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Research Article

# Analogies of Coding Systems of DNA and Elementary Particles

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**Abstract.** We suggest that physical reality can be described in the language of division algebras, which dictates that their symmetries must be manifested in the coding systems of different structures of nature. We compare the structures of DNA and fundamental fermions. In both cases we observe $(3+4)$-element divisions which may arise from the symmetries of the 8-dimensional normed split-algebra. The analogies between the genetic code (given by codons that contain three nucleotide bases) and the properties of the structures of all possible baryons (quark triplets) are discussed. In the genetic code we have the degeneracy of codons built by four standard nucleotides that specify 21 amino acids in humans. Similarly, there are 21 major types of baryons built by four lightest quarks with the degeneration of their spin values. These analogies can help to address some unsolved problems in genetics and physics, like the origin of codon degeneracy, the fermion generation problem and structure of atomic nuclei.

**Keywords.** Coding systems, DNA and RNA, Split octonions, Generations of fermions, Nuclear structure models

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## 1. Introduction

Any process in nature can be characterized in terms of its ability to transfer information. Informational methods are powerful tools in many fields, from computer and physical sciences to genetics and molecular biology. In the simplest case, information can be understood as the number of bits, which allows us to describe it with integers. As was said by Leopold Kronecker, natural numbers were made by god and everything else is the work of men. However, measurements and comparisons of two objects require number systems, where addition, subtraction, multiplication and division is possible. So, the mathematical language needed for information processing is given by a normed composition algebra with an unit element over the real numbers, since any observable quantity, obtained from the measurement, is real. According to Hurwitz theorem, in addition to the usual algebra of real numbers, there are three unique normed division algebras: complex numbers, quaternions and octonions (Baez [4], Schafer [44], Springer and Veldkamp [47]). The real numbers are ordered, commutative and associative, but for each next mentioned hyper-complex number, one such property is lost.

In general, to provide a basic informational framework we do not have to use hyper-complex numbers (even real numbers), since ultimately any measurement boils down to some counting. But hyper-complex numbers make physics more practical and transparent. Multi-dimensional numbers come more often to express solutions to wave equations and are much simpler as opposed to real-valued trigonometric functions. They also incorporate symmetries of corresponding periodic functions, like $U(1)$ for the case of complex numbers. Hyper-complex numbers also have natural connections to multi-dimensional spaces (e.g., plane for complex numbers) that relate geometry to algebra (Feynman *et al*. [11]). If division algebras are adequate language in description of reality, their symmetries must be manifested in the coding systems of different structures of nature.

In this paper we want to compare some aspects of information storing in genetics and particle physics and discuss various analogies between them. Apart from the fundamental differences between particle physics and genetics, the organization of matter exhibits some similarities, in both cases structures fall into several big classes, each of which is constructed out of just a few basic building blocks.

The paper is organized as follows. In Section 2 we review general features of split octonions and their automorphism group $G_2^{NC}$. Section 3 is devoted to the genetic code and its possible links to 8-dimensional algebra of split octonions. In Section 4 it is considered possible importance of the automorphism group of split octonions in particle and nuclear physics, some analogies between genetic code and classification of baryons are discussed. Finally, Section 5 presents our conclusions.

## 2. Split Algebras

It is essential for all normed algebras that they contain a real unit element, $e_0$, and different number of hyper-complex units, $e_A$, whose conjugates have opposite signs,

$$e_A^* = -e_A\,. \tag{2.1}$$

Any element of the algebra is linear combinations of these units:

$$X = x^0 e_0 + x^A e_A\,. \tag{2.2}$$

For the case of complex numbers $A = 1$, for quaternions $A = 3$ and for octonions $A = 7$. The square of the unit element is always positive $e_0^2 = 1$, while the squares of the hyper-complex units $e_A^2 = \pm 1$. If we allow some units to have negative norms, we arrive at so-called split algebras. Norm of a division algebra is Euclidean, while norms of split-algebras are pseudo-Euclidian with equal number of positive and negative elements (Baez [4], Schafer [44], Springer and Veldkamp [47]).

