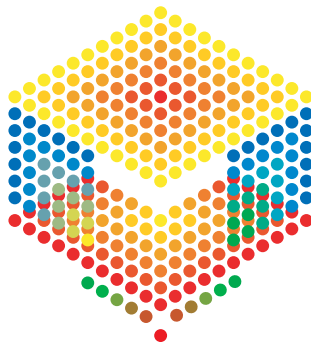


Fourth EACA International School
on Computer Algebra and its Applications

March 20–23, 2018

Santiago de Compostela, Spain



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Fourth EACA International School

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Programme

	TUESDAY 20 MARCH	WEDNESDAY 21 MARCH	THURSDAY 22 MARCH	FRIDAY 23 MARCH
09:30–11:00	I. García Marco AM	I. García Marco AM	V. Levandovskyy AM	I. García Marco AM
10:30–11:00				O. Pérez Barral AM

COFFEE BREAK

11:30–13:00	C. D'Andrea AM	C. D'Andrea (Lab.) I3	C. D'Andrea AM	V. Levandovskyy AM
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LUNCH (Cafetería Facultade de Matemáticas)

15:00–16:30	C. D'Andrea AM	I. García Marco (Lab.) I3	V. Levandovskyy I3	V. Levandovskyy I3
16:30–17:00	J. Cuevas Rozo AM		S. Murodov AM	I. Karimjanov AM

COFFEE BREAK

17:30–18:00	P. Páez Guillán AM	I. Gutiérrez Rodríguez AM	M. Garrote López AM	T. Fakhr Taha AM
18:00–18:30	J. Brox AM	R. Mariño Villar AM	J. Roca Lacostena AM	A. Fernández Fariña AM

- AM Aula Magna
- I3 Aula Informática 3

Speakers

Carlos D'Andrea

Universitat de Barcelona

Elimination Theory

- Algebraic and Geometric Elimination
- The Elimination Theorem
- Resultants and Elimination
- Classical and Modern Resultants
- Computational Tools

Ignacio García Marco

Universidad de La Laguna

Semigroups and its interactions with toric ideals and discrete structures

- Numerical semigroups
- 1-dimensional toric ideals
- The poset of a numerical semigroup: Möbius function and chomp on semigroups
- Noncommutative semigroups: Cayley posets

Viktor Levandovskyy

RWTH Aachen University, Germany

Computing in finitely presented algebras with Letterplace

- Theory of Groebner bases of two-sided ideals over the free associative algebra over a field
 - Monomial orderings, division procedure, normal form. Generalized Buchberger's algorithm. Homogeneous and inhomogeneous input. Truncated finite Groebner bases. Tame and wild infinite Groebner bases.
- Letterplace technique for computing Groebner bases of two-sided ideals
 - Letterplace correspondence of monomials, orderings and Groebner bases.

Practice: First experience with the Singular extension called Singular:Letterplace

- Applications of noncommutative Groebner bases
 - Determining the explicit form of the canonical (wrt a fixed monomial ordering) K-basis of a finitely presented algebra. Algebras of linear partial operators. Computations of K-dimension, Gelfand-Kirillov dimension and an upper bound of the global homological dimension. Establishing Noetherian, prime and semiprime properties.

Practice: Working with Letterplace libraries fpadim.lib and fpaprops.lib

Contributed talks

Algorithms for Grimm's conjecture

Jose Brox, Gerhard Paseman

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Abstract. In 1969, C.A. Grimm ([1]) proposed the following conjecture: If $n, n+1, \dots, n+k$ are composite numbers, then there are distinct prime numbers p_i such that $p_i | n+i$ for $0 \leq i \leq k$. For example, for 24, 25, 26, 27, 28 we can produce 2, 5, 13, 3, 7; on the other hand, we cannot produce distinct prime divisors for 2, 3, 4 (but 3 is prime). If a composite interval satisfies Grimm's conjecture, we say that we have a Grimm map for the interval. This conjecture, if true, would imply prime gap estimates even better than those implied by the Riemann Hypothesis ([2]). In 2006, Laishram and Shorey verified Grimm's conjecture up to 1.9×10^{10} ([4]). In 2016, G. Paseman published an algorithm at MathOverflow (algorithm **S**, [6]), based on a simple modification of Eratosthenes' sieve, which seems to be very close to providing Grimm maps for all composite intervals. We (G.P. and J.B.) report on the effectiveness of the **S** algorithm, with which we have been able to provisionally prove Grimm's conjecture up to 1×10^{12} , finding only 18 failures for **S** (the largest one below 3.5×10^9), which are easily fixed by other means. We have also investigated the behaviour of other algorithms: a simple idea, coming already from Grimm, is to use the greatest prime factor (**GP**) of every $n+i$; this algorithm produces more than 700 failures below 2.5×10^{10} . But if we modify it to be the greatest available prime factor from the right (**GAP**), then there are no failures up to 1×10^9 (nor in the maximum known prime gaps up to 10^{20}). **GAP** has the advantage over **S** of providing a Grimm map for any interval without iterating over previous ones, but in exchange it needs factorizations for all numbers in the interval. There are also other possible options: M. Langevin ([3]) found an elegant argument to provide

