 – 18:10</b>	<b>GUEST SECTION: SERBIAN NATIONAL COST COORDINATOR</b>
17:50 – 18:10	Bratislav Marinković COST ACTIONS AS A WIDE NETWORK OF RESEARCHERS AND INNOVATORS ACROSS EUROPE
<b>18:10 – 18:30</b>	<b>OPEN DISCUSSION</b>
<b>20:30</b>	<b>CONFERENCE DINNER</b>

<b>DAY 2 (16.10.2019.)</b>	
<b>09:00 – 10:10</b>	<b>INFORMATION THEORY</b>
09:00 – 09:30	Bane Vasić GRAPH EXPANSION-CONTRACTION METHOD FOR CALCULATING ERROR FLOOR OF LOW-DENSITY PARITY CHECK CODES
09:30 – 9:50	Mohamed Yaoumi, Elsa Dupraz, Francois Leduc-Primeau, Frederic Guilloud ENERGY-EFFICIENT PROTOGRAPH-BASED LDPC CODES
09:50 – 10:10	Dragana Bajović, Jose M. F. Moura, Dejan Vukobratović DETECTION OF RANDOM WALKS ON GENERIC TOPOLOGIES: OPTIMAL PERFORMANCE CHARACTERIZATION VIA CONVEX OPTIMIZATION
<b>10:10 – 10:30</b>	<b>Coffee Break</b>
<b>10:30 – 11:30</b>	<b>MODELS OF COLLECTIVE BEHAVIOR</b>
10:30 – 11:00	Aleksandra Alorić MARKET FRAGMENTATION AND MARKET CONSOLIDATION AS EMERGENT PROPERTIES IN SYSTEMS OF ADAPTIVE TRADERS AND DOUBLE AUCTION MARKETS
11:00 – 11:30	Simon Schweighofer A BALANCE MODEL OF OPINION HYPERPOLARIZATION
<b>11:30 – 11:50</b>	<b>Coffee Break</b>
<b>11:50 – 13:20</b>	<b>MACHINE LEARNING</b>
11:50 – 12:20	Elsa Dupraz ENERGY-EFFICIENT MACHINE LEARNING ALGORITHMS
12:20 – 12:40	Jelena Milovanović, Branimir Todorović USING DEEP NEURAL NETWORKS FOR INTERNAL BANKING FRAUD DETECTION
12:40 – 13:00	Ivan Petrović, Bratislav P. Marinković, Stefan Ivanović, Violeta Petrović MACHINE VS RULE-BASED LEARNING IN PHYSICS: POSSIBILITIES AND ADVANTAGES
13:00 – 13:30	Michał Bejger APPLICATIONS OF MACHINE LEARNING IN GRAVITATIONAL-WAVE ASTROPHYSICS
<b>13:30 – 14:50</b>	<b>Lunch Break</b>
<b>14:50 – 16:10</b>	<b>COMPLEX NETWORKS</b>
14:50 – 15:20	Ljupčo Kocarev BAYESIAN CONSENSUS CLUSTERING IN NETWORKS
15:20 – 15:50	Slobodan Maletić TOPOLOGICAL ANALYSIS OF COMPLEX DATASETS: TOWARD EXHAUSTIVE RECONSTRUCTION OF RELATIONSHIPS
15:50 – 16:10	Dragorad Milovanović, Zoran Bojković OPTIMAL DEPLOYMENT OF 5G NETWORK SLICING BASED ON COMPLEX NETWORK THEORY
<b>16:10 – 16:30</b>	<b>Coffee Break</b>
<b>16:30 – 17:40</b>	<b>BIONFORMATION SYSTEMS</b>
16:30 – 17:00	Natasa Mišić HIERARCHICAL STRUCTURE OF THE GENETIC CODE
17:00 – 17:20	Francesca Schonsberg GARDNER APPROACH FOR THRESHOLD LINEAR UNITS TO UNDERSTAND MEMORY IN THE BRAIN
17:20 – 17:40	Gordana Simić Medić COMPLEXITY OF CREATING ART
<b>17:40 - 18:00</b>	<b>CLOSING</b> Vemimir Ilić – Conclusion to TINKOS 2019

## INVITED SPEAKERS

Aleksandra Alorić, Institute of Physics Belgrade, Serbia

Michał Bejger, Nicolaus Copernicus Astronomical Center, Polish Academy of Sciences, Poland

Elsa Dupraz, IMT Atlantique, Brest, France

Igor Franović, Institute of Physics Belgrade, Serbia

Vladimir Jaćimović, Faculty of Science and Mathematics, University of Montenegro, Montenegro

Jasmina Jeknić-Dugić, Faculty of Science and Mathematics, University of Niš, Serbia

Ljupčo Kocarev, Macedonian Academy of Sciences and Arts, Macedonia

Jan Korbelt, Complexity Science Hub Vienna, Austria

Jonatan Lerga, University of Rijeka, Croatia

Slobodan Maletić, Vinča Institute of Nuclear Sciences, Serbia

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Miloš Milovanović, Mathematical Institute of SASA, Serbia

Natasa Mišić, Research and Development Institute Lola Ltd, Serbia

Édgar Roldán, ICTP - The Abdus Salam International Centre for Theoretical Physics, Italy

Simon Schweighofer, Complexity Science Hub Vienna, Austria

# Contents

Page No.

<i>Jan Korbel</i> <b>Classification of Generalized Entropies and Applications to Complex Systems</b>	1
<i>Slavko Simić</i> <b>On the Symmetrized S-divergence</b>	2
<i>Zlata Tabachova, Petr Jizba</i> <b>Renyi Entropy Transfer in Deterministic Chaotic System</b>	3
<i>Édgar Roldán</i> <b>Martingale Theory of Stochastic Thermodynamics</b>	4
<i>Gonzalo Manzano Paule, Rosario Fazio, Édgar Roldán</i> <b>Quantum Martingale Theory and Entropy Production</b>	5
<i>Igor Petrović, Jasmina Jeknić-Dugić, Momir Arsenijević, Miroljub Dugić</i> <b>On the Stability of the Quantum Brownian Rotator</b>	6
<i>Miroljub Dugić, Jasmina Jeknić-dugić, Momir Arsenijević</i> <b>Does 'the Old Man' Play Dice?</b>	7
<i>Milos Milovanović, Bojan M. Tomić</i> <b>A Stochastic Theory of Wavelets</b>	8
<i>Jonatan Lerga</i> <b>Local Entropy Measures With Applications in Biomedicine</b>	10
<i>Nicolleta Saulig</i> <b>Complexity Estimation of Nonstationary Signalsby Means of the Rényi Entropy</b>	11
<i>Vladimir Jaćimović</i> <b>Geometry of the Kuramoto Model And Its Extensions: Towards the Theory of Collective Motions on Manifolds</b>	13

<i>Igor Franović</i>		
<b>Macroscopic Dynamics in Heterogeneous Assemblies of Excitable And Oscillatory Units</b>		15
<i>Bratislav Marinković</i>		
<b>Cost Actions as a Wide Network of Researchers And Innovators Across Europe</b>		17
<i>Bane Vasić</i>		
<b>Graph Expansion-contraction Method for Calculating Error Floor of Low-density Parity Check Codes</b>		19
<i>Mohamed Yaoumi, Elsa Dupraz, Francois Leduc-Primeau, Frederic Guilloud</i>		
<b>Energy-efficient Protograph-based LDPC Codes</b>		21
<i>Dragana Bajović, Jose M. F. Moura, Dejan Vukobratović</i>		
<b>Detection of Random Walks on Generic Topologies: Optimal Performance Characterization via Convex Optimization</b>		22
<i>Aleksandra Alorić</i>		
<b>Market Fragmentation and Market Consolidation as Emergent Properties in Systems of Adaptive Traders and Double Auction Markets</b>		25
<i>Simon Schweighofer</i>		
<b>A Balance Model of Opinion Hyperpolarization</b>		1
<i>Elsa Dupraz</i>		
<b>Energy-efficient Machine Learning Algorithms</b>		26
<i>Jelena Milovanović, Branimir Todorović</i>		
<b>Using Deep Neural Networks for Internal Banking Fraud Detection</b>		28
<i>Ivan Petrović, Bratislav P. Marinković, Stefan Ivanović, Violeta Petrović</i>		
<b>Machine vs Rule-based Learning in Physics: Possibilities and Advantages</b>		29



<i>Michał Bejger</i>	
<b>Applications of Machine Learning in Gravitational-wave Astrophysics</b>	31
<i>Ljupčo Kocarev</i>	
<b>Bayesian Consensus Clustering in Networks</b>	32
<i>Slobodan Maletić</i>	
<b>Topological Analysis of Complex Datasets: Toward Exhaustive Reconstruction of Relationships</b>	33
<i>Dragorad Milovanović, Zoran Bojković</i>	
<b>Optimal Deployment of 5G Network Slicing Based on Complex Network Theory</b>	34
<i>Natasa Mišić</i>	
<b>Hierarchical Structure of the Genetic Code</b>	37
<i>Francesca Schonsberg</i>	
<b>Gardner Approach for Threshold Linear Units to Understand Memory in the Brain</b>	39
<i>Gordana Simić Medić</i>	
<b>Complexity of Creating Art</b>	40

Abstracts

# Classification of Generalized Entropies and Applications to Complex Systems

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## Keywords

generalized entropies; Shannon-Khinchin axioms; Shore-Johnson axioms; maximum entropy principle; scaling expansion

## Summary

In this talk, we discuss the concept of entropy and its applications in complex systems. Entropy is a very famous concept in thermodynamics, statistics and information theory. However, it turns out that the original definition due to Shannon might not be accurate for strongly-correlated systems, for systems with emerging structures, or path-dependent processes. For this end, many generalizations of Shannon entropy naturally ap-

peared. In order to understand the meaning of each entropic functional, we discuss several possible classification schemes and point out connections between them. We mention classification based on asymptotic scaling, information-theoretic axiomatics and statistical consistency requirements.

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# On the symmetrized $S$ -divergence

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## Keywords

relative divergence of type  $s$ ; monotonicity; log-convexity

## Summary

In this paper we give a study of the symmetrized divergences  $U_s(p, q) = K_s(p||q) + K_s(q||p)$  and  $V_s(p, q) = K_s(p||q)K_s(q||p)$ , where  $K_s$  is the relative divergence of type  $s$ ,  $s \in \mathbb{R}$ , defined as

$$K_s(p||q) := \begin{cases} (\sum p_i^s q_i^{1-s} - 1)/s(s-1) & , s \in \mathbb{R} \setminus \{0, 1\}; \\ K(q||p) & , s = 0; \\ K(p||q) & , s = 1, \end{cases}$$

where  $\{p_i\}_1^n, \{q_i\}_1^n$  are given probability distributions and  $K(p||q)$  is Kullback-Leibler divergence. It includes the Hellinger and  $\chi^2$  distances as particular cases.