## 2.1 Split Octonions

Let us review some properties of largest normed split algebra, which could form the basic framework for information processing in nature. General element of the 8-dimensional non-associative algebra of split octonions over the field of real numbers $\mathbb{R}$ and its conjugate are

$$\left.\begin{aligned} X &= x_0 + \sum_n (j_n x_n + J_n x_{3+n}) + I x_7\,, \\ \overline{X} &= x_0 - \sum_n (j_n x_n + J_n x_{3+n}) - I x_7\,. \quad (n = 1,2,3) \end{aligned}\right\} \tag{2.3}$$

where $\{x_0, x_n, x_{3+n}, x_7\} \in \mathbb{R}$. Eight basis units in (2.3) are represented by one scalar (denoted by 1), the three vectors like objects $J_n$ ($J_n^2 = 1$), the three pseudo-vectors like elements $j_n$ ($j_n^2 = -1$) and one pseudo-scalar like unit $I$ ($I^2 = 1$). The complete algebra of the basis units can be written as:

$$\left.\begin{aligned} &I^2 = 1\,, \quad j_n I = J_n\,, \quad j_m j_n = -\delta_{mn} + \sum_\ell \epsilon_{\ell mn} j_\ell\,, \\ &J_m J_n = \delta_{mn} + \sum_\ell \epsilon_{\ell mn} j_\ell\,, \quad J_m j_n = \delta_{mn} I - \sum_\ell \epsilon_{\ell mn} J_\ell\,. \quad (\ell, m, n, = 1,2,3) \end{aligned}\right\} \tag{2.4}$$

The quadratic form of split octonions,

$$\mathcal{Q}(X) = \overline{X} X = x_0^2 + \sum_n x_n^2 - \sum_n x_{3+n}^2 - x_7^2\,, \tag{2.5}$$

is pseudo-Euclidean and has $(4+4)$ signature. The form (2.5) is not positively defined and also evaluates to zero for some nonzero elements.

Any split octonion (2.3) with positive $\mathcal{Q}$ might be expressed in the polar form:

$$X = \sqrt{\mathcal{Q}}\,\alpha(\theta)\,, \tag{2.6}$$

where the exponential element,

$$\alpha(\theta) = e^{\epsilon\theta}\,, \tag{2.7}$$

where $\epsilon$ is the $(3+4)$-vector defined by seven basis units $J_n$, $j_n$ and $I$, represents the split octonion with the unit norm. The left multiplication of an octonion $X$ by (2.7), $\alpha X$, can be understood as a rotation by the angles $\theta$ in four orthogonal planes of 8-dimensional octonionic space (2.5). The right product by the inverse of (2.7), $X\alpha^{-1}$, will reverse the direction of rotation in the plane containing $x_0$. So, we can represent rotations that only affect the $(3+4)$-vector part of $X$, applying the unit half-angle octonion twice, multiplying on both the left and on the right (with its inverse),

$$X' = \alpha X \alpha^{-1} = \alpha X \alpha^* = e^{\epsilon\theta/2} X e^{-\epsilon\theta/2}\,. \tag{2.8}$$

These maps are well-defined, since the associator of the triplet $(\alpha, X, \alpha^{-1})$ vanishes. The set of rotations (2.8) of the seven octonionic coordinates $x^A$, in three planes, which do not affect the scalar part $x_0$ of (2.3), contains $7 \times 3 = 21$ angles of the group $SO(3,4)$

of passive transformations of coordinates – the tensorial transformations of the seven parameters $\{x_n, x_{3+n}, x_7\}$ that are leaving invariant the vector part of (2.5) (Gogberashvili and Gurchumelia [15], Gogberashvili and Sakhelashvili [16]).

