The 2nd Conference on

Arithmetic Methods in Mathematical Physics and Biology

August 05-11, 2018 Będlewo, Poland

PLENARY SPEAKERS

Rasha Abu-Eid
Michał Banaszak
Maciej Grześkowiak
Tadeusz Lulek
Jan Milewski
Valery Romanovski

Helmut Ahammer
Dorota Blinkiewicz
Herbert Jelinek
Mirosław Łabuz
Nebojsa Milosevic
Andrij Rovenchak
Przemysław Waliszewski

Grzegorz Banaszak
Andreas Dominik
Piotr Krasoń
Preda Mihailescu
Tomasz Pawłowski
Mihai Tanase

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Arithmetic Methods
in Mathematical Physics and Biology

Book of abstracts

August 5-11, 2018

Contents

Abstracts

The Morphology and Immunology of Head and Neck Cancer

Thursday
August 9
14:30 -
15:30

Rasha Abu-Eid

Institute of Dentistry
School of Medicine, Medical Sciences & Nutrition
University of Aberdeen, Foresterhill Campus
Cornhill Road, Foresterhill,
Aberdeen AB25 2ZR, Scotland, United Kingdom

The incidence of head and neck cancer (HNC) is on the rise. Changes in risk factors such as alcohol and tobacco consumption in addition to human papilloma virus (HPV) infection are thought to be responsible for this increase.

Despite advances in HNC treatment, the mortality rate is still high, which is mainly attributed to late diagnosis.

Oral potentially malignant disorders (OPMD) are a group of conditions associated with a higher risk of malignant transformation. The classification of these lesions is problematic leading to difficulties in predicting malignant transformation.

Therefore, early detection of malignancies is essential to improve the prognosis of HNC. Furthermore, the prediction of malignant transformation in OPMD and characterization of the immune response to these lesions are vital to aid in early diagnosis.

In this study, we aimed at elucidating microscopic patterns in HNC and OPMD through quantification of immune responses, tissue and cell morphological features using image analysis.

Using multiple objective descriptors of cell and tissue morphology and immune scoring of different lesions, it is hoped that a combination of quantifiable factors can be identified for the prediction of disease progression in HNC and OPMD.

With the advances in cancer immunotherapy, full characterisation of the immune response to HNC and OPMD will help in early disease detection and guide the design of novel therapies.

Acknowledgement: This research is supported by funding from Friends of Anchor and NHS Grampian.

Joint work with: Prarthna Clare

Variability of beat to beat contraction strength measured with video recordings

Monday
August 6
9:00 -
10:00

Helmut Ahammer

GSRC-Biophysics, Medical University of Graz, Neue
Stiftingtalstrae 6, A-8010 Graz, Austria

Heart rate variability HRV is an important parameter for character- ising the nonlinear behaviour of the healthy as well as the pathological heart. Commonly, variabilities of interbeat intervals are investigated by analysing electrode measurements obtained from heart (ECG), heart tissue samples or isolated cardiomyocytes. Here we present a new method by analysing high speed video recordings of tissue samples. We present the algorithm to get the temporal contraction signal out of the individual images of a video stream and show the reasons why high speed recordings are necessary. The advantage of this method is that additionally to the interbeat interval, the interbeat contraction strength can be measured and investigated. Two well-known nonlinear measures, the Sample entropy and the Higuchi dimension were computed. The biological model included autorhythmic sinoatrial node tissue SAN and Acetylcholine ACh treatment. The difference between control and ACh treatment was more pronounced with interbeat contraction strengths compared to interbeat intervals.

Joint work with: Susanne Scheruebel, Robert Arnold, Brigitte Pelzmann, and Klaus Zorn-Pauly

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Arithmetic Quantum Mechanics and Galois Theory

Tuesday
August 7
10:30 -
11:30

Grzegorz Banaszak

Adam Mickiewicz University in Poznań
Faculty of Mathematics and Computer Science
Umultowska 87, 61-614 Poznań, Poland

I will discuss connections between the theory of homogenous isotropic Heisenberg ring (XXX-model) and algebraic number theory, in particular Galois theory. The solutions of the Heisenberg eigenproblem and Bethe Ansatz generate interesting families of algebraic number fields. Galois theory yields additional symmetries which not only simplify the analysis of the model but may lead to new applications and horizons. As an example I will discuss the special case of Heisenberg heptagon. The talk is based on joint papers with Dorota Blinkiewicz, Piotr Kraso, Tadeusz Lulek, Mirosaw abuz, Jan Milewski and Ryszard Stargaczyski.