Grimm maps for those intervals such that $n + i$ does not divide $\text{lcm}(1, \dots, k)$ for any $1 \leq i \leq k$. We are trying to extend his result and also analyzing in which proportion of intervals it may be applied. Finally, we are gathering diverse statistics in an attempt to refine Laishram's and Murty's upper bound $g(n) < n^{1/2-1/300}$ (n big enough, [5]), where $g(n)$ denotes the maximum positive integer k such that the interval $n, \dots, n + k$ has a Grimm map (even if there are prime numbers in between).

References

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- [2] P. Erdős and J.L. Selfridge. Some problems on the prime factors of consecutive integers II. *Proc. Washington State Univ. Conf. Number Theory*. Pullman, 13–21, 1971.
- [3] M. Langevin. Plus grand facteur premier d'entiers en progression arithmétique. *Sém. Delange-Pisot-Poitou, Théorie des nombres*, 18(1, exp.3):1–7, 1977.
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Point reduction algorithms and discrete vector fields for finite topological spaces in the Kenzo system

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From the perspective of algebraic topology, finite topological spaces are an important tool to study finite simplicial complexes and their topological invariants, since these spaces allow to find models to describe their associated polyhedra. In 1966, McCord [4] established a connection between such objects: to each finite space X one can associate a simplicial complex $\mathcal{K}(X)$ (its *order complex*) and reciprocally, the *facet poset* $\mathcal{X}(K)$ of a finite simplicial complex K is defined, in such a way that $|\mathcal{K}(X)|$ and X are weakly homotopically equivalent and so are $|K|$ and $\mathcal{X}(K)$.

In this context, given a simplicial complex K , a fundamental aspect consist in finding other spaces that are also models of K , but with a smaller number of elements. Stong in its beautiful article [7] shows that the elimination of linear and colinear points (better known as *beat points* in the literature) preserves the homotopy type of a finite topological space. More recently, Barmak and Minian [1] have proved that deleting from X another special kind of points, called *weak points*, reflects exactly a simple collapse in $\mathcal{K}(X)$ and therefore this operation does not modify the weak homotopy type of X . In [2], some algorithms to decide if an element of a finite space is a beat point or a weak point are proposed, making use of topogenous matrices of the space (incidence matrices of the associated poset), which allow to find its core (a minimal space without beat points with the same homotopy type than the original) and its *weak core* (a core without weak points).

Moreover in [5], Forman's discrete Morse theory for CW-complexes has been adapted to the context of finite topological spaces and used as an alternative method to calculate the homology groups of cellular spaces; such class of spaces contains those that are face posets of some finite simplicial complex, allowing us to apply the results obtained to perform reductions of finite spaces.

The Kenzo system [3], developed by Francis Sergeraert and some coworkers, has been used to compute homology and homotopy groups of complicated spaces and in its computations has applied discrete vector fields to reduce the size of chain complexes. In this talk, an implementation in Kenzo of the algorithms explained in [2] and other new algorithms related with finite topological spaces and posets are presented. In particular, our idea is to generalize the algorithm for computing a discrete vector field for a digital image introduced in [5, Ch. 5] so that it can be applied to any finite topological space.

References

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The non-abelian tensor product of normal crossed submodules of groups

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Abstract.

In this talk the notions of non-abelian tensor and exterior products of two normal crossed submodules of a given crossed module of groups are introduced and some of their basic properties are established. In particular, we investigate some common properties between normal crossed modules and their tensor products, and present some bounds on the nilpotency class and solvability length of the tensor product, provided such information is given at least on one of the normal crossed submodules

References

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Perfect braided crossed modules

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Abstract.

The non-abelian tensor product of groups, given by Brown-Loday, and the non-abelian tensor product of Lie algebras, given by Ellis, determine the universal central extensions of perfect groups and perfect Lie algebras, respectively. We will talk about the extension theory of braided crossed modules of Lie algebras. Moreover, we will prove the braided version of Casas-Ladra theorem and Ellis theorem.

Work supported by Agencia Estatal de Investigación (Spain), grant MTM2016-79661-P (European FEDER support included, UE) and by Xunta de Galicia (Spain), grant ED481A-2017/064.

The rank of positive-semidefinite approximation of low rank matrices and its application in Phylogenetics

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Abstract.