To represent the active rotations in the space of $X$, we would need the transformations to be automorphisms. Automorphisms preserve the norm (2.5) and multiplicative structure of octonions (2.4) as well and allows us to consider octonionic rotations around several axes. An automorphism $U$ of any two octonions, $X_1$ and $X_2$, gives the equation:

$$(UX_1U^{-1})(UX_2U^{-1}) = UX_1X_2U^{-1}, \tag{2.9}$$

which only holds in general if multiplication of $U$, $X_1$ and $X_2$ is associative. So, combinations of the rotations (2.8) around different axes are not unique, i.e., not all octonionic $SO(3,4)$-transformations form a group and can be considered as real rotations. Only the transformations that have a realization as associative multiplications should be considered. Thus, due to non-associativity, the group of rotations of octonionic axes, $J_n$, $j_n$, and $I$, is not equivalent to the group of accompanied passive tensorial transformations of coordinates, $x_A$ that leaves invariant the norm (2.5).

It was found that associative transformations of split octonions can be done by the specific simultaneously rotations in two (and not in three, as for the case of $SO(3,4)$-transformations) orthogonal octonionic planes, which form a subgroup of $SO(3,4)$ with $2 \times 7 = 14$ parameters, known as the non-compact variant of smallest Cartan's exceptional Lie-group, denoted as $G_2^{NC}$. The Lorentz-type transformations of $G_2^{NC}$ can be divided formally in three distinct classes: Euclidean rotations of the spatial and time-like coordinates ($x^n$ and $x^{3+n}$) by the compact 3-angles; Boosts, mixing of spatial and time-like coordinates by the two hyperbolic 3-angles; Diagonal boosts of the spatial coordinates and corresponding time-like parameters by the hyperbolic angles (Gogberashvili and Gurchumelia [15], Gogberashvili and Sakhelashvili [16]).

## 2.2 Generators of the Non-compact G2

For the completeness let us present the generic block decomposition of generators of non-compact $G_2^{NC}$ (Günaydin and Gürsey [13]):

$$G = \begin{pmatrix} S & \widetilde{V} & \sqrt{2}U \\ -\widetilde{U} & -S^T & \sqrt{2}V \\ \sqrt{2}V^T & \sqrt{2}U^T & 0 \end{pmatrix}, \tag{2.10}$$

where $S$ are $3 \times 3$ matrices that generate the group $SL(3,R)$,

$$\left.\begin{aligned} &S_1 = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & -1 \end{pmatrix}, \quad S_2 = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & -1 \end{pmatrix}, \quad S_3 = \begin{pmatrix} 0 & 1 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad S_4 = \begin{pmatrix} 0 & 0 & 1 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \\ &S_5 = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 1 \\ 0 & 0 & 0 \end{pmatrix}, \quad S_6 = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ -1 & 0 & 0 \end{pmatrix}, \quad S_7 = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & -1 & 0 \end{pmatrix}, \quad S_8 = \begin{pmatrix} 0 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \end{aligned}\right\} \tag{2.11}$$

$U$ and $V$ are 3-component $1 \times 3$ block column matrices,

$$U_1 = \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix}, \quad U_2 = \begin{pmatrix} 0 \\ 1 \\ 0 \end{pmatrix}, \quad U_3 = \begin{pmatrix} 0 \\ 0 \\ -1 \end{pmatrix}, \quad V_1 = \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix}, \quad V_2 = \begin{pmatrix} 0 \\ 1 \\ 0 \end{pmatrix}, \quad V_3 = \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix}, \tag{2.12}$$

and $\widetilde{U}$, $\widetilde{V}$ are the $3\times 3$ dual matrices $\widetilde{U}_{ij}=\epsilon_{ijk}U_k$.

Note that the transposed matrices $G_A^T$ are related to the original matrices $G_A$ by

$$G_A^T=-KG_AK\,, \tag{2.13}$$

where the involution $K$ has the block structure

$$K=\begin{pmatrix}0&1&0\\1&0&0\\0&0&-1\end{pmatrix}. \tag{2.14}$$

The real matrix representing the coset $G_2^{NC}/(SL(2,R)\times SL(2,R))$ may be chosen to have the symmetrical block structure

$$M=\begin{pmatrix}A&B&\sqrt{2}U\\B^T&C&\sqrt{2}V\\\sqrt{2}U^T&\sqrt{2}V^T&S\end{pmatrix}, \tag{2.15}$$

where $A$ and $C$ are symmetrical $3\times 3$ matrices, $B$ is a $3\times 3$ matrix, $U$ and $V$ are 3-component column matrices, and $S$ is a scalar, such that the inverse matrix reads

$$M^{-1}=KMK=\begin{pmatrix}C&B^T&-\sqrt{2}V\\B&A&-\sqrt{2}U\\-\sqrt{2}V^T&-\sqrt{2}U^T&S\end{pmatrix}. \tag{2.16}$$