Self-assembly of biopolymers and protein-like polymers

Wednesday
August 8
14:30 -
15:30

Michał Banaszak
Adam Mickiewicz University in Poznań
Faculty of Physics
Umultowska 85, 61-614 Poznań, Poland

TBA

Joint work with:

Commensurability principles for algebraic tori with examples

Friday
August 10
9:00 -
10:00

Dorota Blinkiewicz
Adam Mickiewicz University in Poznań
Faculty of Mathematics and Computer Science
Umultowska 87, 61-614 Poznań, Poland

In 1975, A. Schinzel solved the linear detecting problem for 1-dimensional tori over number fields. He shows that for greater dimension such property does not hold. We will discuss the relations between local to global detecting properties and local to global commensurability properties for abelian groups with finite torsion. We will apply these results to Mordell-Weil groups of tori and we will give example of a class of tori where the local to global commensurability properties hold. We will also focus on examples where they fail. These examples extent recursively the Schinzel's example. At the end of the lecture we will also give a criterion for commensurability using only finite number of reductions.

Joint work with: Grzegorz Banaszak

Lempel-Ziv complexity measure in biomedical applications

Monday
August 6
17:15 -
17:30

Marta Borowska
University of Białystok, Poland

Understanding the mechanism of biomedical signal generation is a significant problem in understanding many diseases. In this study we used Lempel-Ziv complexity measure with its extension for quantifying the dynamical changes of electrohysterogram (EHG). The Lempel-Ziv complexity measure can characterize the degree of order or disorder. In the first step of calculation these measure, the signal must be converted by a coarse-graining process into a finite sequence whose elements contains zeros and ones. The sequence of zeros and ones can be obtained in many ways: transform the original signal by comparing the signal with threshold (the mean value or the median value) of the window time series; generate signal which include a total of m! types of symbols, where m is the number of data points in each motif. Traditional Lempel-Ziv complexity algorithms based on single-scale do not include multiple electrical activities of the uterus. Therefore, combination permutation Lempel-Ziv complexity methods and a multiscale approach can be useful for quantifying the dynamical changes of EHG signals.

Improving Medical Decisions by Considering Non-Linearity of Biological Signals

Tuesday
August 7
9:00 -
10:00

Andreas Dominik
THM University of Applied Sciences, Gießen, Germany

Today, medical decisions are based on the interpretation of vast amounts of biological data obtained from a multitude of diagnostic instruments, such as 2D- and 3D-imaging (X-ray, CT, NMR, etc.), time series registration (ECG, EEG, etc.) or data from molecular biology (gene expression, genomics, epigenomics, metagenomics, etc.). Naturally, understanding the data requires understanding the underlying biological processes which can be described as giant feedback control systems, spanning scales from molecular level to entire organisms.

However, biological systems differ from technical systems in many ways. Because of their emergence, it is not possible to describe the behaviour of biological systems by analysing microscopic processes - only complete (and *living*) organisms show the typical characteristics that include non-linearity and fractal patterns. This is one reason for the increasing interest in systems biology research.

The talk will show examples for clinical data ubiquitously used for diagnosis in indications such as cancer or cardiovascular disease. Opportunities and challenges that arise from analysis of non-linearity will be illustrated and discussed.

Just as in all fields of data analytics, in medicine the development of reliable classifiers depend on the availability of reliable data. Unfortunately, publication of complete sets of raw data is unusual in medicine and hence only small data sets are available in literature. Simulations of complete biological systems might provide the necessary loophole and allow access to huge data sets of biological signals - presupposed that the simulated system covers enough of the biological system to generate signals with realistic characteristics.

Therefore, a brief introduction to techniques for multi-scale modelling of biological systems and their applications will complete the talk.

On generating primes with applications to cryptology

Wednesday
August 8
10:30 -
11:30

Maciej Grześkowiak
Adam Mickiewicz University in Poznań
Faculty of Mathematics and Computer Science
Umultowska 87, 61-614 Poznań, Poland

Let G be a finite abelian group and let H be a proper subgroup of G. Let $(G : H)$ denote the index of H in G. Let $\mathcal{F}$ be the fixed family of finite abelian groups. An algorithmic solution the following computational problem will be presented. Construct $G, H \in \mathcal{F}$ such that H is a proper subgroup of G and $(G : H)$ is as small as possible. The proposed algorithm should work in polynomial time with respect to the number of bits of the order of the group G.