In many areas of applied linear algebra, it is necessary to work with matrix approximations. A usual situation occurs when a matrix obtained from experimental or simulated data is needed to be approximated by a matrix that lies in a statistical model or satisfies some specific properties. In this talk we will study symmetric and positive-semidefinite approximations (see [2]) and we will show that the positive and negative indices of inertia of the symmetric approximation and the rank of the positive-semidefinite approximation are always bounded from above by the rank of the original matrix.

We will show how this results can be applied while we are using algebraic tools in phylogenetic reconstruction. One main goal of phylogenetic reconstruction is recovering the ancestral relationships among a group of current species. In order to reconstruct phylogenetic trees it is usual to model evolution adopting a parametric statistical model which allows us to define a joint probability distribution at the leaves of the trees. When these models are algebraic one is able to deduce polynomial relationships between these probabilities, known as phylogenetic invariants. One can study these polynomials and the geometry of the algebraic varieties that arise from them and use it to reconstruct phylogenetic trees.

There is a special situation when these theoretical probabilities can be placed into a matrix that has to be positive-semidefinite of low rank, say k , in order to correspond to a distribution arising from a hidden Markov process on a certain phylogenetic tree (see Proposition 4.5 in [1]). The corresponding

$(k + 1)$ -minors are phylogenetic invariants and their vanishing provide interesting information about the tree topology. But unfortunately these conditions and polynomial relationships are not always satisfied when working with real or simulated data.

The aim of our research is to use phylogenetic invariants and the stochasticity of the parameters of the general Markov model to provide insight into phylogenetic inference and to design new methods for phylogenetic reconstruction.

References

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- [2] Higham, N. J. Computing a Nearest Symmetric Positive Semidefinite Matrix *Linear Algebra and its Applications*, **103**, 103–118, 1988.

Application of Gröbner bases solving geometric problems

I. Gutiérrez-Rodríguez

Joint work with E. Calviño-Louzao, X. García-Martínez, E. García-Río and R. Vázquez-Lorenzo

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Abstract. The theory of Gröbner bases provides very powerful tools to solve large polynomial systems of equations. We pleasantly found that these methods can be very useful to classify homogeneous geometric structures such as: Einstein metrics, Bach flat structures or Ricci solitons. In this talk we will give the classification of Bach-flat Lie groups and Ricci solitons in dimension 4 using Gröbner bases.

References

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- [2] D. Cox, D. Little, and D.O’Shea, Ideals, Varieties, and Algorithms, Undergraduate Texts in Mathematics
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Leibniz algebras constructed by representations of general diamond Lie algebras

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Abstract.

The Ado's theorem in Lie Theory states that every finite-dimensional complex Lie algebra can be represented as a matrix Lie algebra, formed by matrices. However, that result does not specify which is the minimal order of the matrices involved in such representations. In [1], the value of the minimal order of the matrices for abelian Lie algebras and Heisenberg algebras \mathfrak{h}_m , defined on a $(2m+1)$ -dimensional vector space with basis $X_1, \dots, X_m, Y_1, \dots, Y_m, Z$, and brackets $[X_i, Y_i] = Z$, is found. For abelian Lie algebras of dimension n the minimal order is $\lceil 2\sqrt{n-1} \rceil$.

The real general Diamond Lie algebra \mathfrak{D}_m is a $(2m+2)$ -dimensional Lie algebra with basis $\{J, P_1, P_2, \dots, P_m, Q_1, Q_2, \dots, Q_m, T\}$ and non-zero relations

$$[J, P_k] = Q_k, \quad [J, Q_k] = -P_k, \quad [P_k, Q_k] = T, \quad 1 \leq k \leq m.$$

The complexification (for which we shall keep the same symbol $\mathfrak{D}_m(\mathbb{C})$) of the Diamond Lie algebra is $\mathfrak{D}_m \otimes \mathbb{C}$, and it shows the following (complex) basis:

$$P_k^+ = P_k - iQ_k, \quad Q_k^- = P_k + iQ_k, \quad T, \quad J, \quad 1 \leq k \leq m,$$

where i is the imaginary unit, and whose nonzero commutators are

$$[J, P_k^+] = iP_k^+, \quad [J, Q_k^-] = -iQ_k^-, \quad [P_k^+, Q_k^-] = 2iT, \quad 1 \leq k \leq m.$$

In this work we constructed a minimal faithful representation of the $(2m+2)$ -dimensional complex general Diamond Lie algebra, $\mathfrak{D}_m(\mathbb{C})$, which is isomorphic to a subalgebra of the special linear Lie algebra $\mathfrak{sl}(m+2, \mathbb{C})$. We

also constructed a faithful representation of the general Diamond Lie algebra \mathfrak{D}_m which is isomorphic to a subalgebra of the special symplectic Lie algebra $\mathfrak{sp}(2m+2, \mathbb{R})$. Furthermore, we describe Leibniz algebras with corresponding $(2m+2)$ -dimensional general Diamond Lie algebra \mathfrak{D}_m and ideal generated by the squares of elements giving rise to a faithful representation of \mathfrak{D}_m .