## 3. Genetic Code

The total information content of the *deoxyribonucleic acid* (DNA) and *ribonucleic acid* (RNA), which are responsible for the storage and reading of genetic information of life (Pray [42]), still remains a mystery (Craig *et al*. [10]). DNA and RNA molecules are polymers made up of long chains of nucleotides, each of which contains one of four nitrogenous base – *Adenine* (A), *Guanine* (G), *Cytosine* (C) and *Thymine* (T) in DNA, or *Uracil* (U) instead of Thymine in RNA. DNA and RNA molecules, which responsible for storing and implementing genetic information, consist of 4 different nucleotide bases. Through this 'nucleotide alphabet', information is written using sets of 3 nucleotides. These triplets are called codons and there are in total 64 of them (see, Lin *et al*. [32] and references therein). Codons instruct cells to create protein chains, encoding a particular amino acid, or signaling the termination of protein synthesis.

Several attempts to describe the genetic code in terms of symmetry properties and group theory have been developed by Antoneli and Forger [2], Gonzalez *et al*. [17], Hornos and Hornos [21], Kwon *et al*. [29], Lehmann and Libchaber [30], Lenstra [31], Negadi [36], Rietman *et al*. [43], Schafer [45]. Group theoretical approach for codon representation suggests selecting a simple Lie algebra having irreducible representation of dimension 64 (Hornos *et al*. [22]). This can be achieved by a 8 dimensional algebra (Hill and Rowlands [20]), all possible combinations of 8 units (including the different signs) makes 64 objects. For instance, the general linear group over the field of real numbers $GL(8,R)$ is a real Lie group of dimension $8^2=64$. Examples of the groups which admit a 64-dimensional irreducible representation are $G_2$ (the only such exceptional Lie algebra) and its subgroup $SU(3)$ (McKay and Patera [35]), which are widely used in particle physics.

The genetic code can be represented as a RNA codon table of all possible combinations produced by a triplet code of the four standard nucleotides (Table 1), with indications of particular amino acids that are encoded by these codons. For some reason, out of many types of amino acids in nature, there are only 22 of them that are found in living organisms (Table 2). Note that, in addition to 20 standard amino acids, there exists two atypical ones, Selenocysteine (Sec) and Pyrrolysine (Pyl) (the last two in Table 2), which are encoded by codons that normally function as stop signals (Zhang *et al*. [50]). Since Pyrrolysine (Pyl) is not used in human protein synthesis, there are only 21 different amino acids encoded in the human DNA.

**Table 1.** Codons made of standard nucleotide 'letters'

**Second Letter**

| First Letter | U | | C | | A | | G | | Third Letter |
|---|---|---|---|---|---|---|---|---|---|
| U | UUU | **Phe** | UCU | **Ser** | UAU | **Tyr** | UGU | **Cys** | **U** |
| | UUC | | UCC | | UAC | | UGC | | **C** |
| | UUA | **Leu** | UCA | | **UAA** Stop | | **UGA Sec**/Stop | | **A** |
| | UUG | | UCG | | **UAG Pyl**/Stop | | UGG | **Trp** | **G** |
| C | CUU | **Leu** | CCU | **Pro** | CAU | **His** | CGU | **Arg** | **U** |
| | CUC | | CCC | | CAC | | CGC | | **C** |
| | CUA | | CCA | | CAA | **Gln** | CGA | | **A** |
| | CUG | | CCG | | CAG | | CGG | | **G** |
| A | AUU | **Ile** | ACU | **Thr** | AAU | **Asn** | AGU | **Ser** | **U** |
| | AUC | | ACC | | AAC | | AGC | | **C** |
| | AUA | | ACA | | AAA | **Lys** | AGA | **Arg** | **A** |
| | **AUG Met**/Start | | ACG | | AAG | | AGG | | **G** |
| G | GUU | **Val** | GCU | **Ala** | GAU | **Asp** | GGU | **Gly** | **U** |
| | GUC | | GCC | | GAC | | GGC | | **C** |
| | GUA | | GCA | | GAA | **Glu** | GGA | | **A** |
| | GUG | | GCG | | GAG | | GGG | | **G** |