Some basic properties as symmetry, monotonicity and log-convexity are established. An important result from the Convexity Theory is also proved i.e.,

If  $f$  is a convex function defined on  $I := [a, b]$  and

$$F(x, y) := f(x) + f(y) - 2f\left(\frac{x+y}{2}\right),$$

then

$$\max_{x, y \in I} F(x, y) = F(a, b).$$

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# Rényi entropy transfer in deterministic chaotic system

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## Keywords

complex systems; transfer entropy; Rényi  $\alpha$ -entropy; information flows; causality

## Summary

Complex dynamical system is a system composed of several subsystems (with given properties) interacting between each other and surrounding environment. These interactions brings to the whole system new properties, absent in composing parts. Locating and identifying information flows within a dynamical complex systems is fundamental for understanding its causal structure.

In recent years the Shannon transfer entropy, introduced in [5], has been actively used as the directional measure of information flows between stochastic processes. In [1] it was then generalized in terms of information measures called the Rényi  $\alpha$ -entropies and used to detect information flows between financial data [2, 3] for specific value of  $\alpha$ .

In our research we focus on studying the whole spectrum of transfer  $\alpha$ -entropies. Especially, we concentrate on transfer entropies for  $\alpha < 1$  since they measure the information flows caused only by marginal events. We can characterize Rényi transfer  $\alpha$ -entropies with the following assumptions:

- Transfer entropies generalize the usual linear causality tests (e.g., Granger causality) to non-linear dynamics, in order to explain internal dynamics and information transfer in complex systems with extreme events.
- The generalization represented by the Rényi family of entropies provide a beautiful inside look to the geometrical properties of the conditional distributions. Rényi TE can be used for studying mutual in-

fluences between time-series in various dissimilar fields, ranging from neuroscience to financial markets.

- RTE is able to detect simple linear and non-linear correlations between stochastic processes.

We illustrate the utility of Rényi  $\alpha$  transfer entropies in analyzing causality within subsystems of the Lorenz system and also between two coupled Lorenz systems. Shannon TE also known as Conditional Mutual Information between chaotic deterministic systems was studied in [4].

The Lorenz system is a system of ordinary differential equations with chaotic solutions. Even though the next step (solution) of the system is uniquely defined by the current one, the long term predictions are not possible. The latter is a consequence of the sensitivity on the initial conditions.

Nevertheless we show that the RTE can detect structured information flows within the subsystems of the the Lorenz system.

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# Martingale Theory of Stochastic Thermodynamics

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## Keywords

stochastic thermodynamics; nonequilibrium physics; martingales; heat engines; biophysics

## Summary

Stochastic thermodynamics is an emerging field that describes the fluctuating nature of particle and energy fluxes at mesoscopic scales. Fluctuation theorems derived over the last two decades have unveiled universal properties of the finite-time distributions of entropy production, work and heat at the mesoscale. These results have inspired novel nanotechnological applications in single-molecule biophysics, colloidal systems, etc. However little is known yet about further statistical properties in stochastic thermodynamics, e.g. what are the extreme-value and first-passage-time statistics of fluctuating energy and entropy fluxes?

We derive equalities and inequalities for the extreme-value, stopping-time and passage statistics of the fluctuating entropy production and the housekeeping heat for

classical and quantum mesoscopic systems driven away from equilibrium. These results are derived using martingale theory, a mathematical framework widely used in gambling and finance. In this talk, I will discuss recent work within the framework of the "martingale theory" for stochastic thermodynamics of classical systems, both in the theoretical and experimental context. Furthermore, I will briefly discuss applications of this refreshing framework to extreme-value statistics of molecular motors.

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# Quantum Martingale Theory and Entropy Production

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## Keywords

quantum thermodynamics; entropy production; martingales; quantum trajectories; non-equilibrium thermodynamics

## Summary

Thermodynamics can be extended far beyond macroscopic systems composed by a large number of classical or quantum particles. For example, when reducing the size of the systems under consideration, fluctuations becomes dominant. In such situations, the system may be easily driven out of equilibrium and the laws of thermodynamics are blurred, since they are only expected to be fulfilled on average. Nevertheless, studying the statistics of fluctuations has revealed a deeper structure of thermodynamics in the form of equalities for the fluctuating versions of work, heat or entropy, the so-called fluctuation theorems [1].

Fluctuation theorems have been developed for small quantum systems, mostly in the case of ideal thermal equilibrium environments. Going beyond this assumption has attracted increasing attention in the last decade, both because of the effective finite-size of real thermal reservoirs in practical applications, and the possibility of engineering non-thermal reservoirs with quantum properties in the lab [2, 3].

This extension can be carried out within the formalism of quantum jump trajectories, which describes the evolution of an open quantum system conditioned on environmental monitoring. In such case, entropy production can be meaningfully defined along single trajectories in the

Hilbert space, and fluctuation theorems be derived [4]. Furthermore, the present formalism allows the study of martingale theory for entropy production in nonequilibrium steady states in the quantum realm [5]. We find that, even if quantum fluctuations spoil the classical theory in its original form, an extension can be developed, leading to several new results spotting the role of coherence in thermodynamics. In particular, we identify a decomposition of entropy production into an exponential martingale and a purely quantum term, both obeying integral fluctuation theorems. Moreover we derive a set of genuine universal results for stopping-time and infimum statistics of stochastic entropy production. We complement the general formalism with numerical simulations of a qubit system.

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# On the stability of the quantum Brownian rotator

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## Keywords

quantum many-particle systems; quantum Brownian rotator; master equation method; stability of rotation

## Summary

The standard quantum mechanical theory is insensitive to the number of particles. Therefore description of the quantum many-particle systems remains an open issue in the foundations of the theory. To this end, additional complications come from the fact that the realistic systems are with the definite geometrical size and shape as well as exposed to the environmental influence. For this reason, only the toy-models bearing high degree of spatial symmetry for both the system as well as for its environment are used.

The walk and progress in modern technology, such as nanotechnology, demands theoretical elaboration of the proper quantum models. In this regard, the large-molecule (the natural as well as artificial) rotators represent one of the basic 'setups' for the desired nano- and quantum-technological procedures [1, 2, 3]. The theoretical models are rather simplified, e.g. [4], and hardly of any use for certain realistic physical situations. Nevertheless, to this end, an elaborate approach and the basic results have recently been put forward [5, 6].

The propeller-shaped large-molecules rotators can be modeled by a single (rotational) degree of freedom as a rigid system that is open to the environmental influence and can be modelled by the so-called Caldeira-Leggett master equation [7]. The model argues for the linear dependence of both the moment of inertia and the damping

factor on the number  $N$  of blades of the propeller [5, 6]. A number of interesting theoretical predictions regarding stability of rotation are obtained exhibiting nontrivial (including nonlinear) dependence on the  $N$ .

Interestingly, in effect, some kind of *optimization*, which is characteristic for the macroscopic classical engineering, is needed for the proper control of the molecular rotators even for the one-dimensional model. The desired quantum optimal-control methods are in infancy yet.

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# Does 'the Old Man' play dice?

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## Keywords

quantum ensembles; quantum Markov processes; quantum unraveling; randomness

## Summary

In 1926, Einstein wrote to Born [1]: *'Quantum mechanics commands much respect. But an inner voice tells me that it is not Mr. Right. The theory delivers a lot, but it hardly brings us closer to the mystery of the Old Man. Anyway, I'm sure he does not play dice.'*

This quote carries the very essence of the 'quantum puzzle(s)' and provides an intimate link with the mathematical problem of interpretation of probability [2, 3, 4, 5]. In the narrower physical context, this is a never-ending debate about determinism versus randomness, which Einstein (like most of the working physicists) could not easily adopt for the 'simple' reason that 'pure randomness' seems to be elusive [5]—the concept of probability appears to be vague in the context of the *single* physical system. For this reason, it is widely believed that dynamics of a quantum ensemble can be 'unraveled', i.e. that carries at least one dynamically well-defined ensemble decomposition. More precisely, a ('mixed') quantum ensemble is imagined to consist of subensembles, each of which is in a uniquely-defined ('pure') quantum state that dynamically evolves in time independently of the others. Much of the interpretations of quantum theory adopt the unraveling as assumed, if not explicitly introduced. Furthermore, the ensemble unraveling as briefly described above is essential also for some important quantum information processing [6]. However, quite recently, the ab-

sence of the ensemble unraveling has been put forward for an important class of the quantum linear dynamical processes (dynamical maps) [7].

For some typical quantum Markovian processes, it proves that the ensemble unraveling is *not* possible. Formally, the mixed ensembles appear basically equal with the 'pure' ensembles—every single element of the mixed ensemble is in the same mixed state for those quantum dynamical processes. This, technically simple, observation [7] unexpectedly revives and directs the old debate on whether or not 'the Old Man' plays dice.

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# A Stochastic Theory of Wavelets

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## Keywords

stochastic processes; time operator; multiresolution; real and  $p$ -adic analysis

## Summary

*Wavelet* (in French *ondelette*) is a term originating from Roger Balian, that was finally adopted by Jean Morlet [1, 2]. It implies a function generating base for decomposition of the finite energy signals both in spatial and in frequency domain concurrently. Given a wavelet  $\psi$ , the base of  $L^2(\mathbb{R})$  is generated through translations and dilatations  $\psi_{j,k}(x) = \psi(2^j x - k)$  whereby the integers  $j$  and  $k$  indicate spatial position and dyadic scale of a basic element. Their emergence corresponds to the base proposed by Alfréd Haar in the doctoral thesis under Hilbert's supervision (1909) and his paper published in the *Mathematische Annalen* [3]. The Haar wavelet

$$\psi(x) = \begin{cases} 1 & 0 < x < 1/2 \\ -1 & 1/2 < x < 1 \end{cases} \text{ generates a complete orthonormal system of compact support which is not regular in terms of continuous differentiability [4].}$$

Succeeding precursors to wavelets include the Franklin orthonormal system (1927), the Littlewood-Paley theory (1930), the Calderon identity (1960), a modification of the Franklin base given by Strömberg (1981), the Gabor atoms in signal processing (1946), subband coding (1975), pyramidal algorithms (1982), zero-crossings (1982), spline approximations, the Rokhlin multipole algorithms (1985), refinement schemes in computer graphics, coherent states in quantum mechanics, and renormalization in quantum field theory [2]. Construction of wavelets that have compact support and arbitrary high regularity (1988) is ultimately done by Ingrid Daubechies [5].

Independent of the other theories, Karl Gustafson et al. developed a view in which wavelets are regarded to be stochastic processes [6]. The context arose naturally from the time operator formalism of statistical mechanics. Gustafson and Misra looked at models for the decay

of quantum particles, having realised that regular stationary stochastic processes imply multiresolution property which was an indication of the time operator [7].