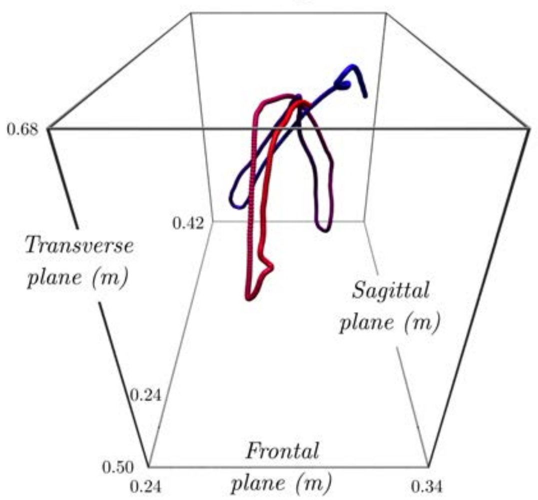
For cryptographic purposes the following groups are important: the multiplicative group of finite fields, the group of point of elliptic curves over finite field and the Jacobian group of hyperelliptic curve over finite fields.

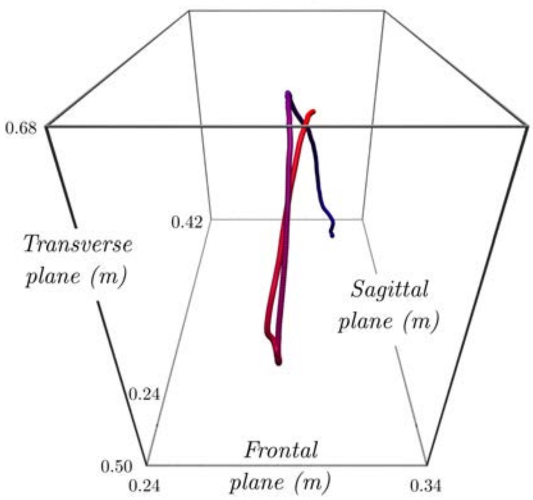
Temporal 3-dimensional spatial analysis of Centre of Mass during a postural balance test and effect of Static Taping

Herbert Jelinek
Charles Sturt University, Albury, Australia

Friday
August 10
10:30 -
11:30

Postural stability or postural sway is a common feature investigated in clinical and sports settings. Centre of mass (CoM) and centre of pressure (CoP) are the main features available to quantify postural stability, with centre of mass being a 3-dimensional movement whereas centre of pressure varies in two dimensions. Temporal and 2-dimensional data have been intensively studied for both CoM and CoP including fractal analysis. The current study applied a 3-dimensional representation of planar and vertical data to investigate changes in CoM whilst undertaking a balance test. The box-counting fractal analysis method was applied in 3-dimensions and the fractal dimension of CoM dispersion determined. Eight participants were recruited to undertake the Y-Balance Test, which requires participants to stand on their dominant leg and maximally stretch the non-dominant leg in the anterior, posterior-lateral and posterior-medial direction. Participants were tested with and without support taping (static tape, ST) applied to the ankle, lower leg and thigh. 3-dimensional motion capture data and ground reaction forces were used to calculate CoM following kinetic and kinematic assessment of the pelvis and lower limb. Static taping significantly decreased complexity of CoM dispersion (postural sway) compared to no taping ($\bar{x}\pm$SD; 1.29 ± 0.05 & 1.20 ± 0.04; $p = 0.003$). Our results indicated that 3-dimension fractal analysis is a robust method to investigate postural stability, it provides objective data on the complexity of CoM dispersion during a balance test and the effect of taping. The 3-dimensional analysis provides a more complete indication of complexity compared to current 2-dimensional CoM/CoP measures, as too much or too little complexity in CoM dispersion indicates instability and vertical changes should be taken into account in addition to horizontal sway. Future work will include a larger sample size and investigate factors that may contribute to increased or decreased complexity and effect of taping.


No tape


Static tape

Joint work with: Ahammer, H., Heale, L., Bourke, P. and Donnan, L.

DeepHRV - Discovering fractal properties of HRV series with help of deep neural networks

Tuesday
August 7
17:15 -
17:30

Julia Jelitzki

THM University of Applied Sciences, Gießen, Germany

In modern medical diagnostics measurement of biological signals is used to characterise the underlying complex system *Homo sapiens* (i.e. the patient). Therefore all detected signals in medicine are expected to display fractal patterns to some degree and entropy estimation of clinical signals is widespread. In many cases entropy corresponds surprisingly well with the health status of the examined organism.