With the four bases, A, G, C and U(T), there are $4^3 = 64$ possible codons, from which 3 are used as stop signals. However, it was noted the possibility of increasing the number of replicable nucleotides in DNA and RNA from the four standard ones (used in Table 1) to six, by nonstandard P and Z nucleotides (Piccirilli *et al*. [38], Switzer *et al*. [48]) (or even to eight [24]). The extra two nucleotides seem to have a nitro functionality not found in standard DNA. This increment in the number of genetic 'letters' may also lead to expansion of the functional potential of nucleic acids (Zhang *et al*. [51]).

In each codon the arrangement of nucleotide bases is strictly determined. For instance, GUA and GAU codons are different, even though their composition is the same. This reflects the fact that there is no symmetry with respect to transmission of bases in genetic code and that they show qualitative differences based on their structure. $64 \to 22$ mapping in Table 1 is obviously not one-to-one, several (synonymous) codons can code for a single amino acid, i.e., genetic code structure is redundant. While two amino acids (Met and Trp) are encoded by a single codon in the standard genetic code, the majority of amino acids are encoded by multiple codons. The most redundancy is observed for three residues (Arg, Leu, Ser), which are each encoded by six codons (see the Table 2). The genetic codon degeneracy occurs mainly due to the variance in third position, e.g. the amino acids Glycine is encoded by four codons GGU, GGC, GGA, GGG that differ only in third base.

**Table 2.** Amino acids made up of the first four standard nucleotide bases

| # | Amino acid name | Messenger RNA codons | Degeneracy |
|---|---|---|---|
| 1 | Alanine (Ala) | **GCU, GCC, GCA, GCG** | Quartet |
| 2 | Arginine (Arg) | **CGU, CGC, CGA, CGG, AGA, AGG** | Sextet |
| 3 | Asparagine (Asn) | **AAU, AAC** | Doublet |
| 4 | Aspartic Acid (Asp) | **GAU, GAC** | Doublet |
| 5 | Cysteine (Cys) | **UGU, UGC** | Doublet |
| 6 | Glutamic acid (Glu) | **GAA, GAG** | Doublet |
| 7 | Glutamine (Gln) | **CAA, CAG** | Doublet |
| 8 | Glycine (Gly) | **GGU, GGC, GGA, GGG** | Quartet |
| 9 | Histidine (His) | **CAU, CAC** | Doublet |
| 10 | Isoleucine (Ile) | **AUU, AUC, AUA** | Triplet |
| 11 | Leucine (Leu) | **UUA, UUG, CUU, CUC, CUA, CUG** | Sextet |
| 12 | Lysine (Lys) | **AAA, AAG** | Doublet |
| 13 | Methionine (Met) | **AUG** (Start) | Singlet |
| 14 | Phenylalanine (Phe) | **UUU, UUC** | Doublet |
| 15 | Proline (Pro) | **CCU, CCC, CCA, CCG** | Quartet |
| 16 | Serine (Ser) | **UCU, UCC, UCA, UCG, AGU, AGC** | Sextet |
| 17 | Threonine (Thr) | **ACU, ACC, ACA, ACG** | Quartet |
| 18 | Tryptophan (Trp) | **UGG** | Singlet |
| 19 | Tyrosine (Tyr) | **UAU, UAC** | Doublet |
| 20 | Valine (Val) | **GUU, GUC, GUA, GUG** | Quartet |
| 21 | Selenocysteine (Sec) | **UGA** (Stop) | Singlet |
| 22 | Pyrrolysine (Pyl) | **UAG** (Stop) | Singlet |

The codon redundancy is still an unsolved problem, theories on the origin of the genetic code can be grouped in at least five different categories (see, Giulio [14]).