The wavelet theory received a key impetus from interest by mathematicians and physicists cooperating with geologists from the oil companies. In particular, the wavelet transform was developed by Grossmann and Morlet who was the geologist having suggested that seismic traces should be analyzed by translations and dilatations of a suitable function [8]. Grossmann was a theoretical physicist and mentor of investigating coherent states by Ingrid Daubechies wherein wavelets have also emerged, although in her study there was no relation to multiresolution and stochastic processes [9]. In that respect, the quantum theory indubitably played a significant role concerning wavelets [6].

Due to Meyer and Mallat, multiresolution analyses has become an essential tool in exploring wavelets [10, 11]. It corresponds to nested subspaces  $\mathcal{A}_j$  of  $L^2(\mathbb{R})$  satisfying axioms among which a central one is the property  $f(\cdot) \in \mathcal{A}_j \Leftrightarrow f(2\cdot) \in \mathcal{A}_{j+1}$ .  $\mathcal{A}_j$  is termed the *approximate subspace*, whilst its orthocomplement  $\mathcal{D}_j$  such that  $\mathcal{A}_{j+1} = \mathcal{A}_j \oplus \mathcal{D}_j$  is the *detail subspace* of a multiresolution. The structure is intimately related to that of the Kolmogorov automorphisms, which belong to the framework of regular stationary stochastic processes [12]. A prime example is induced by the Baker map

$$B(x, y) = \begin{cases} (2x, y/2) & x < 1/2 \\ (2x - 1, y + 1/2) & x > 1/2 \end{cases} \text{ which is a measure preserving transformation of the unit square.}$$

The time operator of the Kolmogorov system governed by the evolution  $Vf(x) = f(Bx)$  has been explicitly constructed [13].

Given the evolutionary operator  $V$  of a system, the time is defined to be the operator  $T$  satisfying  $[T, V] = V$ , i.e.,  $[T, V^t] = tV^t$ . If the evolution  $V^t f(x) = f(B^t x)$  is induced by a measure preserving group  $B^t$ , it is equivalent to the uncertainty relation  $[T, L] = iI$  whereat

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$V^t = e^{-iLt}$ , i.e., the Liouvillian  $L$  is an infinitesimal generator of  $V^{t\dagger} = e^{iLt}$  in regard to the Stone theorem. Since wavelets on the real line are not related to preservation of any finite measure, one requires reducing their domain onto the interval  $\mathbb{I} = [0, 1]$  which is done through periodization  $\tilde{\psi}_{j,k}(x) = \sum_l \psi_{j,k}(x+l)$  [14]. A multiresolution on the interval  $\mathbb{I} = [0, 1]$  corresponds to the Renyi map  $R$  inducing the exact system governed by the evolutionary operator  $Uf(x) = f(Rx)$ . It is extended naturally to the Kolmogorov system  $Vf(x) = f(Bx)$  induced by the Baker map that is measure preserving. The time operator of the system  $U$  is determined by the Haar wavelets due to the eigenequation  $T\psi_{j,k} = j\psi_{j,k}$  having natural extension to that of  $V$  [12].

In that manner, detail subspaces of the multiresolution analyses are regarded to be the age eigenstates wandering in terms of the evolution. However, only the Haar wavelet constitutes a multiresolution on the interval since it is undisturbed by periodization. Other ones satisfy the multiresolution property just approximately considering that they are partially localized in the period. Nevertheless, the wavelet domain hidden Markov model concerning statistics of the detail coefficients fits as well to all of them [15]. The Markovian structure  $S = (S_{j,k})$ , composed by hidden variables of the model, represents causal states whose informational content  $H(S)$  is termed to be the global complexity of a system. It indicates an increase of local complexity  $H(S_{j,k})$  in the temporal domain corresponding to eigenvalues  $j$  of the time operator  $T$ , which is the definition of self-organization by Shalizi [16]. The complexity is proven to be a measure of the decomposition optimality, which is also evident by a superior denoising related to the optimal wavelet [17].

The statistical model regards a signal and its coefficients to be random realizations, which is achieved through natural extension of the unilateral shift  $U$  to the bilateral one  $V$ . It actually maps a unilateral sequence of binary digits  $\dots i_0 i_1 \dots$  from  $\mathbb{I}$ , which is the domain of  $R$ , to the bilateral string  $\dots i_1 i_0 i_{-1} \dots$  that represents an element of  $\mathbb{I} \times \mathbb{I}$  whereon  $B$  acts shifting the representation right. Such a shift corresponds to division by 2 in terms of dyadic numbers whose only multiresolution analysis is the Haar one, although there are many other wavelets generating it [18]. In that manner, dyadic analyses should dissolve the problem concerning a lack of the multiresolution property due to periodizing wavelets on the interval. A usage of  $p$ -adic probabilities on the other hand makes irrelevant the problem of positivity preservation which is the main discordance between multiresolution analyses and stochastic processes [6]. The negative probabilities – that correspond to their stabilization in a  $p$ -adic norm – is crucial contradistinction of quantum and classical viewpoints [19]. Considering that, the quantum theory plays once again a major role in conjunction to the  $p$ -adic numbers whose interrelationship should be elucidated by the wavelet theory which is regarded to be a  $p$ -adic spectral analysis [20].

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# Local Entropy Measures with Applications in Biomedicine

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## Keywords

Rényi entropy; local entropy measures; time-frequency distributions; biomedicine

## Summary

Real-life signals are often non-stationary and multi-componential [1]. This is also true for signals found in biomedicine, like electrocardiogram (ECG), electroencephalogram (EEG), electromyogram (EMG), and many others. Detecting and tracking these nonstationarities is of crucial importance since they may contain information on underlying pathophysiological processes.

One of the traditional approaches for analyzing medical signals imply visual pattern recognition. This is, of course, time-consuming and expensive process done by medical experts. In order to reduce the costs, as well as to improve the accuracy, recent approaches implement computer-aided signal processing methods resulting in more objective techniques capable to quantify hidden signal features.

One of the first tools for processing non-stationary time-series is based on the well-known Fourier transform. This mathematical tool provides insight to the spectral components of the analyzed data. Namely, the Fourier transform performs signal spectral decomposition enabling detection of the signal frequency domain features. However, its main shortcoming is loss of the time localization of frequencies present in the analyzed data [2].

In this talk, we will refer to advanced and computationally more demanding tools for non-stationary signal processing, such as joint time-frequency distributions (TFDs). It will be shown that utilizing the TFDs for biomedical signals analysis provide in-depth insight to signal frequency content varying over time as a two-dimensional representation. In additions, TFDs enable detection of the number of signals components and their instantaneous frequencies [2].

Another limitation of the traditional inspection is caused by the presence of inevitable noise in real-life scenarios. Additive noise presents a challenge both for visual inspection and traditional frequency domain analysis tools, especially in case of low signal to noise ratios. Thus, a preprocessing (i.e. denosing) is necessary prior to the signal analysis. Various techniques for denoising were proposed in the last few decades (both temporal and transfer-domain based) [3, 4].

In addition, studies have shown that additional information regarding the content of the TFDs can be obtained by entropy based measures (due to the similarity of the TFDs to probability density functions) [5]. In this talk, a modification of the Rényi entropy for the estimation of the number of signal components from noisy TFDs will be presented. Namely, the algorithm based on the short-term Rényi entropy was applied to analysis of EEGs both in noise-free and noisy environments [6]. Upgraded by an iterative algorithm which additional enhanced the original approach, and combined with instantaneous frequency estimation, the proposed method was shown to be an efficient technique providing spectral description of brain activities at each electrode location up to moderate noise levels.

As it will be shown in the talk, the obtained information concerning the number of EEG signal components and their dominant instantaneous frequencies extracted from the TFDS (both in noise and noise-free environments) show potentials to enhance diagnostics and treatment of neurological disorders for patients with motor control illnesses.

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# Estimation of signal complexity using the Rényi entropy

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## Keywords

Rényi entropy; time-frequency distributions; nonstationary signals

## Summary

The entropy measure is a well-known tool for estimating the information associated to a probability density function. It has been adapted to the  $(t, f)$  plane in order to quantify the information content and complexity of individual signals, as well as the concentration and resolution quality of TFDs [1]. The generalized Rényi entropy, when applied to a TFD, acts as an indicator of the number of components present in a given signal. Several important restrictions are assumed: one of the signal components must be known a priori, all components must present equal time and frequency supports in the  $(t, f)$  plane, and they need to exhibit similar spectral amplitudes. Since in real-life applications these highly limiting conditions are rarely satisfied [2], the signal information content is generally evaluated with respect to a reference signal, obtaining the information on how many reference signals are required to form the analyzed signal [3].

These limitations have served as a motivation for a generalization of the counting property of the Rényi entropy. Recently, a methodology has been proposed for estimating the instantaneous (local) number of components in a nonstationary multicomponent signal based on the local application of the Rényi entropy counting propriety [4]. The presented estimation avoids the need for prior information on the analyzed signal and puts no limitations on the signal structure. Unlike the classic approaches for estimation of the local number of signal components, which involve counting the peaks in the  $(t, f)$  plane at each time instant for as long as the peak amplitude exceeds a fixed threshold, the estimation based on the Short-term Rényi entropy detects a component whenever it locally presents the entropy characteristics of a reference signal. The reference signal is an arbitrarily chosen analytic signal, with constant or variable IF. The applicability of the Short-term Rényi entropy is supported by the fact that the estimated number of components is invariant to the parameters that characterize the selected TFD or the entropy order. When the counting property of the Short-term Rényi

entropy is extended to nonstationary signals, important insights on the signal structure (i.e. components crossings and components ending/starting times) are obtained from the features of the entropy-based estimated number of components. The presented approach allows to resolve ambiguities in the case of local decrements of the number of components, and to obtain information on the time locations of components crossings [5]. When this information is combined with the entropy-based estimate of the number of components, a correct estimation of the total and local number of components present in a signal can be made. However, the results obtained by the Short-term Rényi entropy are highly biased by the amplitude ratio of the signal components present in the analyzed time slice of the TFD. Since in engineering applications one deals with real-life signals, being mixtures of dominant and weaker spectral components, a refined algorithm is proposed, especially well-suited to situations of unequal spectral amplitudes. This iterative method exhibits pronounced sensitivity to low energy components, and it is robust to moderate levels of additive noise. Also, the result obtained by the proposed algorithm is an integer valued function which eases procedures for blind source separation based on "peak detection and tracking" techniques. In addition, the information on the time instants of the starts/ends of the signal components allows to estimate the total number of components. This information can turn advantageous from a computational optimization prospective, allowing dynamic memory allocation, and prevention of memory overflow.

The main contribution of the presented study consists in proving that the Short-term Rényi entropy can estimate the local number of components in a nonstationary signal, without any prior information on the signal. Other future research directions will include implementation of the information on the local and total number of components, obtained by the Short-term Rényi entropy, in advanced blind source separation methods and clustering algorithms. This would lead to more efficient computing solutions and memory handling. Finally, the Short-term Rényi entropy information can be used in applications for signal denoising as a classifier of the output of the K-means algorithm.