In this study complexity of biological signals was analysed with help of deep artificial neural networks. For a first proof-of-concept, lists of heart beat intervals (RR-series) were analysed. RR-series are commonly used for studying heart rate variability (HRV) and correlation between their complexity (described by entropy or fractal dimension) and heart disease is well known.

Data preparation included normalisation and transformation into the frequency domain by computing the wavelet spectrogram. Analysis of the spectrogram was performed by means of a multi-layer convolutional neural network (CNN). Transfer learning was applied for the training of the CNN by using artificial training sequences as representatives for different types of patterns, such as fractal, random, periodic or almost-periodic. We call the output of the neural network for each of the four classes the response for the respective channel.

The fully trained CNN was used to predict the level of complexity of clinical RR-series without further training or adaption to the real-life signals by monitoring the response of the different channels of the CNN.

Validation was performed with Physionet data sets: samples for *diseased* have been taken from the Congestive Heart Failure RR Interval Database (chf2db); examples for *healthy* from a manually curated version of the Normal Sinus Rhythm RR Interval Database (nsr2db).

First results look promising: response of the CNN differs significantly when RR-series from patients with various grades of cardiovascular disease are processed. However, interpretation of the results remains a challenge, because every CNN learnes to identify different sets of patterns. In consequence, response of the neural network is not reproducible even though each network sucessfully separates between *diseased* and *healthy*.

Joint work with: Gernot Ernst, Andreas Dominik

Application of non-standard analysis to singular solutions of Bethe Ansatz

Wednesday
August 8
9:00 -
10:00

Piotr Krasoń
University of Szczecin
Mathematics Department
70-451 Szczecin, ul.Wielkopolska 15, Poland

In this work we suggest a rigorous mathematical approach for explanation of singular solutions of Bethe Ansatz by means of Robinson complex hypernumbers. There are several approaches towards these singular solutions eg. formal infinitesimals or germs of meromorphic functions. Our aim is to make them precise using non-standard analysis and show that they are essentially equivalent.

Joint work with: A. Koper and J. Milewski

Examples of breaking and enhancing of Galois symmetry of Bethe pseudoparticles in isotropic heptagonal magnetic ring

Monday
August 6
14:30 -
15:30

Tadeusz Lulek
Adam Mickiewicz University in Poznań
Faculty of Physics
Umultowska 85, 61-614 Poznań, Poland

We demonstrate examples of breaking and enhancing of Galois symmetry of Bethe pseudoparticles - elementary constituent bricks of exact eigenstates of the XXX model - for the case of the ring of $N = 7$ magnetic nodes with the spin 1/2 and isotropic nearest neighbour interaction. Admissible quanta of phase for such pseudoparticles responsible for the doublet with energy $E = -5$ at the centre of the Brillouin zone in the sector of $r = 3$ spin deviations from the ferromagnetic saturation are roots of the 6-degree polynomial f with integer coefficients, indecomposable over the prime number field $\mathbb{Q}$ of rationals. We apply the combinatoric version of the Weyl duality to demonstrate various types of the related Galois symmetry in construction of the three-particle states ($r = 3$) from roots of f. We explain the physical meaning of some statistical constraints for Bethe pseudoparticles, resulting from conservation laws for energy and quasimomentum.

String hypothesis for short Heisenberg magnets

Wednesday
August 8
16:00 -
17:00

Mirosław Łabuz

Department of Theoretical Physics
Faculty of Mathematics and Natural Sciences
University of Rzeszów
Pigonia 1, 35-310 Rzeszów, Poland

It is well known, that exact Bethe Ansatz solutions for the Heisenberg eigenproblem of a linear magnetic chain base upon the hypothesis of strings. This hypothesis is presumed to work in the thermodynamic limit $N \to \infty$, but it works pretty well also in the finite case.

I present some details of analysis performed for short magnetic chains. In particular, I exploit Galois symmetry associated with the secular eigenproblem in determining rigged string configurations.

Numbers, classes and relations

Monday
August 6
10:30 -
11:30

Preda Mihailescu

Georg-August-Universität, Mathematisches Institut, Göttingen, Germany

I will talk about units and class groups in the p-cyclotomic field.

The presentation will probably not bring new help for fighting skin cancer, but prove some interesting expectations that may delight those who know about the subject, and hopefully captivate the attention of those who do not know, too.