- *The stereo-chemical origin:* It is based on the hypothesis that codons can selectively bind to assigned amino acids via a stereo-chemical specificity.
- *The co-evolution theory*: It postulates that the codon assignation to new amino acids proceeds by inheriting part of the codon set pertaining to the precursor amino acids (amino acids that generate the new one by biosynthetic modification).
- *The adaptive hypothesis*: It postulates that the main evolutionary pressure is minimization of mutation errors; moreover, it implies that similar amino acids are coded by similar codons.

- *The operational code*: It proposes an ancestral link between the operational code (which determines mainly in the acceptor stem the affinity with the cognate amino acid) and the genetic code (implemented with the codon–anticodon pairing).
- *The frozen accident*: It postulates a random origin of the codon assignation to amino acids and a successive evolution due to different evolutionary pressures, until a point in which any further modification becomes deleterious (determining the freezing of the code).

None of the approaches described above is centered on the degeneracy distribution as a key feature, degeneracy is more of a consequence than a property directly related to the physico-chemical origin of the code. But experience accumulated in physics has revealed that degeneracy of systems is usually associated with some symmetries. So, one can use the algebraic approach to decipher the structure that underlies the genetic code. Several attempts have been made to describe the codon degeneracy from mathematical standpoint (see Antoneli and Forger [2], Gonzalez *et al*. [17], Hornos and Hornos [21], Kwon *et al*. [29], Lehmann and Libchaber [30], Lenstra [31], Negadi [36], Rietman *et al*. [43], Schafer [45] and references therein). Assuming importance of the 8-dimensional normed algebra with $(3+4)$-splitting as an underline structure of nature, the question arises whether the degeneracy of the genetic code can also be related to symmetry properties of coding and decoding molecules and their possible stereo-chemical interactions.

An important branch of stereochemistry, which explores the relative spatial arrangement of atoms that form the structure of molecules and their manipulation, is the study of chiral molecules that lack a plane of symmetry and are, therefore, non-superimposable on their mirror images. Chiral molecules exist in two reflected structures that are often referred to as "left-handed" or "right-handed" molecules. It turns out, all amino acids found in living organisms (except for Glycine, which is not chiral) are left-handed. In addition to that, each of the four standard nucleotide bases of the genetic code, consist of deoxyribose – DNA's sugar, which is also chiral, but comes only in right-handed form. As it appears, nature uses only one form, left-hand amino acids and right-hand sugars to create life that we are familiar with today. This is sometimes called homochirality and it can be considered as an intrinsic property of all life forms. Thus, based on the chiral properties of both, cognate codons (anticodons) and encoded amino acids, there can be some physico-chemical affinity between the two (Koonin and Novozhilov [28]). Thus, particle physics suggests that one should consider the stereo-chemical theory as the leading model on origin and evolution of the code.

Note that the standard model of particle physics is also a chiral theory, where right- and left-handed fermions transform differently. Where does chirality come from, or why does homochirality dominate life forms are among the many important questions in science. We can only assume, that at some point, some kind of symmetry breaking must have occurred, which caused left-handedness and right-handedness to separate from each other and predominate in different structures. This is similar to the disturbance of the balance between matter and antimatter in the early universe, which finally has led to the dominance of matter. Moreover, as a result, only left-handed neutrinos exist, while antineutrinos are right-handed.

## 4. Particle Structures

The universe is built by information, objects in nature are distinct only by different arrangements of same underline fermion structures. In quantum field theory the role of the observer and information is central (Popper [41]), primary object is a field which exhibits itself in the form of discrete objects (particles) only under measurements. Elementary particles are just field excitations, which appear in space-time with some specific classical characteristics (like mass, charge or trajectory) in the process of obtaining information in terms of countable sets (bits).