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# Geometry of the Kuramoto model and its extensions: towards the theory of collective motions on manifolds

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## Keywords

Kuramoto model, low-dimensional dynamics, Möbius transformations, Lie groups, symmetric spaces

## Summary

Our talk is focused on some geometric and group-theoretic aspects of the Kuramoto model. This line of research has been initiated by Watanabe and Strogatz who reported a change of variables that reduces the dynamics of a large (or infinite) number of globally coupled oscillators to 3-dimensional dynamical system that describes the evolution of global variables of the system, see [1].

This low-dimensional dynamics in the Kuramoto model with identical oscillators and global coupling has further been explained from the group-theoretic point of view in the paper [2]. About the same time, Ott and Antonsen have derived a simple ODE for the order parameter in the model with non-identical oscillators under some severe mathematical assumptions in their famous paper [3]. This brought new insight into relations between the Kuramoto model and some classical mathematical constructions from Complex Analysis and Hyperbolic Geometry, see [4–6].

On the other side, Kuramoto model has been extended to some higher-dimensional manifolds, such as spheres [7, 8], homogeneous spaces and Lie groups [9, 10]. The geometry of these higher-dimensional Kuramoto models is currently subject of research interest with some intriguing insights already available, see [11].

In whole, this set of ideas seems to be evolving into a unified theory of collective motions on manifolds, where many results from higher-dimensional complex geometry, Lie group theory and theory of harmonic functions obtain interesting interpretations and applications.

In addition, this unveils a hidden presence of the Kuramoto model (and its extensions) in some theories of mathematical physics, including analytic representation of quantum states,  $SU(1,1)$  coherent states [12] and general notion of coherent states on symmetric spaces in the sense of Perelomov [13].

At the end of our talk we briefly point out some parallel developments in the field of distributed and cooperative

control on non-Euclidean spaces that have recently been unified into a new subdiscipline named *Geometric consensus theory*, see [14–16].

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# Macroscopic dynamics in heterogeneous assemblies of excitable and oscillatory units

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## Keywords

diversity; excitable and oscillatory dynamics; collective mode; stability and bifurcation analysis; noise and coupling delay

## Summary

We consider the macroscopic regimes, as well as the scenarios for the onset and the suppression of collective oscillations in a heterogeneous population of active rotators comprised of excitable or oscillatory elements [1]. Heterogeneity in local bifurcation parameters is often encountered in neuronal and other biophysical systems, and may, depending on a particular context, alternatively be referred to as diversity, variability, impurities, or quenched noise. The setup we discuss is fundamentally distinct from the classical Kuramoto scenario [2], where the diversity is manifested only at the quantitative level, such that all the system elements are self-oscillating, but display different intrinsic frequencies. Within the Kuramoto paradigm, the crucial point is the description of the onset of collective oscillations in terms of a continuous phase transition, whereby increasing the coupling strength counteracts the disordering effect of diversity. Our study reveals two generic scenarios for the onset and the suppression of collective mode in systems with a qualitative heterogeneity between the units. After gaining a comprehensive understanding of the macroscopic regimes and the associated stability boundaries for the noiseless and the delay-free case, we demonstrate how the underlying bifurcation scenario is modified in presence of small noise or small coupling delay.

We study the noise- and the delay-free setup within the framework of Ott-Antonsen reduction method [3, 4, 5], analytically determining the macroscopic stationary states, their local structure and the respective stability domains in terms of the characteristics of the rotators' frequency distribution, namely the mean frequency and the associated distribution width. We establish that the

system may display three macroscopic regimes, namely the homogeneous stationary state, the oscillatory state and the heterogeneous stationary state. The local structure of macroscopic stationary states, analyzed by solving for the so-called local mean-field, is revealed to be governed by the relationship between the units' intrinsic frequency and the macroscopic excitability parameter.

Depending on the main features of the frequency distribution, we find five characteristic domains supporting different forms of the system's collective behavior [1]. Three of them involve monostable dynamics, whereas two of them admit bistability, manifested either as the coexistence between the two stationary solutions, or the coexistence between a stationary and a periodic solution. We find that the transitions between the characteristic domains involve a complex bifurcation structure, organized around three codimension-two bifurcation points, including a Bogdanov-Takens point, a cusp point, and a fold-homoclinic point. It is shown that the onset of the collective mode may occur via two generic scenarios, guided by a SNIPER or the Hopf bifurcation, such that the transition from the homogeneous to the heterogeneous stationary state under increasing diversity may follow the classical paradigm, with macroscopic oscillations at an intermediate stage [6], but may also be hysteretic, reflecting the existence of two bistability domains [1]. We demonstrate that the basic bifurcation structure holds qualitatively in presence of small noise or small coupling delay, having explicitly calculated the shift of the relevant bifurcation curves in the latter case. It is found that noise influences the effective positions of all the relevant bifurcations, whereas the delay makes an impact only on the Hopf bifurcation.

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# COST Actions as a wide network of researchers and innovators across Europe

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## Keywords

COST; interdisciplinarity; OECD fields; network

## Summary

The European Cooperation in Science and Technology (COST) is a funding organisation for the creation of research networks [1]. COST is an intergovernmental framework consisting at present of 38 Members and 1 Cooperating Member country. The networks projects are called Actions and approved projects are funded for four years with the average fund of 134,500 EUR per year. These networks offer an open space for collaboration among scientists across Europe (and beyond) and thereby give impetus to research advancements and innovation [1].

COST Association does not fund research itself but it funds collaboration activities (workshops, conferences, working group meetings, training schools, short-term scientific missions - STSM, and dissemination and communication activities). At present there are 1178 completed Actions, 213 running Actions and from the next month new 35 Actions will start their 4 year terms. As of 2018, approximately 45,000 researches has been involved in COST Actions. Only in that year 2,457 STSMs have been accomplished [2].

### Main OECD Fields of

Science and Technology	OC-2018-1	OC-2018-2
Natural sciences	25.8%	25.9%
Engineering and technology	22.4%	24.1%
Social sciences	20.9%	20.8%
Medical and health sciences	17.1%	16.7%
Agricultural sciences	5.4%	6.7%
Humanities	8.4%	5.8%

Different disciplines of the Actions are categorized as 6 OECD fields of science and technology:

- Natural sciences;
- Engineering and technology;
- Social sciences;

iv) Medical and health sciences;

v) Agricultural sciences; and

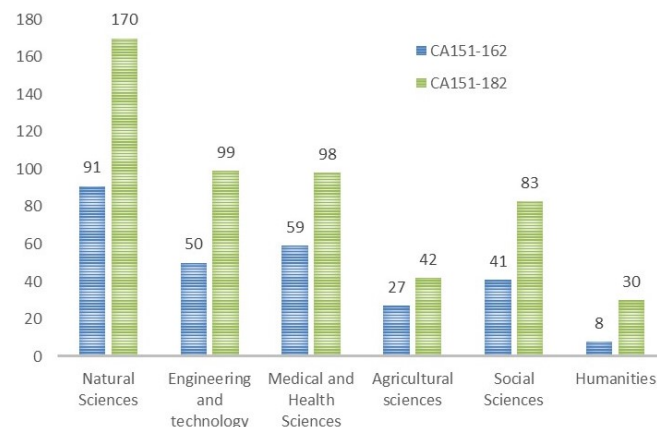
vi) Humanities.

One of the COST priorities is to foster interdisciplinary research for breakthrough science. During two calls for Action proposals approximately 50% of proposals required expertise in two or more fields. The distribution of the fields within the Open Calls 2018-1 and -2 is presented in Table 1 [3].

Involvement of Serbian researchers in COST Actions is constantly increasing so that country representation in COST Actions starting from 73% in 2014 achieved 90% in 2018. Also, leadership positions in COST Actions held by Serbian participants is steadily increasing, from 16 in 2014 to 29 in 2016 and even to 42 in 2018. Participation in network activities comprises 106 STSMs, 190 trainees and 16 trainers in 2018. The total budget received by Serbian participants hits almost 1 million euros [4].

Distribution of OECD fields among Serbian research community is presented in Figure 1. On the graph the first columns in blue represent data from the 4 open calls (2015-2016) while the second columns in green are those from all 7 open calls (2015-2018).

## SCIENCE FIELDS



\*The author is COST National Coordinator.

Many other statistical data is available for considerations, such as participation of Inclusiveness Target Countries (ITC), gender balance, number of ECI - Early Career Investigators, distributions of marks of evaluated proposals, etc. All data and knowledge accumulated within COST demonstrates the complexity of research network in Europe.

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# Predicting Trapping Set Criticality in LDPC Codes

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## Keywords

error correction; low-density parity check codes; iterative decoding; trapping sets; error-floor

## Summary

Low-density parity check (LDPC) codes are typically decoded using iterative algorithms in which messages are passed over edges of the code's Tanner graph. A message over an edge is computed based only on the messages arriving to neighboring nodes, which leads to low decoding complexity as the Tanner graph is sparse. However, due to this local nature of computing messages, iterative decoding algorithms fail to converge to a codeword when the transmitted codeword is corrupted by some low-weight error patterns even when an LDPC code has large minimum distance [1]. On the binary symmetric channel (BSC), this leads to a changed slope of the frame error rate (FER) curve at small crossover probabilities  $\alpha$  and is known as an error floor phenomenon. Despite tremendous efforts and significant theoretical results in the past two decades (see [2] for a survey), characterizing error floor phenomenon analytically or semi-analytically remains an open problem. Predicting whether a decoding algorithm operating on a given Tanner graph will fail due to a specific error pattern is crucial for designing good codes and decoders, but is theoretically supported only when decoders propagate binary messages (Gallager B decoder) and variable nodes have degree three [3, 4, 5]. On the other hand, very little is known or published for decoders of practical interest such as min-sum algorithm or finite alphabet iterative decoding (FAID) algorithms [6] and codes where variable nodes have degree-four or irregular degrees.

Experimental evidence indicates that the topology of subgraphs induced by the corrupt variable nodes, also known as *trapping sets*, greatly affect decoding failures and clearly at small  $\alpha$ s subgraphs induced by a small number of variable nodes are most harmful. The code design can exploit this fact and attempt to make a Tanner graph that is free of such small harmful subgraphs.

Avoiding larger number of harmful graphs leads to better error correction capability, but also lowers code rate. To maintain a high rate, only the most harmful subgraphs must be avoided in the code design procedure. Thus, it is of importance to classify the subgraphs based on their harmfulness to the decoding algorithm. Such classification is difficult due to a large number of subgraphs, especially in irregular LDPC codes [7, 8, 9], and due to complexity of a decoding algorithm.

As opposed to the significant effort in enumeration of trapping sets [10, 8, 9], very little is known about how a given topology affects the actual FER performance. In this talk we establish the connection between a subgraph topology and its "harmfulness" to a decoding algorithm. The topology is specified by parameters the number of variable nodes and expansion, as well as neighborhood of degree-three check nodes, and harmfulness is expressed through the critical number and strength [1].

