Escuela de investigación
Álgebras de Evolución y Estructuras no Asociativas

Lugar: Escuela de Ingenierías Industriales. Málaga
Fecha: 15 al 17 de octubre de 2018
Aula: 0.26

Conferenciantes

María Inez Cardoso (U. F. de Santa Catarina)

Cristina Draper (U. Málaga)

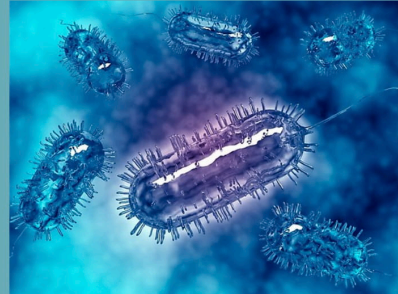Raúl Falcón Ganfornina (U. Sevilla)

Cristóbal Gil Canto (U. Málaga)

Alberto Márquez (U. Sevilla)

Cándido Martín González (U. Málaga)

Bakrom Omirov (U. Uzbequistán)

Irene Paniello (U. P. de Navarra)

María Victoria Velasco Collado (U. Granada)

https://algebraygrafos.sciencesconf.org/

Contacto: Cristóbal Gil Canto
cgilc@uma.es

Departamento de Matemática Aplicada

Departamento de Álgebra, Geometría y Topología

Red NCAlg

ESCUELA DE INGENIERÍAS INDUSTRIALES

UNIVERSIDAD DE GRANADA

Mathematical Modelling of Cellular Reactions

Altintan Derya
altintan@selcuk.edu.tr
Department of Mathematics, Selçuk University,

Understanding the dynamics of cellular reactions has an important role to explain the dynamics of entire organisms. Cellular reactions can be considered as reaction networks formed by many different species interacting via different reaction channels. There are two very well-known approaches to model the behavior of reaction systems: deterministic approach and stochastic approach. The deterministic approach, which is the traditional approach, is based on the idea that time evolution process of the reaction systems is continuous and deterministic. Then, it models the dynamics of these processes by the Ordinary Differential Equations (ODEs), called the Reaction Rate Equations (RREs) [4]. Although this approach is appropriate for many systems, it will not be appropriate when the number of species in the system is so low and stochastic fluctuations have an important role on the dynamics of reactions. Therefore, the stochastic modeling approach is proposed as an alternative to deterministic approach [3]. Different from the traditional approach, the stochastic approach is based on the idea that the dynamics of the system is discrete and stochastic. Then, it models the system using the Random Time Change Model (RTCM) or the Chemical Langevin Equation (CLE). Furthermore, the time derivative of the probability function satisfies the Chemical Master Equation (CME) or the Fokker-Planck Equation [2]. In cellular reactions, the abundance of species and also the rates of reactions can change in a wide range. Pure approaches, such as deterministic and stochastic, can be inefficient to model processes with multi-scale nature. Therefore, hybrid models which combine pure deterministic and stochastic approaches are proposed [1]. In this talk, we will explain the basics of stochastic modeling approach and its relation with the traditional deterministic modeling. Furthermore, we will talk on some hybrid methods that models processes with multi-scale nature by using deterministic and stochastic approaches in the meantime. Keywords: Deterministic approach, Stochastic approach, Chemical Langevin equation, Chemical master equation, Fokker-Planck equation References [1] A. Ganguly, D. Altıntan, and H. Koeppl, Jump-diffusion approximation of stochastic reaction dynamics: Error bounds and algorithms. Multiscale Model. Simul. 13 (2015), no. 4,1390-1419. [2] D. T. Gillespie, The chemical Langevin and Fokker-Planck equations for the reversible isomerization reaction. J. Phys. Chem. A 106 (2002), 5063-5071. [3] N. G. van Kampen, Stochastic processes in physics and chemistry. North Holland, 3rd edition, 2007. [4] D. J. Wilkinson, Stochastic modeling for systems biology Boca Raton, FL : Taylor & Francis, 2006.