References

- [1] D. Burde. Leibniz On a refinement of Ado's theorem. *Arch Math (Basel)*, 70(2) (1998), 118–27.

A classification on weakly-Einstein manifolds

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Abstract. Einstein metrics on Riemannian manifolds (M^n, g) are critical metrics for different curvature functionals like the one given by the L^2 -norm of the curvature tensor. Nevertheless, there are another metrics which are critical but not Einstein. For instance if the Ricci tensor is Codazzi (i.e., its covariant derivative is totally symmetric), a metric is critical for $g \mapsto \int_M \|R\|^2$ if and only if $\check{R} = \frac{1}{n}\|R\|g$, where \check{R} is the symmetric $(0, 2)$ -tensor field given by $\check{R}_{ij} = R_{iabc}R_j^{abc}$. It was proved that any Einstein metric in dimension four satisfies this equality [1], so a Riemannian manifold is called *weakly-Einstein* if $\check{R} = \frac{1}{n}\|R\|g$, but not Einstein.

The main aim of this work is to give a classification of locally conformally flat weakly-Einstein manifolds through the study of the its algebraic structure, showing that either (M, g) is locally a product $N_1^m(c) \times N_2^m(-c)$ of equally-dimension manifolds of constant opposite curvature or otherwise (M, g) is locally a warped product $\mathcal{I} \times_f N(c)$ for some specific warping function f and fiber $N(c)$ of constant curvature. Moreover, it is shown that a locally conformally flat manifold of dimension four is weakly-Einstein if, and only if, has vanishing scalar curvature.

References

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Locally conformally flat weakly-Einstein manifolds To appear.

Property transitions of chains of evolution algebras

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Abstract.

The notion of evolution algebra was introduced by J.P. Tian in [3] and the notion of chain of evolution algebra was introduced by J.M. Casas, M. Ladra, U.A. Rozikov in [2].

This chain presents a dynamical system, the state of which at each given time is an evolution algebra. The sequence of matrices of structural constants of this chain of evolution algebras satisfies the Chapman-Kolmogorov equation.

In this note we give the behavior of properties depending on time of a class of chains of two-dimensional evolution algebras constructed in [1, 2].

References

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Dealing with negative conditions in automated proving

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Abstract.

In the algebraic-geometry-based theory of automated proving and discovery, it is usually required that the user includes, as complementary hypotheses, some intuitively obvious non-degeneracy conditions. Traditionally, there are two main procedures to introduce such conditions into the hypotheses set. The aim of this talk is to present these two approaches, namely Rabinowitsch's trick and the Ideal Saturation computation, and to discuss in detail the close relationships and subtle differences that exist between them, highlighting the advantages and drawbacks of each one. Moreover, we will analyse the impact of each of these two methods in the formulation of statements with negative thesis, yielding rather unexpected results if Rabinowitsch's trick is applied.

Work supported by Agencia Estatal de Investigación (Spain), grant MTM2016-79661-P (European FEDER support included, UE) and by FPU scholarship, Ministerio de Educación, Cultura y Deporte (Spain).

Ruled hypersurfaces with constant mean curvature in complex space forms

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Abstract. In this talk it is shown that ruled real hypersurfaces with constant mean curvature in the complex projective and hyperbolic spaces are minimal. Therefore, by a classification result by Lohnherr and Reckziegel [1] such hypersurface is one of:

1. a Clifford cone in $\mathbb{C}P^n$ or $\mathbb{C}H^n$ or,
2. a bisector in $\mathbb{C}H^n$ or,
3. a Lohnherr hypersurface in $\mathbb{C}H^n$.

References

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On the embedding problem for evolutionary Markov matrices

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Abstract.

DNA substitution models describe the evolutionary process through nucleotide substitution matrices. Assuming that nucleotide mutations always happen at the same rate through time leads to continuous-time models, which only consider matrices that are the exponential of rate matrices. A different approach appears when one regards the evolutionary process as a whole and considers matrices whose entries are given by the substitution probabilities between nucleotides. The understanding of the connection between these two approaches is fundamental for modeling evolution as it has practical and theoretical consequences, such as the identifiability of rates from experimental biological data. In this talk, we will give a description of the embedding problem, and see some new results about embeddability when restricted to Kimura 3-substitution-types model and its submodels.

List of participants

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Álvarez Díaz, Beatriz	Universidade de Santiago de Compostela
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Fernández Vilaboa, José Manuel	Universidade de Santiago de Compostela
Gago, Felipe	Universidade de Santiago de Compostela
García Marco, Ignacio	Universidad de La Laguna
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