Diagonalisation of the Heisenberg Hamiltonian for two spin deviations and Chebyshev polynomials

Thursday
August 9
10:30 -
11:30

Jan Milewski

Institute of Mathematics
Poznań University of Technology
ul. Piotrowo 3A, 60-965 Poznań, Poland

The characteristic polynomial of the Heisenberg Hamiltonian for the ring with number of nodes N deviations is expressed by Chebyshev polynomials.

Four types of Chebyshev polynomials depending on parity N and quasimomenta k are considered.

Bethe parameters are derived by means of Inverse Bethe Ansatz.

Monofractal analysis of digital images of the human dentate nucleus: correlation, classification and morphometric analysis

Thursday
August 9
16:00 -
17:00

Nebojša Milošević
Department of Biophysics, Medical faculty, University of Belgrade, Serbia
and
Instituto Tecnológico de Santo Domingo, Santo Domingo, República Dominicana

Introduction: Dentate nucleus, the largest and phylogenetically most recent of the cerebellar white matter nuclei, plays an important role as major relay center between the cortex and the other parts of the brain (1). Neurons in the human dentate nucleus are usually classified into two types according to their topology (1): to central and border neurons. Although, neuronal images from the dentate nucleus have been previously quantified by various techniques (2-4), the goal of this work can be summarized in: a) investigate or improve actual classification scheme and b) investigate morphological differences between groups. The goals have been achieved with monofractal parameters which describe space-filling and shape of the neuron, as well as both complexity and irregularity of dendritic tree. In additi, correlation between Euclidean and monofractal parameters which quantifies the neuron size and shape, have been investigated.

Material and Methods: The specimens of the dentate nuclei were separated from 10 adult human brains, without pathological changes in the brain structure. A pool of 272 multipolar neurons was collected by recording histological samples on a light microscope. Multipolar neurons were initially classified in central (156) and border (116) group (1). Five monofractal parameters, quantifying three aspects of neuron morphology (surface area and shape of whole neuron, as well as the branching complexity of dendritic tree) were measured (3), by the box-counting method (5). Classification scheme was investigated by both histogram evaluation and cluster analysis. Morphological and topological differences were analyzed either by Kruskal-Wallis or Mann-Whitney (U) test (6).

Results: First, the correlation between the monofractal and Euclidean parameters of the surface, shape of the neurons and the density of the dendritic tree was examined, with the aim to show that the three indirectly describe these properties. Then, the distribution of five monofractal parameters was examined, with the aim of their correct presentation and further statistical analysis. The classification was performed simultaneously with histogram and cluster analysis using surface of the neuron and density of dendritic tree. Neurons were classified with cluster analysis only, into four types. The Kruskal-Vallis test indicates that there were statistical differences between the types, while Mann-Whitney test shows precise differences in five monofractal parameters between types. Finally, morphology of four cell types was analyzed according to the topological classification. Between the central and border neurons, there was a difference in D_{NF} only, while morphological differences in four monofractal parameters (D_N , D_{out}, D_{skel} and Λ) were found only for type 1 cells.

Conclusion: The results of this study corroborate with previous studies (4), which show that the topological of neurons from the human dentate nucleus is inferior to their morphological classification. On the other hand, this study improves previous conclusions (1), showing that the monofractal parameters could completely describe difference in morphology of neuronal types. The combination of morphological and topological classification indicates the need for a large sample. The obtained neuronal differences were discussed further in relation to the function of the cerebellar network.

Joint work with: Veličko Vraneš

References:

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Loop Quantum Cosmology: from polymer quantization to Early Universe dynamics

Tuesday
August 7
14:30 -
15:30

Tomasz Pawłowski
Center for Theoretical Physics of the Polish Academy of Sciences
Al. Lotnikow 32/46, 02-668 Warsaw, Poland

Loop Quantum Cosmology is an application of a nonstandard (that is based on a representation different from Schroedinger one) quantization procedure applied to quantize the spacetime itself in context of (simple) cosmological models of Universe. I will present a very brief outline of the theory and its main results. Further I will discuss its advantages, caveats and challenges following from its reliance on the nonstandard (the so called polymeric) quantization, in particular the issues of Hilbert spaces (non)separability and the effect of the ambiguities in the quantization procedure on physical predictions.