In case of higher degree variable nodes, enumerating all possible trapping sets as combinatorial objects is computationally infeasible. Even if it was feasible, analyzing decoding errors based on an isolated trapping set would be inaccurate for strong decoders as it ignores the effect of messages from the trapping set neighborhood passed towards the trapping set. These outside messages strongly depend on the location of the trapping set in the Tanner graph, and this exact location is critical for accuracy. In this talk we discuss an approach which starts with a list of all shortest cycles together with their locations in the Tanner graph, and then finds their sufficiently large neighborhoods to ensure that the messages in the interior of such subgraph accurately represent actual messages in a decoding algorithm operating on an entire graph. Unlike previous approaches, our method does not make any a priori assumptions about what graph topologies make a trapping set harmful. On the contrary, these topologies are identified by the procedure.

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# Energy-Efficient Protograph-Based LDPC codes \*

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## Keywords

LDPC codes; protographs; energy optimization; Min-Sum decoder

## Summary

Energy consumption of electronic systems has become a major issue, both for environmental reasons and to augment the learning ability of systems with strict energy budgets. In communication systems, the standard approach consists of reducing transmission energy. However, it was shown in [1] that for short-distance communications, the energy consumption of the receiver becomes non-negligible compared to the transmission energy. In this context, this paper considers the design of Low Density Parity Check (LDPC) codes that both show energy efficiency and good decoding performance.

For this problem, [6] considers hard-decision decoders, and proposes two models to represent the energy consumption. The first model considers the decoding complexity, and the second one measures the energy needed for data transfer inside the decoder. In addition, [4] considers discrete message alphabets and evaluates the memory requirements of the decoder. To finish, [5] optimizes the code degree distribution in order to reduce the decoding complexity, but does not explicitly relate this complexity to the decoder energy consumption.

In this paper, we consider a quantized Min-Sum decoder which, due to its discrete nature, can be easily implemented on a circuit. In addition, we consider LDPC codes constructed from protographs. Protographs allow to build Quasi-cyclic LDPC codes which are also very convenient for LDPC encoder and decoder implementation [3]. We use density evolution to evaluate the decoding performance of the Min-sum decoder for a given protograph, and we apply the method of [2] to predict the finite-length performance of the decoder.

We then introduce two models to evaluate the decoder energy consumption of the quantized Min-Sum decoder for a given protograph. The first model evaluates the number of operations realized by the decoder, and the

second model measures the energy needed to write data into memory. From these two models, we propose to optimize the protograph so as to minimize the decoder energy consumption, while guaranteeing a certain performance level fixed as a criterion. As a result, we obtain two protographs that minimize the decoder energy consumption, while showing performance close to the protograph optimized without energy constraint.

To finish, we extend our approach to the case where the LDPC decoder operates under faulty hardware. We incorporate into the energy models the proportion of faults introduced inside the decoder. We then optimize both the amount of faults and the quantization level so as to minimize the decoder energy consumption.

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# Detection of random walks on generic topologies: Optimal performance characterization via convex optimization

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## Keywords

random walks; hypothesis testing; large deviations; Lyapunov exponent; convex optimization

## Summary

We study detection of hidden random walk that runs over an arbitrary graph, according to a certain transition matrix. The graph nodes are able to sense their environment over time and produce noisy measurements of the local activity that they sense. Specifically, when a graph node is visited by the walk, the measurement of that node will exhibit a positive shift in the mean value. Also, outside of the walk's path nodes measure only noise.

The above problem has many practical applications. For example, it can be used to model the activity of an intruder in a region monitored by a network of cameras, where the camera locations are the graph nodes, and nearby cameras are connected by an edge, describing the next possible steps of an intruder. In [1], the authors present the electron spin detection problem modelled as a random telegraph signal that switches between two states (a random walk on two nodes). In our previous work [2] we presented a random access communication scheme that exploits frequency hopping to combat possibly unknown frequency selective fading, where hopping over different frequencies is guided by a random walk.

There are several interesting aspects of this problem. First, although the problem clearly exhibits a combinatorial nature (likelihood functions depend on a specific path that the random walk took, and there is a combinatorial number of them), it turns out that the optimal likelihood ratio test can be represented as a simple linear recursion. In particular, the likelihood ratio at time  $t$  can be expressed as a product  $\Pi_t$  of  $t$  matrices of identical statistics, where each of the matrices decomposes as the product of the transition matrix  $P$  of the walk and a diagonal matrix  $D_t$  with measurement dependent values. This has been shown in [3] for the two node case, and in the general case in [4] and [2], where [4] studied the

setup with equal SNRs while [2] analyzed the setup with arbitrarily different SNRs across the network. Further, by the generalized Stein's lemma for ergodic processes [5], the type-I error exponent is computed as the almost sure limit of the scaled log-likelihood ratios (known also in the literature as asymptotic Kullback-Leibler divergence). Since the likelihood ratio is expressed as the product  $\Pi_t$  of i.i.d. random matrices, the latter yields a simple Monte-Carlo scheme for finding the error exponent numerically. Finally, the random walk detection problem exhibits a threshold effect: if the expected SNR of the random walk observations is higher than the entropy of the walk, the walk is detectable. The latter result was known for lattices [7], [6], and was generalized more recently for generic topologies in [4] and [2].

In contrast with the existing works that either assume symmetry in the network topology (e.g., lattice [7] and [6]) or in the nodes' observation statistics ([1], [4]), we consider the problem in full generality by studying completely generic topologies, and also where each node's mean value can be chosen arbitrarily. The latter is particularly relevant in practice, since the random walk's path may be closer to some sensing locations than to the others, and therefore the mean value at those locations should be higher. Our goal in the paper is characterization of the exponential speed of decay of the probability of a miss, for a given bound on the false alarm probability – i.e., the type-I error exponent. By the equivalence of the error exponent and the Lyapunov exponent for product  $\Pi_t$ , exact computation of the error exponent is therefore difficult. Building on the notion of Markov types by Davisson, Longo and Sgarro [8], we extend this to Gauss-Markov types that besides the empirical number of transitions from one state to another (Markov type), accounts also for the average of signal values at each of the nodes obtained from the measurements during the random walk visits at each of the node's locations. We prove that the Gauss-Markov type satisfies the large deviations principle and we use this result to find a tractable lower bound

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on the error exponent. A highly novel result in the literature is that the lower bound we obtain can be (equivalently) reformulated as a convex optimization problem. This has not been shown before, even for the symmetric topologies or identical SNRs across nodes. We evaluate the derived bound by means of numerical simulations for several classes of topologies, showing that the bound closely follows the true error exponent.

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# A Balance Model of Opinion Hyperpolarization

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## Keywords

polarization; opinion dynamics modeling; balance theory; issue constraint; backfire effect

## Summary

Political polarization is surging in many democratic countries, endangering the stability of political systems. Most political science and opinion dynamics literature focuses on polarization as *extremeness* [4]. However, there is another aspect of polarization called *issue constraint* [3], meaning the correlation between positions on different issues. Polarization, defined as the emergence of two equal sized groups with complete consensus within, and complete contradiction between them, can only emerge if there is issue positions are extreme and correlated.

So far, no opinion dynamics model can satisfactorily explain the emergence of both extremeness and constraint. We develop an opinion dynamics model based on an extended form of cognitive balance theory [5, 2], which we call *weighted balance theory* (WBT). We apply this theory to triads consisting of two individuals,  $i$  and  $j$ , and one or several policy issues  $d_1, \dots, d_D$  (such as gay marriage, cannabis legalization, carbon tax etc.). Classical balance theory postulates that such a triad is balanced either if  $i$  and  $j$  agree on  $d$  and like each other, or if they disagree on  $d_1, \dots, d_D$  and dislike each other. WBT takes into account the weight of the attitudes of  $i$  and  $j$  towards  $d_1, \dots, d_D$  and towards each other.

WBT predicts i) the attitude of  $i$  towards  $j$  based on the attitudes of both  $i$  and  $j$  towards  $d_1, \dots, d_D$ , and ii), how  $i$  will adapt its attitudes towards  $d_1, \dots, d_D$ , based on its

attitude to  $j$ . We test the first prediction on empirical data from the 2016 American National Election survey, and find that it can be confirmed, but that respondents tend to be more extreme in their interpersonal attitudes than predicted by WBT - a property we call 'evaluative extremeness'.

We design an opinion dynamics model based on WBT, where agents adapt their opinions to increase balance with other agents. We find that our model is able to generate both opinion extremeness and issue constraint, even for high numbers of opinion dimensions  $D$ . Furthermore, we find that our model can shed new light on two other enigmatic phenomena in opinion research, group mono-polarization and the backfire effect [1].

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# Market fragmentation and market consolidation as emergent properties in systems of adaptive traders and double auction markets

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## Keywords

collective behaviour; econophysics; agent-based modelling; fragmentation vs consolidation

## Summary

Technological progress is leading to proliferation and diversification of trading venues, thus increasing the relevance of the long-standing question of market fragmentation versus consolidation and its potential advantages and disadvantages. In a consolidated or concentrated market, the majority of trades occurs in one (or a few) as opposed to numerous trading venues and it is our goal to investigate whether these different states can emerge spontaneously. We address this issue by devising a stylised model, we analyse systems of adaptive traders that choose where to trade based on their previous experience. We find that when the typical scale of market returns (or, at fixed scale of returns, the intensity of choice) become higher than some threshold, the preferred state of the system is fragmented: both buyers and sellers are divided into subgroups that are persistently loyal to one market over another. We demonstrate that only based on aggregate parameters about trading venues, such as the demand to supply ratio, we can assess whether a population of traders will prefer fragmentation or specialization towards a single venue.

We investigate what conditions lead to market fragmentation for populations with a long memory and analyse

the stability and other properties of both fragmented and consolidated steady states.

We find a rich variety of steady states in spite of the simplified nature of our models for markets and traders. These include: market coexistence - where both markets attract all types of traders present in the population, and where market/trader specialisation occurred; single market dominance; market indifference; general vs. specialised markets, where a single market attracts all groups of agents while the other can be viewed as specializing towards only one group. Interestingly, all these different steady states arise without imposing any heterogeneity onto the agents and fragmentation is the preferred state even when the markets have identical properties.

Finally we investigate the dynamics of populations with finite memory; when this memory is long the true long-time steady states are consolidated but fragmented states are strongly metastable, dominating the behaviour out to long times.

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# Energy-Efficient Machine Learning Algorithms \*

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## Keywords

Machine Learning; Faulty Hardware; Energy optimization; Binary Recursive Estimation

## Summary

Machine Learning algorithms are known to be highly energy consuming due to the large amount of data and computation operations required by these algorithms. It is of high importance to lower this energy consumption in order to reduce the environmental impact and also to improve the learning performance under limited computational resources.

When designing electronic systems, a standard technique to reduce the energy consumption consists of aggressively downscaling the voltage supply. However, due to physical limitations, further reducing the power supply of next generations of electronic devices will make computational units unreliable, which may introduce faults in the computation operations realized on these chips [3]. On the other hand, tolerating faults in the computation operations gives us the opportunity to address a tradeoff between algorithm performance and energy consumption. This is the issue we consider in this talk.