Mutations in evolution algebras by means of isotopisms

Raúl Manuel Falcón Ganfornina
rafalgan@us.es
Departamento de Matemática Aplicada. Universidad de Sevilla.

Any mutation of genotypes that occurs during the mitotic cell cycle in an eukaryotic cell can be algebraically represented by an isotopism of the evolution algebra that describes the genetic pattern of the inheritance process. This talk deals with the theory of isotopisms of non-associative algebras and, particularly, with the distribution of evolution algebras into isotopism classes in order to determine the spectrum of genetic patterns, up to mutation, that describe the mentioned inheritance process of a mitotic cell cycle.

Connections between evolution algebras and graphical model of hereditary disease

Ian Morilla

morilla@math.univ-paris13.fr

Université Paris 13, Laboratoire d'excellence Inflamex, France.

In Biology, genes interactions are usually described in terms of graphs. Certain of those genes dispose in bi-functional modules within the graph according to their (anti)correlation to a state of functioning (e.g., permittivity to a genetic disorder of codominant traits) [1]. A disease may be characterised by a finite number of those modules. For a given module, there exist some allelic variants at risk (i.e., genetics risk factor) leading to a permissive state what eventually would cause disease in an individual if the other modules were also in the same permissive state. At present, the effective modelling of all these inherited genetics factors is impossible in biomedicine. However, within the framework of evolution algebras, it can be possible. In this work, we will explore connections between random walks on disease graphs [2-3] and the evolution algebra determined by the same graph.

[1] Victor JM, Debret G, Lesne A, Pascoe L, Carrivain P, et al. Network Modeling of Crohn's Disease Incidence. PLOS ONE 11(6)(2016): e0156138.

[2] Jianjun Tian & Xiao-Song Lin, Continuous time Markov processes on graphs, Stochastic Analysis and Applications, Vol. 24(2006), no. 5, 953-972.

[3] Jianjun Paul Tian & Zhenqiu Liu, Coalescent random walks on graphs, Journal of Computational and Applied Mathematics, 202(2007), no. 1, 144-154.

Alberto Márquez
almar@us.es

A CLASS OF NILPOTENT EVOLUTION ALGEBRAS

Bakhrom Omirov
omirovb@mail.ru
National University of Uzbekistan

Recently, by A. Elduque and A. Labra a new technique and a type of an evolution algebra are introduced. Several nilpotent evolution algebras defined in terms of bilinear forms and symmetric endomorphisms are constructed. The technique then used for the classification of the nilpotent evolution algebras up to dimension five. In this talk we discuss about this technique for high dimensional evolution algebras and we show that, except the cases considered by Elduque and Labra, this construction of nilpotent evolution algebras does not give all possible nilpotent evolution algebras.

Coálgebras genéticas

Irene Paniello
irene.paniello@unavarra.es
Universidad Pública de Navarra

Las coálgebras con realización genética fueron propuestas por J. Tian y B-L. Li en 2004 [9], como ejemplo de estructura algebraica no asociativa que permitiese rastrear la transferencia de la información genética en aquellos sistemas genéticos que se comportan de acuerdo a las leyes de Mendel. Más concretamente, dada una población genética mendeliana, su objetivo era definir una estructura algebraica que, para cada uno de los tipos genéticos existentes en la población, permitiese identificar las características genéticas de sus ancestros.