Periodic solutions in some biochemical models

Thursday
August 9
9:00 -
10:00

Valery Romanovski
CAMTP - Center for Applied Mathematics and Theoretical Physics
of the University of Maribor, Maribor, Slovenia
Faculty of Electrical Engineering and Computer Science
Faculty of Natural Science and Mathematics
University of Maribor, Maribor Slovenia

We give an introduction to algorithms of the elimination theory and methods for solving of polynomial systems and show how they can be used for the qualitative investigation of autonomous systems of ordinary differential equations arising in modeling of biochemical networks. An application to the study of two polynomial systems of ODEs, which model some ecological and chemical processes, is presented. In particular some integrals and periodic solutions in the systems are found and limit cycle bifurcations are investigated.

Bridging biology, linguistics, and physics: Some preliminary results for the distribution of nucleotides in mitochondrial DNA

Monday
August 6
16:00 -
17:00

Andrij Rovenchak
Department for Theoretical Physics
Ivan Franko National University of Lviv, Lviv, Ukraine

The three branches of science mentioned in the title intercross in the presented research, each in its own aspect. The subject of study, mitochondrial DNA (mtDNA) is a closed-circular, double-stranded molecule containing, in the case of mammals, 1600017000 base pairs (1). It is believed to be of bacterial evolutionary origin and thus might be considered as a nearly universal tool to study all eukaryotes. The rankfrequency distributions of nucleotide sequences in mtDNA are defined in a way analogous to the linguistic approach, with the highest-frequent nucleobase serving as a whitespace (2). The obtained sequences are analyzed with respect to parameters entropy and mean length which discriminate two mammal families, *Felidae* (cats) and *Ursidae* (bears) (3). The observed relation between the parameters is explained by a simple model yielding a correct qualitative description. Physics enters into the research not only via entropy but also through the analysis of so-called frequency spectra of the nucleotide sequences, which are modeled by nonadditive generalizations of the Bose-distribution (4). The use of nonadditive distributions is typical in studies of complex systems (5). While in the presented study the separation of families is not very sharp, the distributions for *Felidae* (cats) have on average longer tails comparing to *Ursidae* (bears) (3).

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On the Collatz conjecture

Tuesday
August 7
16:00 -
17:00

Mihai Tanase
Georg-August-Universität, Mathematisches Institut, Göttingen, Germany

The Collatz function takes any even integer x to $x/2$ and any odd integer x to $3x + 1$. The Collatz conjecture states that the iterations of the Collatz function on any starting integer greater than zero will eventually reach 1. In other words, no divergent or cyclic trajectories are possible (other than the trivial cycle $1 - 4 - 2 - 1$). However, the overall behavior of the iterates appears to be unpredictable. Illustrative for this fact is the Collatz fractal which is obtained when the Collatz function is extended to the field of complex numbers. One may associate to each trajectory a formal power series with the iterates as coefficients. In this presentation we reveal an unexpected property of these associated formal power series.

The Fibonacci Constant Limits Self-organization of Epithelial Cells and the Local Connected Fractal Dimension Predicts Their Metastatic Potential

Friday
August 10
14:30 -
15:30

Przemysław Waliszewski
Department of Urology, Lahn-Dill Clinics, Dillenburg, Germany

Both epithelial and mesenchymal cells interact each other at the various levels of their hierarchical organization forming tissue; a complex dynamic system. We show that the Fibonacci constant determines a limit for self-organization of epithelial cells into tissue structures of the higher order, such as glands or rosettes. Tumorigenesis alters the existent fractal structure to the point at which intercellular interactions are very weak. The mapping of the local connected fractal dimension allows the identification of cancer cells with increased metastatic potential providing an important tool for digital pathology of prostate carcinoma. The co-application of both complexity and diversity measures allows the subordination of those carcinomas into the classes of equivalence, and defines quantitative criteria for low- or high risk carcinomas. In particular, entropy indicates the direction of natural evolution in those tissue systems and the increment of complexity. Transformation of digitalized images of the electronically isolated cell nuclei into the grey intensity curves enables their analysis by a number of algorithms designed for the evaluation of nonlinear time series and the calculation of the Hurst coefficient, the embedding correlation dimension, and fragmentation dimension. All the latter dimensions confirm the existence of non-random, fractal structure in the spatial distribution of cancer cell nuclei. In particular, two of those algorithms, R/S and R/L, calculate the values of the Hurst coefficient that allow the identification of low- vs. high aggressive carcinomas. The statistical characteristic of those intensity curves indicates the non-ergodic nature of the underlying process.

Speakers