The first part of this talk reviews existing works on fault-tolerant computation and learning. Linear computation requires to (almost) retrieve the exact value of the function output, and fault-tolerant linear computation was studied in [5, 6, 10, 15]. In addition, many machine learning problems have been considered recently under faulty hardware. For instance, noisy hypothesis testing and noisy parameter estimation were considered in [1], logistic regression was studied in [14], and neural networks were described in [12]. In the field of error-correction, noisy Low Density Parity Check (LDPC) decoders have also been widely investigated in [4, 7, 8, 13]. Unlike linear computation, the above problems are naturally robust to errors introduced by the hardware. But the above works mainly focus on fault-tolerance, and do not make the con-

nection with energy consumption.

In a second part of this talk, we consider the problem of recursive binary estimation under faulty hardware. Recursive binary estimation [2, 9] consists of estimating a sequence of statistically dependent hidden states from their noisy observations. It is considered in many applications such as target tracking, speech, or image processing, see [11] for a review. To the best of our knowledge, the problem of noisy recursive binary estimation was not studied yet in the literature.

We first focus on studying the robustness to faults of recursive binary estimation. We propose a theoretical analysis that bounds the expected gap between the noisy recursion and the noiseless one. We prove that this gap converges to a fixed point, which shows the robustness of the recursive binary estimation. Finite-length simulations show the accuracy of the proposed analysis. Then, we derive a model that relates the amount of faults in the computation to the energy required to performed the computation. We consider two energy allocation strategies. In a first case, we assume that energy allocation can vary from time to time, while in the second case, we assume that energy allocation can vary from bit to bit. In the two cases, we exhibit optimal energy allocation strategy in order to maximize the performance of the recursion under energy constraints.

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# Using deep neural networks for internal banking fraud detection

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## Keywords

cyberattacks, system log, anomaly detection, deep neural networks, banking security

## Summary

According to The Global Banking and Finance Review cyberattacks have cost near \$360 billion per year [1] and cases involving bank insiders account for about 70 percent of that total [2]. Artificial intelligence is recognized as being a most powerful weapon for both sides – hackers and authorities. Anomaly detection technique is more common solution for fraud detection than predictive and prescriptive analytics as it can process a huge amount of continuous stream of unlabeled data and notify deviations from a normal behavior. Deep Neural Networks (DNN) based anomaly detection has received increasing attention in recent work [3]. Logs, which record system runtime information, are widely used for anomaly detection [4]. Long-Short Term Memory Networks (LSTMs) that model a system log as a natural language sequence, have a great potential to automatically learn log patterns from normal execution. In this paper [5] they automatically detect anomalies when log patterns deviate from the model trained from log data under normal execution system.

Research [5] has tended to focus on detecting process deviation from normal execution by predicting what will happen next. By adding two additional softmax groups of neurons in the last layer of LSTM network to predict the user account and workstation in the next log, we extended the approach to detect five types of anomalies:

- User logged on to a workstation that he never used before
- User is using a software (creates a process) that has never been used by that user
- Workstation has a process started that have never been used before on that workstation
- User is creating a process on a workstation that has

never been used on that workstation by that user

- Abnormal child process created (parent process started a child process that it has never started before)

Model was trained on System monitor (Sysmon) logs from the internal banking system to simultaneously predict what will happen next, who will do that and on which machine. The outputs of the neural network are probability distributions over all possible values for each of the above elements. Output probabilities are sorted in descending order to give an alert if an event has occurred that is ranked below the given threshold that is tuned on a validation dataset.

For a given test set, that was built by experts in cybersecurity in banks, proposed system detected all attacks. This test revealed that recurrent neural networks can be used for detecting various types of frauds in internal banking system. We hope that further tests that should be performed, including deploying model in banking system and testing on real-time data, will be successful as well.

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# Machine vs Rule-based Learning in Physics: Possibilities and Advantages

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## Keywords

machine learning; expert system; python; databases

## Summary

Machine learning (ML) is understood to be one of artificial intelligence (AI) fields [1]. Broadly speaking, AI distinguishes rule-based and machine learning techniques. A computer system that achieves AI through a rule-based technique is called rule-based system (expert system as one), while that achieves AI through a machine learning technique is called a learning system. It can be found a hybrid approach which combines both techniques [2]. The general goal of ML is to recognize statistically significant patterns in the available data. ML is widely used in computer science as one continuously developing field with numerous applications [3].

Beside of improvements on some “commercial” technologies such as image recognition, as well as industrial application, ML is becoming very important for many research areas in physics such as the computational study of condensed matter or atomic/molecular/optical physics, quantum information, forecasting meteorological parameters [4], for astronomical data streams [5], etc. New concepts of database set-ups and distributed approach to data entries is prevailing [6] and the number of data nodes is constantly increasing [7], even more traditional and old databases like NIFS [8] are becoming a part of such large networks.

Rule-based learning uses a series of IF-THEN statements to reach conclusions. The whole process is based on expert knowledge and experiences (facts). That is why rule-based system is called expert system. An expert system (ES) referred to as knowledge-based system is computer software that emulates the decision-making ability of a human expert [9].

ML uses experience implemented in algorithms [3] which enable the pattern recognition, i.e. concerning with the automatic recognition of regularities in observed data and classifying them into different categories. Based on that, ML can transform row (experimental) data into structured though the learning algorithms [10].

The comparison between rule-based and ML approach can be found in the many different areas [11, 12]. One very illustrative example which explains difference between these two techniques, and at the same time shows limitations of the rule-based, and advantages of ML technique can be found in [12]. In situation when confronted with an unknown sample, researches perform mass spectrometry and compare the observed spectrum with those at a library. Identification can be done in the case of positive match. This is the same principle how rule-based system works. It can deal only with data in database, otherwise it is useless. This is the major limitation of these systems. On the other hand, ML can, based on existing, predict synthetic spectra which can be used in mass spectrometry to expand the coverage of molecular spectra which can be identified. In many papers this improvement of the classification “skills” is pointed as the main advantage of ML technique. Within the fast process’s physics (with which we deal), ML classification technique as referred to as multivariate analysis in order to emphasize contrast to traditionally used approaches [13]. According to [11], a determination of a peak (event) quality can be expected as well.

For both techniques quality and quantity of obtained results is significantly better than classical experimental result analysis, and the process is considerably faster. The abstract is going to review our previous researches on ES methods in the different fields of collisional atomic and molecular physics. We started with analysis of the atomic

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and molecular threshold spectra [14, 15, 16]. Based on some criteria (theoretical and empirical), we developed methodology for classification different physical events, presented by peaks. Moreover, for twoatomic molecules spectra we developed procedures for spectra generation which enable us to analyze spectra in the area where because of big peak density and peak's overlapping, classical methodology, based on subjective estimation of a person that performs an experiment, fails and leads to wrong interpretation of experimental results [14, 15, 16]. We showed that using ES improve the quality and quantity of obtained results and conclusions, remove the inevitable noise influence and measurement errors on experimental data and significantly speed up the process of spectra analysis regarding on the classical approach. Later, we extended our researches on the atomic photoionization process [9] where, for linearly polarized laser field, we observed the influence of the different effects such as ponderomotive and Stark shift, as well as the laser beam shape on the tunneling transition rate for alkali and noble atoms. All mentioned we considered for three theories, Keldysh, PPT and ADK [17, 18, 19]. But, in spite of all improvements in the process of analysis, caused by using ES methodology, we noticed some limitations basically related to ES impossibility to predict any situation and behavior out of those already involving in ES, i.e. database.

The purpose of this abstract is to open (point) new possibilities of ML which could improve results obtained by using ES method in fields of interest. According to [13, 20] ML enables accurate predictions which are not available in the input data.

On the end, authors expect significant increase of using ML algorithms in many areas of physics, especially in those with a big data analysis [21].

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# Applications of Machine Learning in Gravitational-wave Astrophysics

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## Keywords

gravitational waves; data analysis; machine learning; parameter estimation; denoising

## Summary

Gravitational-wave detections [1, 2] by means of state-of-the-art interferometers - LIGO, Virgo and now also KAGRA - create a new way of studying the Cosmos [3]. However, the astrophysical signals are weak and buried in the detectors' noise [4]: the sensitivity is generally limited by the presence of transient, non-Gaussian noise artifacts as well as stationary disturbances. In this talk I will describe the problems that have to be faced while facilitating routine detections and parameter estimation of interesting signal types, as well as opportunities, as most of these tasks may be alleviated with various machine learning techniques (as the growing list of publications show [6]).

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# Bayesian Consensus Clustering in Networks

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## Keywords

exchangeable random structures, Bruno de Finetti, Bayesian consensus, stochastic blockmodels, multiplex networks

## Summary

The close relationship between exchangeable sequences of random variables and Bruno de Finetti's development of predictive inference and Bayesian statistics will be reviewed [1–3]. Exponential random graph models and exchangeable random graphs [4] will be discussed. By combining models from statistics and sociology, stochastic block models, with tools from computer science and machine learning, consensus and Bayesian consensus clustering, the Bayesian consensus stochastic block model for multiplex networks [5] will be suggested.

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# Topological analysis of complex datasets: toward exhaustive reconstruction of relationships

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## Keywords

simplicial complex; data analysis; algebraic topology; complex systems; filtration stages

## Summary

Complex datasets are generated at an extraordinary rate by academia, industry and general public, and tackling problems emerging from big amounts of data impose the need for new scalable methods to analyze and classify these data automatically. The huge amount and complex structure of datasets challenge the capability of traditional data analytics techniques, hence it is necessary to provide well-founded mathematical, statistical and algorithmic methods to exploit structures in data. The common sources of these large amounts of datasets are complex systems, therefore the reconstruction of relationships within the dataset is of certain importance for the reconstruction of complex systems' behavior. Recently, the research in applications of algebraic topological methods put forward an alternative to usual statistical methods, and established a fast emerging framework of Topological data analysis [2]. The core idea of Topological data analysis is to find the shape of data [1], and extract useful relationships inherent in complex dataset. Simplices, and their aggregations into simplicial complexes [4], are the main mathematical objects for representing relations of the elements of datasets, whereas the methods of Topological data analysis are based on the so called persistent homology [2]. It comprises computation of Betti numbers as the ranks of homology groups of simplicial complex, that is groups generated by the non-bounding cycles of simplices, which build higher-dimensional holes. Generally, introducing, and changing, a free parameter related to dataset, gives rise of a sequence of simplicial complexes, called filtrations, which is further followed by the change of existence of the non-bounding cycles. The homology group gen-

erators which stay unchanged for a wide range of free parameter values are persistent.