De manera general, una coálgebra con realización genética puede entenderse como un espacio vectorial real de dimensión finita n, provisto de una aplicación lineal, o comultiplicación, $\Delta: C \to C \otimes C$, que para una base distinguida, llamada natural, $B = \{e_1, \ldots, e_n\}$, permite escribir $\Delta(e_k) = \sum_{i,j=1}^{n} \beta_{ij}^k e_i \otimes e_j$ con k={1,...,n} para ciertos $0 \leq \beta_{ij}^k \leq 1$, i, j, k =1,...,n, tales que $\sum_{i,j=1}^{n} \beta_{ij}^k = 1$, para todo k = 1,...,n. Los elementos de la base natural podían en este caso considerarse como un conjunto completo de representantes de los distintos tipos genéticos existentes en la población genética objeto de estudio. En su trabajo de 2004 [9] Tian y Li revisaron las principales propiedades de las coálgebras con realización genética, proporcionando una interpretación biológica para algunas de ellas. Igualmente formularon una serie de cuestiones relativas al papel que esta estructura podía desempeñar en el estudio y modelización de la transferencia de la información genética. La mayoría de estas cuestiones quedaron abiertas después de este trabajo. Posteriormente en 2011 en [2] se estableció una correspondencia entre las coálgebras con realización genética y las llamadas matrices cúbicas estocásticas de tipo (1,2). Estas matrices habían sido previamente estudiadas por Maksimov en [1]. Esta correspondencia, entre coálgebras con realización genética y matrices cúbicas estocásticas de tipo (1,2), ha sido fundamental para el posterior estudio de diversas cuestiones relacionadas con las coálgebras con realización genética [3, 4, 5]. Más recientemente, en 2018, siguiendo las pautas establecidas por Tian y Li en su artículo de 2004 [9], se han considerado igualmente nuevas coálgebras con significado genético que intentan reflejar el comportamiento de poblaciones no mendelianas [6] así como el de las llamadas "chicken populations" [7]. Nuestro objetivo será proporcionar una visión general del papel de las coálgebras genéticas en la modelización del comportamiento de los sistemas genéticos. Para ello, y tras un breve repaso de algunas definiciones y propiedades básicas relativas a las coálgebras [8], revisaremos la noción de coálgebra con realización genética introducida por Tian y Li en [9], así como su correspondencia con las matrices cúbicas estocásticas de tipo (1,2) establecida en [2]. Esta correspondencia nos permitirá, por ejemplo, identificar los caracteres y los operadores de evolución de tales coálgebras, así como sus estados de equilibrio.

A continuación consideraremos distintas cuestiones relativas a la estructura de estas coálgebras proporcionando una caracterización de su simplicidad (en sentido genético) basada en trigrafos orientados. Para analizar se comentarán brevemente diversos aspectos relativos a las llamadas coálgebras de evolución, recientemente introducidas en [6].

[1] V. M. Maksimov, Cubic stochastic matrices and their probability interpretation, Theory Probab. Appl. 41 (1) (1997) 55- 69.

[2] I. Paniello, Stochastic matrices arising from genetic inheritance, Linear Algebra and its Applications 434 (2011) 791-800.

[3] I. Paniello, Marginal distributions on genetic coalgebras, J. Math. Biology 68 (5) (2014) 1071-1087.

[4] I. Paniello, On evolution operators of genetic coalgebras, J. Math. Biology 74 (1-2) (2017) 149-168.

[5] I. Paniello, Backwards genetic inheritance through coalgebragraphs, Linear and Multilinear Algebra 65 (5) (2017) 943-961.

[6] I. Paniello, Evolution coalgebras, aceptado en Linear and Multilinear Algebra (2018).

[7] I. Paniello, Evolution coalgebras on chicken populations, aceptado en Linear and Multilinear Algebra (2018).

[8] M. E. Sweedler, Hopf Algebras, Mathematics Lecture Note Series, W. A. Benjamin, Inc. New York, 1969.

[9] J. Tian, B-L. Li, Coalgebraic structure of genetic inheritance, Mathematical Biosciences and Engineering 1 (2) (2004) 243-266.

The classification of n-dimensional algebras with (n − 2)-dimensional annihilator.

Amir Fernández Ouaridi
amir.fernandezouaridi@alum.uca.es
Universidad de Cádiz

The classification of algebras is an important and interesting problem in the modern algebra. There are algebraic classifications [5], geometric classifications [3, 4], degeneration level classifications [6] and some other. In this work, we use the algebraic classification of 2-dimensional algebras [5] and some generalizations of ideas from [1, 2], to establish a complete classification, up to isomorphism, of all n-dimensional algebras with (n − 2)-dimensional annihilator over an algebraically closed field.

