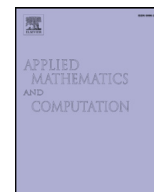




Contents lists available at ScienceDirect

## Applied Mathematics and Computation

journal homepage: [www.elsevier.com/locate/amc](http://www.elsevier.com/locate/amc)

# Algebraic computation of genetic patterns related to three-dimensional evolution algebras

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## ARTICLE INFO

Article history:  
Available online xxx

MSC:  
17D92  
68W30

Keywords:  
Computational Algebraic Geometry  
Evolution algebra  
Classification  
Isotopism  
Isomorphism

## ABSTRACT

The mitosis process of an eukaryotic cell can be represented by the structure constants of an evolution algebra. Any isotopism of the latter corresponds to a mutation of genotypes of the former. This paper uses Computational Algebraic Geometry to determine the distribution of three-dimensional evolution algebras over any field into isotopism classes and hence, to describe the spectrum of genetic patterns of three distinct genotypes during a mitosis process. Their distribution into isomorphism classes is also determined in case of dealing with algebras having a one-dimensional annihilator.

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## 1. Introduction

Evolution algebras were introduced by Tian and Vojtechovsky [22,23] to simulate algebraically the self-reproduction of alleles in non-Mendelian Genetics. In the last years, these algebras have been widely studied without probabilistic restrictions on their structure constants [3,6,8,10,13,17–19,21]. A main problem to be solved in this regard is the distribution of evolution algebras into isomorphism classes. Besides, Holgate and Campos [7,16] exposed the importance in Genetics of considering also the distribution of such algebras under isotopism classes, because they constitute a way to formulate algebraically the mutation of genotypes in the inheritance process.

The mentioned distribution into isomorphism classes has already been dealt with for two-dimensional evolution algebras over the complex field [5,9] and for nilpotent evolution algebras of dimension up to four over arbitrary fields [15]. More recently, the authors [14] have characterized the isomorphism classes of two-dimensional evolution algebras over arbitrary fields and have established their distribution into isotopism classes. The latter gives rise to the spectrum of genetic patterns of two distinct genotypes during mitosis of eukaryotic cells. More specifically, if  $u$  and  $v$  are two distinct non-zero elements of the algebra under consideration, then the mentioned spectrum is formed by the next four genetic patterns:  $(0, 0)$ , for which no offspring exists;  $(u, 0)$ , for which exactly one of the two genotypes does not produce offspring;  $(u, u)$ , for which the offspring has always the same genotype, whatever the initial one is; and  $(u, v)$ , for which the genotype of the offspring depends directly on that of the cell parent. This spectrum was obtained in [14] by means of distinct aspects on Computational Algebraic Geometry, all of them based on the fact that the algebraic law defined by the structure constants of any evolution algebra, together with the relations among basis vectors described by any isotopism of algebras, constitutes the

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set of generators of an ideal of polynomials whose reduced Gröbner basis establishes the algebraic relations that must hold, up to mutation, the genetic patterns of the mitosis process. This paper also focuses on the computation of such relations, particularly in case of dealing with three-dimensional evolution algebras. This enables us to distribute these algebras into isotopism classes, whatever the base field is, and describe mathematically the spectrum of genetic patterns of three distinct genotypes during a mitosis process. The distribution of such algebras into isomorphism classes is also determined in case of dealing with algebras having a one-dimensional annihilator.

## 2. Preliminaries

In this section, we expose some basic concepts and results on evolution algebras, isotopisms and Computational Algebraic Geometry that are used throughout the paper. For more details about these topics we refer the reader to the respective manuscripts of Tian [22], Albert [1] and Cox et al. [11].

### 2.1. Evolution algebras

A *gene* is the molecular unit of hereditary information. This consists of *deoxyribonucleic acid (DNA)*, which contains the code to determine the attributes or *phenotypes* that characterize each organism. Genes are disposed in sequential order giving rise to long strands of DNA called *chromosomes*. Genes related to a given phenotype can have distinct forms, which are called *alleles*. They always appear at the same position in chromosomes and constitute the *genotype* of the organism with respect to such a phenotype.