Nevertheless, focusing only on the non-bounding cycles of simplices, the other structures built by simplices, and accordingly elements of complex datasets which they represent, may remain overlooked. These structures represent connected chains of same-dimensional simplices, which are not non-bounding cycles. Finding non-bounding cycles of simplices, as well as equivalence classes of connected chains of  $k$ -dimensional simplices, partitions the  $k$ -dimensional chain group into  $k$ -dimensional subgroups. We propose a method for getting more complete picture of the shape of data by focusing on these chains as well, via the calculation of eigenvalue spectra of higher-order combinatorial Laplacian [3, 5], and tracking changes of the non-zero eigenvalues when free parameter is changed. It turns out that this approach represents an extension of common Topological data analysis methods, since the multiplicity of zero eigenvalues is equal to the rank of homology group, that is the Betti number.

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# Optimal deployment of 5G network slicing based on complex network theory

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## Keywords

network slicing; mapping algorithms; topology information; deployment policies

## Summary

5G is the new generation of reference architecture for the global mobile and fixed telecommunication network. It is an evolution of previous generations in terms of performance as well as support diversified vertical services, targeting different types of users. 5G constitutes a larger ecosystem, with more complex relationships, more heterogeneity and more dynamicity, so an optimization process is inevitable. For details and implementation, overview papers, keynote speeches, special issues and the latest books are presented through our references [1, 2, 3]. Three classes of innovative 5G service scenarios are defined:

- eMBB (enhanced mobile broadband) services characterized by very high data rates and very high density of users, for instance virtual reality and augmented reality, requiring extremely high quality mobile video distribution, and, in general, support of the expected increases in video consumption.
- mMTC (massive machine type communications) services characterized by very high data rates and very high density of users, for instance virtual reality and augmented reality, requiring extremely high quality mobile video distribution, and, in general, support of the expected increases in video consumption.
- uRLLC (ultra-reliable and low latency communications) services related to scenarios with demanding requirements in terms of latency and reliability, such as smart factories, smart grid, intelligent transportation systems, automated driving.

For 5G communication systems, network slicing has emerged as a key concept to meet the diverse requirements of three typical service scenarios. How to fast deploy the end-to-end slices based on policies is the main issue in a multi-domain network infrastructure [4]. To efficiently utilize the limited physical resources, a service-oriented deployment is proposed by offering different

deployment policies for typical slices (eMBB, mMTC, uRLLC). Complex network (CN) theory is proposed to obtain the topological information of slices and infrastructure network [5, 6].

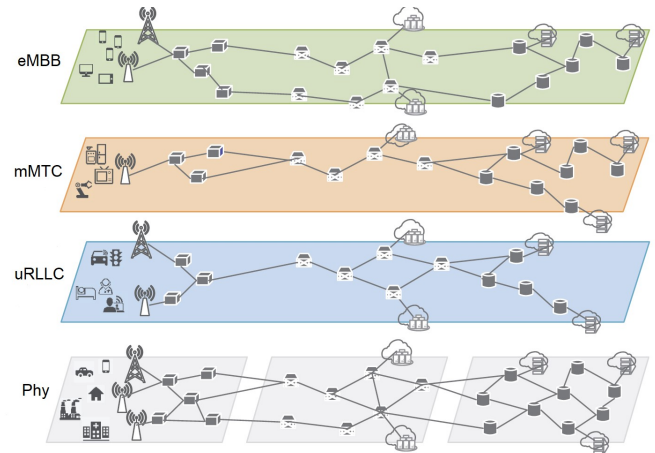


Figure 1: An example of mapping three typical network slices on 5G physical infrastructure.

The network slicing (NS) problem is combined optimization problem of placing 5G network functions over a set of candidate locations and deciding their interconnections (Fig. 1). Network slices are the chains of virtualized network functions (VNF). Researches focus is on service description, resource virtualization, and service mapping. We have presented NS model that allows telecom operators to define slice requests and map them to the limited network resources to suit a particular 5G use case [4]. The main challenge is fast end-to-end deployment based on policies for typical slices [5]. The objectives of typical slices are to efficiently take advantage of network resources. Usage of eMBB in high user density area requires very high traffic capacity, low mobility and higher user data rate. Usage of mMTC covers a huge number of connected devices which transmit relatively low volume of non-delay sensitive data. Usage of uRLLC has strict requirements in throughput, latency and availability. The collected network slice requests are possible to classify and implement by different mapping algorithms for VNF placement and the selection of link paths. The network slice request could be deployed as

static (permanent) or dynamic (recycled).

**Topological information.** Complex network (CN) theory is proposed to obtain the topological information of slices and infrastructure network [6]. A node importance metric is defined to rank the nodes in node mapping. Topological properties of degree and betweenness centrality of nodes are proposed to capture structural characteristics of infrastructure network. The degree of a node measures the number of edges that connect to it, which reflects the level of influence.

$$d_i = \sum_{j \in N} \delta_{ij} \quad (1)$$

The parameter  $\delta_{ij}$  takes the value 1 if node  $i$  and node  $j$  are directly connected, otherwise it takes the value 0. *Betweenness centrality* quantifies the number of times a node acts as a bridge along the shortest path between two other nodes. It is defined as the fraction of shortest paths between any pair of nodes that travel through the node

$$b_i = \sum_{s \neq i} \frac{\sigma_{st}(i)}{\sigma_{st}} \quad (2)$$

In this equation,  $\sigma_{st}$  is the total number of shortest paths from node  $s$  to node  $t$  and  $\sigma_{st}(i)$  is the number of those paths that pass through node  $i$ .

**Mathematical model.** In order to describe end-to-end network slice deployment, infrastructure network model, network slice request (NSR) model and slice deployment model are proposed. Topological information of infrastructure network include the structural characteristics of physical nodes (base stations - BS, optical switches - OS, core nodes - CN). The infrastructure network can be abstracted as undirected weighted graph  $G_I = (N_I, E_I, C_I, B_I)$  of set of physical nodes, physical links, capacity of physical nodes, bandwidth set of physical links, respectively. We only take into consideration the capacity of nodes and bandwidth of links.

**Deployment policies.** By analyzing different features of three use cases, three service-oriented deployment algorithms and three optimization objectives are used for eMBB slice, mMTC slice and uRLLC slice accordingly [5]. The objective are take advantage of network infrastructure resources efficiently.

- eMBB usage in hotspots area with high user density, requires very high traffic capacity, while the requirement for mobility is low and user data rate is higher. This kind of slice does not require strict delay and plentiful resources. Hence, the deployment objective of eMBB slices should be maximizing the remaining resources of physical nodes:

$$\max \left[ \sum_{n_I \in N_I} C_I(n_I) - \sum_{n_R \in N_R} C_R(n_R) \cdot \mu_{n_R, n_I} \right] \quad (3)$$

- uRLLC usage scenario has stringent requirements for throughput, latency and availability. The QoS guarantee of this use case is low latency, which causes that the deployment objective should be minimizing the delay of slices. The transfer delay time is expressed in the number of network hops, so minimizing the delay means minimizing each physical path length. Hence, deployment objective of uRLLC slices should be minimizing physical path length of network segments:

$$\max \left[ \sum_{e_I \in E_I} B_I(e_I) - \sum_{e_R \in E_R} B_R(e_R) \cdot \nu_{e_R, e_I} \right] \quad (4)$$

- mMTC usage scenario has plenty of connections, which results in the requirement of high computing resources and low congestion rate. Therefore, the deployment objective of mMTC slices should be maximizing the remaining bandwidth on physical links:

$$\min \sum_{e_R^{wl} \in E_R^{wl}} \nu_{e_R^{wl}, e_I^{wl}} + \sum_{e_R^{ol} \in E_R^{ol}} \nu_{e_R^{ol}, e_I^{ol}} \quad (5)$$

**Mapping algorithms.** After the arriving of *network slice request* (NSR), these requests are classified, than implemented by different mapping algorithms [5]. The mapping process of network slice requests to the 5G infrastructure network (Fig. 1) consists of placement virtual network functions and selection link paths chaining them:

1. placing VNFs means to select the physical nodes of substrate network as host for the virtual nodes of NSRs under the condition of satisfying the capacity requirements;
- 2 procedure of creating paths that interconnect the VNFs placed nodes would be achieved on the basis of k-shortest paths (KSP) algorithm.

Also, the *resource efficiency* (RE) and *acceptance ratio* (AR) of network slices request are calculated. Resource efficiency is defined as the revenues and cost ratio. Acceptance ratio is the ratio of the number of NSRs which have been successfully mapped and the total number. Extensive simulations will be conducted to validate the performance of proposed algorithm and analyze the average execution time.

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# Hierarchical Structure of the Genetic Code

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## Keywords

origin of life; code degeneracy pattern;  $p$ -adic modelling; nucleon numbers; scale invariance

## Summary

Complexity is an important prominent feature that has raised the biotic from the abiotic nature. Scientific efforts to obtain the "minimal" cells by removing as much complexity as possible resulted in the simple organisms by biological standards, but still extremely complex by chemical ones [1]. This complexity is reflected in the fact that living systems, even in their minimal form, are ordered in numerous different ways at many scales, either in terms of composition, spatial configuration, or dynamics. Life's innovative solution for the emergence, maintenance and evolution of its complexity has given through information flow from storage to functional molecules (inside an individual organism), as well as through information inheritance from ancestor to offspring (between the organisms).

The main flow of genetic information within the biological systems is based on the three sequence-defined biopolymers, nucleic acids DNA/RNA and polypeptides, through the three information processing systems, replication (DNA→DNA), transcription (DNA→RNA) and translation (RNA→polypeptides). Protein synthesis during the translation process is an essential and central biological process in a living cell and, at the same time, the final and most complex step of the genetic information flow. However, microbial phylogenetic studies have revealed that the *translation* process was highly developed in the last universal common ancestor (LUCA) at the root of the universal phylogenetic tree, even in comparison to the simpler process of transcription, while a modern type of genome replication mechanism still did not exist at that level [13]. The fact that the translation apparatus was the most mature information processing system at the root of the universal tree makes it one of the main framework for understanding the origin of life.

The simplest abstract description of the complex translation process is given by the *genetic code* as a map of the set of 64 *codons* (the ribonucleobase triplets,

$b_1b_2b_3$ ,  $b_i = \{C, G, U, A\}$ , where  $C$ ,  $G$ ,  $U$ , and  $A$  are respectively the ribonucleobases cytosine, guanine, uracil, and adenine) onto the set of 20 *amino acids* and translation termination *release factors*. This strong surjective property of the mapping implies that the genetic code is a highly degenerate (redundant) code. The degeneracy pattern is regular in the *general* form of 4-fold degenerate codon half (denoted as the set  $4^*$ ), determined only by the doublets  $b_1b_2$ , and 2-fold degenerate codon half (the set  $2^*$ ), determined by additional discrimination of pyrimidines  $Y = \{C, U\}$  from purines  $R = \{G, A\}$  at  $b_3$  [11]. The transformation  $4^* \leftrightarrow 2^*$  is obtained by double transposition  $C \leftrightarrow A$  and  $G \leftrightarrow U$  known as *Rumer's transformation*  $CGUA \leftrightarrow AUGC$  [11], which means that  $4^* \leftrightarrow 2^*$  is  $M/K$  invariant since the amino bases are  $M = \{C, A\}$  and the keto  $K = \{G, U\}$ . Moreover, using notation for the strong bases  $S = \{C, G\}$  and the weak bases  $W = \{U, A\}$ , the two degeneracy codon classes can be given in a compact way  $4^* = \{SS, SU, WC\}$  and  $2^* = \{WW, WG, SA\}$ , showing the prevailing of strong bases in the  $4^*$  codon half and the weak in the  $2^*$  codon half. Such  $M/K$  invariant and  $S/W$  regular bipartition of codon space in 32 codons as 8 *four*codon families and 32 codons as 16 *two*codon subfamilies can be regarded as the most significant signature of the hierarchical structure of the genetic code [7, 2]. According to the long-standing hypothesis, the code degeneracy is related to the noise immunity of genetic information, in particular error-detection and error-correction.