[1] Hegazi A., Abdelwahab H., The classification of n-dimensional non-associative Jordan algebras with (n − 3)-dimensional annihilator, Communications in Algebra, 46 (2018), 2, 629–643.

[2] Hegazi A., Abdelwahab H., Calderon Martin A., The classification of n-dimensional non-Lie Malcev algebras with (n–4)-dimensional annihilator. Linear Algebra Appl. 505 (2016), 32–56.

[3] Ismailov N., Kaygorodov I., Volkov Yu. The geometric classification of Leibniz algebras, International Journal of Mathematics, 29(2018), DOI: 10.1142/S0129167X18500350.

[4] Kaygorodov I., Popov, Yu. Pozhidaev A., Volkov Yu. Degenerations of Zinbiel and nilpotent Leibniz algebras, Linear and Multilinear algebra, 66 (2018), 4, 704–716.

[5] Kaygorodov I., Volkov Yu., The variety of 2-dimensional algebras over an algebraically closed field, arXiv:1701.08233. 6. Kaygorodov I., Volkov Yu., The degeneration level classification of algebras, arXiv:1710.08943

Cayley graphs, groups and Fibonacci-like sequences

Cristóbal Gil Canto
cristogilcanto@gmail.com
Universidad de Málaga

Given a finite (directed) graph E we can define its corresponding graph monoid M_E in a natural way. We will give some conditions on the graph which yield that this monoid is in fact a group. This happens for the case of Cayley graphs: for n a positive integer and for each $0 \leq j \leq n\text{-}1$ we let C_n^j denote Cayley graph for the cyclic group Z_n with respect to the subset $\{1, j\}$. We will totally describe the structure of these groups when $j=2,3$. The analysis is surprisingly related to a collection of integer sequences described by Haselgrove in the 1940s, to the classical Fibonacci sequence in the $j=2$ case and to a Fibonacci-like sequence, called Narayana's cows sequence, in the $j=3$ case. Finally, as a consequence, we will be able to use the description of these groups to get really nice information about the structure of the so-called Leavitt path algebras of Cayley graphs.

Classification of some functions in a special rings : A survey

Abdellah Mamouni
a.mamouni.fste@gmail.com
FST Errachidia, Morocco

The purpose of this work is to prove results concerning the classification of somme functions on prime and semi-prime rings. Hence, we provide examples to show that the assumed conditions can not be relaxed.

STORIES ON G_2

Cristina Draper Fontanals
cdr@uma.es
Universidad de Málaga

In this workshop on non-associative structures we will deal with one of the most studied
such creatures, the Lie algebra structure. In particular, we will dwell on one fascinating example, the Lie algebra g_2. In spite of being relatively small (dimension 14), it is undoubtedly versatile. Since its discovery (Killing, 1887), researchers have tried to understand the role of this algebra (and its related group G_2) as well as the other exceptional algebras (resp. groups). But this task is far to be finished. The number of search results of the algebra g_2 in Google is more than one million... We will give reasons to explain why this structure is so entangled with many others, and why it arises pervasively...

 [1] C. Draper Fontanals. Notes on G2: the Lie algebra and the Lie group. Differential Geom. Appl. 57 (2018), 23–74.

Squares and two-dimensional evolution Algebras

María Inez Cardoso Gonçalves
minezcg@gmail.com
Universidade Federal de Santa Catarina. Florianópolis. Brasil.

We associate an square to any two dimensional evolution algebra, an square is an equivalence class (or a union of them) whose combinatorial objects are equivalent to graphs. This geometric object is uniquely determined, does not depend on the basis and describes the structure and the behaviour of the algebra. To illustrate the use of the squares we prove that simplicity of a two dimensional evolution algebra is equivalent to a geometric property of the associated square. We also recover the classification of two-dimensional evolution algebras without restriction on the characteristic of the based field, paper that we discovered after we completed the classification (for a classification of two-dimensional algebras over an algebraically closed field. We determine the identities of degrees at most four, as well as derivations and automorphisms. We look at the group of automorphisms as an algebraic group, getting in this form a new algebraic invariant.