In *eukaryotic* cells, DNA is primordialily contained in the *nucleus*, although it also appears in organelles as mitochondria and chloroplasts, which are located in the cytoplasm. *Mitosis* is an asexual form of reproduction that consists of the division of an eukaryotic cell into two daughter cells in such a way that the nuclear genetic material of the former duplicates giving rise, up to rare mutation, to homologous nuclear chromosomes. In the final stage, the two daughter cells split having each resulting cell its corresponding copy of nuclear genetic material, whereas the extra-nuclear genetic material in the cytoplasm of the parent cell is randomly distributed between both of them by *vegetative division*. There exist distinct probabilistic laws that regulate the theoretical influence of all of this genetic material in the genotype of the offspring. Tian and Vojtechovsky [23] introduced evolution algebras to represent mathematically these laws. Specifically, an *evolution algebra* defined on a set  $\beta = \{e_1, \dots, e_n\}$  of distinct genotypes with respect to a given phenotype of an asexual organism is an  $n$ -dimensional algebra of basis  $\beta$  over a field  $\mathbb{K}$  such that  $e_i e_j = 0$ , if  $i \neq j$ , and  $e_i e_i = \sum_{j=1}^n c_{ij} e_j$ , for some  $c_{i1}, \dots, c_{in} \in \mathbb{K}$ . The elements  $c_{ij}$  are called the *structure constants* of the algebra. Here, the product  $e_i e_j = 0$ , for  $i \neq j$ , is due to the uniqueness of the genotype of the parent cell; the product  $e_i e_i$  represents self-replication in the mitosis process; and each structure constant  $c_{ij}$  constitutes the probability, due to vegetative division, that the genotype  $e_i$  becomes the genotype  $e_j$  in the next generation.

### 2.2. Isotopisms of evolution algebras

Two  $n$ -dimensional algebras  $A$  and  $A'$  are *isotopic* [1] if there exist three non-singular linear transformations  $f, g$  and  $h$  from  $A$  to  $A'$  such that  $f(u)g(v) = h(uv)$ , for all  $u, v \in A$ . The triple  $(f, g, h)$  is called an *isotopism* between  $A$  and  $A'$ . If  $f = g$ , then the triple  $(f, f, h)$  is called a *strong isotopism* and the algebras are said to be *strongly isotopic*. If  $f = g = h$ , then the isotopism constitutes an *isomorphism*, which is denoted by  $f$  instead of  $(f, f, f)$ . To be isotopic, strongly isotopic or isomorphic are equivalence relations among algebras. Throughout the paper, we refer the former and the latter as  $\sim$  and  $\cong$ , respectively.

Isotopisms of evolution algebras can be interpreted as mutations of the genetic material of parent and daughter cells in the mitosis process with respect to a given phenotype. Specifically, if  $(f, g, h)$  is an isotopism between two  $n$ -dimensional evolution algebras  $A$  and  $A'$ , then  $f$  and  $g$  represent the respective possible mutation of each one of the two homologous chromosomes in which the nuclear genetic material of the parent cell duplicates during the first part of the mitosis process, whereas  $h$  represents a possible mutation of the genotype of the offspring in the final step of the process. For each  $\alpha \in \{f, g, h\}$ , the corresponding expression  $\alpha(e_i) = \sum_{j=1}^n a_{ij} e_j$  involves the genotype  $e_i$  to mutate to  $e_j$  with probability  $a_{ij}$ . Since  $A'$  is also an evolution algebra, the mitosis process only finishes if the genotypes of both homologous chromosomes that have been created after the mutations  $f$  and  $g$  coincide. If these genotypes do not coincide, then there is no offspring.

Hereafter,  $\mathcal{E}_n(\mathbb{K})$  denotes the set of  $n$ -dimensional evolution algebras over the base field  $\mathbb{K}$  with basis  $\{e_1, \dots, e_n\}$ , whereas  $\mathcal{T}_n(\mathbb{K})$  denotes the direct product  $\prod_{i=1}^n \langle e_1, \dots, e_n \rangle$ . Every evolution algebra in  $\mathcal{E}_n(\mathbb{K})$  is uniquely determined by an *structure tuple*  $T = (t_1, \dots, t_n) \in \mathcal{T}_n(\mathbb{K})$ , where  $t_i = e_i e_i$ , for all  $i \leq n$ . The structure tuple  $T$  also determines the *genetic pattern* of the corresponding mitosis process.

**Proposition 2.1** ([14]). *Let  $\mathbb{K}$  be a field. The next results hold.*

- a) Any two structure tuples in  $\mathcal{T}_n(\mathbb{K})$  that are equal up to permutation of their components and basis vectors give rise to a pair of strongly isotopic evolution algebras.
- b) Let  $T$  be a structure tuple in  $\mathcal{T}_n(\mathbb{K})$ . There always exists a structure tuple  $T' = (\sum_{j=1}^n c_{1j} e_j, \dots, \sum_{j=1}^n c_{nj} e_j) \in \mathcal{T}_n(\mathbb{K})$  such that
  - a) If  $c_{ii} = 0$ , for some  $i \geq 1$ , then  $c_{jk} = 0$ , for all  $j, k \geq i$ .
  - b) If  $c_{ii} \neq 0$ , for some  $i \geq 1$ , then  $c_{ij} = 0$ , for all  $j \neq i$ .
  - c) The evolution algebra in  $\mathcal{E}_n(\mathbb{K})$  of structure tuple  $T'$  is strongly isotopic to that one of structure tuple  $T$ .

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