The genetic code is almost universal across all life forms, and this universality is attributed exclusively to the standard genetic code (SGC), which is implicitly assumed to have been carried by LUCA [6]. The SGC has only two single exceptions to the general degeneracy pattern where the codon families in  $2^*$  are not divided as  $2+2$  codon subfamilies but as  $3+1$  and  $2+1+1$ , which is why the set  $2^*$  is more generally defined as the non-4-fold degenerate codon half (the set  $\bar{4}^*$ ). However, the "ideal" degeneracy pattern is found in some nonstandard genetic codes, which emerged by minor variations of SGC in the post-LUCA epoch. One such is the *vertebrate* mitochondrial code (VMC), which is the most symmetrical (e.g.,

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satisfies  $4^* \equiv 2^*$ ) and, therefore, it is occasionally hypothesized that the VMC-like codes were characteristic for the pre-LUCA or early LUCA epoch.

One of the approaches to understand the genetic code is an *ultrametrics* which enables the description and analysis of information with a complex, discrete, and hierarchical structure by defining informational order and similarity. An ultrametric distance is the main description tool, defined as the distance that satisfies the strong triangle inequality  $d(x, y) \leq \max\{d(x, z), d(z, y)\}, \forall z$ , while a metric space endowed with such a distance is an ultrametric space. The most elaborated and informative ultrametric spaces are with the  $p$ -adic distances  $d_p(x, y) = |x - y|_p$ , where  $p$  is a prime number and  $|x|_p = p^{-k}$  is the  $p$ -adic norm of a non-zero number  $x$ , defined as the highest  $p^k$  dividing  $x$ , while  $|0|_p := 0$ .  $p$ -Adic modeling of the genetic code and genome [3] is given by introducing the  $p$ -adic codon space  $C_p$  and  $p$ -adic amino acid space  $A_p$  as subsets of the set  $\mathbb{Z}$  of usual integer numbers where the measure of codon-codon similarity and codon-amino acid assignment closeness expressed as the distance between the corresponding  $p$ -adic integers. For the 5-adic model, the degeneracy pattern or Rumer's  $4^*/4^*$  (or  $4^*/2^*$ ) division of codon space can be described by specifying the 4-fold degenerate codons by the smallest 5-adic distance  $\frac{1}{5^2}$ , while the 2-fold degenerate codons by both  $\frac{1}{5^2}$  of 5-adic distance and  $\frac{1}{2}$  of 2-adic distance [3, 4, 5]. All properties of  $p$ -adic numbers cannot be represented in Euclidean space whose geometry is based on the usual absolute value.  $p$ -Adic numbers express a scale-invariant (self-similar) structure as a consequence of the power-law behavior of  $p$ -adic distances, so they are often illustrated as a tree, dendrogram, or fractal. By using 1-, 2-, or 3-component *digit* vectors, it is possible to represent a  $p$ -adic distance by the usual Euclidean distance and a  $p$ -adic set as a linear, planar, or spatial model (e.g., Sierpinski-like tetrahedron) [10]. Therefore, the Euclidean representations that are naturally derived from the 5-adic genetic code model [9, 5] may coincide with some other genetic code models although they were not originally defined by the  $p$ -adic approach.

Another remarkable feature of the degeneracy pattern of SGC is the regular distribution of nucleon numbers, both at the amino acid and nucleobase levels, predominantly in the form of the multiplies of decimal number 37 [12]. Among the numerous arithmetical regularities [12], Rumer's  $4^*/4^*$  division *most consistently reflects the 37 divisibility* compared to other divisions of SGC, while SGC compared to nonstandard genetic codes [9]. Such an uncommon phenomenon primarily indicates the need to demarcate whether these regularities are the accidental occurrences or the results of a globally acting ordering process inherent to some multiscale phenomena. Supporting evidence for some multiscale phenomena follows from the relation of the number 37 to the golden mean  $\Phi$  and its multiplicative inversion  $\psi$ . Simple modification of  $\Phi, \phi$ -polynomials gives the irrationals,

$\Psi$  and  $\psi$ , which integrate the self-similarity and the scaling by powers of 10, i.e.,  $\Psi\psi = 10$  and  $\Psi - \psi = 1$ , where  $\Psi^2\psi = 10\Psi = 37.015\dots \approx 37$ . Values  $\Psi$  and  $\psi$  also satisfy two basic relations:

- (i)  $[10\Psi] + [10\psi] = 37 + 27 = 64 = [10(\Psi + \psi)]$  and
- (ii)  $[10\Psi^2] - [10\psi^2] = 137 - 73 = 64 = [10(\Psi^2 - \psi^2)]$ ,

where the function  $[\cdot]$  rounds to the nearest integer [8, 9]. This approach revealed that a nucleon number distribution in SGC is as follows: (a) Rumer's division exactly satisfies the relation (ii), (b) so-called Gamow's division closely satisfies the relation (i), and (c) the average nucleon numbers are very close to  $10\Psi^2 \approx 137$  for the total amino acid set,  $100\Psi \approx 370$  for the total DNA codon set and consequently  $10(\Psi^2 + 10\Psi) = 10\Psi^3 \approx 507$  for both sets (valid only for the reduced codon spaces of SGC by 3 termination codons) [9].

All of these approaches can contribute to a better understanding of the universal properties of life and the underlying physics that governed and shaped life, what is the necessary condition for modeling the origins of life.

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# Gardner approach for threshold linear units to understand memory in the brain

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## Keywords

neural networks; storage capacity; Gardner approach; memory

## Summary

The creation of new memories and the possibility to consciously retrieve them is a complex feature occurring within networks in the brain.

From a theoretical point of view, memories can be regarded as attractor states: network dynamics lead to one or another attractive configuration of activity, depending on the initial condition, i.e. one or another memory is retrieved depending on the initial cue given by the external agent, e.g. a sensory percept, or another memory [1]. The attractors (i.e., the memories) are stored in the connections between the units, in neuronal terms they are stored in the synaptic strengths.

A real neuron gets activated and elicits a spike when the sum of the inputs it receives from other neurons outdo a threshold, when a neuron spikes it provides inputs to all neurons connected to it, each weighted by a specific synaptic strength.

In a model, the ability of a network to store memories depends on the states each unit can take as well as on the way different attractors are learned, i.e. the way the connectivity matrix of the 'synaptic' weights is organized. The Hopfield model has been influential in explaining how a network of binary units can store un-correlated memories and retrieve them separately [2]. The storage capacity of the Hopfield network was derived for two learning strategies in [3] and [4]. Amit, Gutfreund and Sompolinsky assumed a Hebbian rule to learn the connections, Elisabeth Gardner assumed optimality in the connectivity matrix. Hebbian associative learning is a key neuroscience paradigmatic that has led to a simple for-

mula, or 'learning rule' to specify the weights of a neural network that has stored memories.

In [5] Treves introduced threshold-linear units and derived the storage capacity when they are arranged in a Hopfield network connected by Hebbian weights. Threshold-linear units describe a more realistic behavior of neuronal responses as compared to binary units.

We took up again the Gardner approach and applied it to Hopfield networks with threshold-linear units, we derived the maximal storage capacity for uncorrelated attractors and its dependence on the activity level [6].

Recent experimental results with spatial memory tasks have shown correlated attractor states, which challenge the applicability of a simple Hebbian learning rule. Further extensions of our calculations in the case of correlated attractors will enable an approach to understand these new results.

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# Complexity of Creating Art

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## Keywords

complexity; brain; disease; creativity, neuroaesthetics

## Summary

Since the early ages art has been involved with rituals of healing and different kinds of interacting with nature or divine forces. Today, music in particular is a discipline which can be applied in different fields such as education, social services as well as medicine and psychotherapy [1, 12]. Music is recognized as a powerful way for giving support and fostering recovery from complications in patients suffering from a wide variety of neurologic diseases [2]. But, not only neurologic diseases have been treated with music therapy.

Some evidence for music therapy shows that it can improve medical outcomes and quality of life in different ways. Some of them are: improving invasive procedures, restoring lost speech, reducing side effects of cancer therapy, pain relief, improving the quality of life for dementia patients. In fact, there are more studies which show that music therapy can help to recall memories and assist communication, or even can be used as a diagnostic assessment tool [3]. Some interesting case studies might indicate that some kind of changes in behaviour can be treated as indicators for some kind of disease but also put a light on the emergence of different kinds of creativity [4].

For example, there was the case of cell biologist Anne Adams who started to paint in her middle age. At some point, she became obsessed with Maurice Ravel's "Bolero". This famous repetitive composition inspired her to put an elaborate visual rendition of the song to canvas. But, when Anne Adams completed Unravelling Bolero, her brain was starting to be affected by neurodegenerative disease called primary progressive aphasia. She was diagnosed and referred to Dr. Bruce Miller, who has shown that some patients with progressive aphasia develop a passion for creating art.

A group of neurologists led by Dr. Miller and William Seeley claim that their scientific search suggests that structural and functional enhancements in non-dominant posterior neocortex may give rise to specific forms of visual creativity that can be liberated by dominant frontal cortex injury. Miller suggests that these areas may have sprouted new neural connections in Anne's brain as her

language centers began to deteriorate [4].

Surprisingly, Ravel also suffered from a brain disease with identical symptoms. He composed "Bolero" when he began to show signs of his illness with spelling errors in musical scores and letters [5].

Dr. Miller claims that Anne's figures are arranged in an orderly manner like the music, countered by a zigzag winding scheme. The transformation of sound to visual form is clear and structured. We can conclude that creativity is a complex process, even if the precise mechanisms are still unknown. These precise mechanisms should include the way our brain perceives and interprets the signals in terms of self-organization and complexity [6, 10, 11]. This makes an interesting case for neuroaesthetics, which includes the examination of information-processing models in neural architecture and its relation with emotional and cognitive processes [7]. Using neuroimaging techniques allows documentation of which brain areas are active in creating and perceiving art [8]. These plastic brain changes are correlated with the signal processing model of aesthetic perception indicating capability of its computational foundation [9]. Neuroaesthetics, therefore, has an impact not only to education, psychology of art and creativity but to science and therapeutic practices as well.

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