According to the standard model of particle physics, the fundamental fermions that constitute the building blocks of matter in our universe are organized into three generations, each consisting of two leptons and two quarks (Griffiths [18]). This structure is reminiscent of the (3+4) pattern found in DNA, where three families of four fundamental fermions can be identified. This analogy suggests that split octonions and their automorphism group might play an important role in particle physics. For example, the Lorentz-type group $G_2^{NC}$, in addition to its association with DNA symmetries, can also be linked to spacetime symmetries (Gogberashvili and Sakhelashvili [16]).

It is noteworthy that visible matter, composed of particles that allow us to study information in terms of countable sets, constitutes less than 5% of the universe (Particle Data Group *et al*. [37]). This percentage can be loosely compared to the proportion of non-coding DNA, which plays a significant role in the creation of life as we know it today (Piovesan *et al*. [39]). While the exact figures may differ, with non-coding DNA comprising about 98% of the human genome, the analogy emphasizes the relatively small, yet crucial, role of visible matter and coding DNA in their respective domains.

In this section we want to indicate possible manifestations of split octonion symmetries in different structures of elementary particles.

### 4.1 Particle generations

The standard model of particle physics is very successful and has been tested by experiments with high precision. However, from the theoretical perspective, there still exist several puzzles, such as the origin of the fermion masses, their mixing and three generations structure. Between generations, particles differ by their flavour quantum number and mass, but their electric and strong interactions are identical. The flavor problem is the fact that the nature and principles behind the flavor sector are much less understood than those of the gauge sector (see, Zupan [52]). At present, it seems that we do not have a satisfactory theoretical framework to explain these phenomena and an extension of the standard model is believed to be necessary.

There have been several approaches to address the problem of generations beyond the standard model. A popular way is the introduction of the family symmetry – discrete or continuous, global or local (Grimus and Ludl [19], King and Luhn [26]). Continuous horizontal symmetries can be classified into three categories: Models with an abelian group $U(1)_F$, which naturally account for the hierarchical mass structures of the three chiral generations of quarks and leptons (Froggatt and Nielsen [12]); Models with non-abelian group symmetries, the most popular are $SU(2)_F$ (Barbieri *et al*. [5]) and $SU(3)_F$ (King and Ross [27]); a model with a noncompact non-abelian group symmetry $SU(1,1)_F$, which offers the opportunity to understand chiral generations of elementary particles and their hierarchical mass structures through spontaneous symmetry breaking (Inoue [23]). To address problems in flavor physics, finite groups (Wilson [49]) and large extra dimensions (Arkani-Hamed and Schmaltz [3]) have also been proposed. However, such extra symmetries or extra dimensions remain hypothetical.

Observations of symmetries of split octonions in different structures of nature suggest to consider $G_2^{NC}$ as the family symmetry group. Due to the unaccounted $SO(3)$ symmetry group present in $G_2^{NC}$, one can try to obtain three families of fermions by rotating the first generation of fermions in the octonionic space.

Note that, in general, it is problematic to consider a non-compact family symmetry group, like $SU(1.1)_F$ or $G_2^{NC}$, since for the non-compact case the quadratic form for a non-zero group elements can be negative or zero. This implies that certain quantum states will have a negative norm and are thus unhealthy. However, there are a few ways to handle the potential pathology: It can be introduced a selection rule which results in a zero overlap between the healthy and unhealthy (negative norm) states Becchi *et al*. [6], Margolin and Strazhev [33, 34]; the Killing form can be promoted to a dynamical field and given by a gauge covariant derivative (Cahill and Özenli [7], Cahill [8, 9], Julia and Luciani [25]); a variant of gauge can be considered, which removes some components and force the quadratic form to be positive definite (Alexander and Manton [1]). All these approaches share the common thread of projecting the healthy states into a maximal compact subgroup of the non-compact group.

## 4.2 Baryons as Codons

In elementary particle physics, baryons consist of three valence quarks, analogous to how genetic information is encoded using sets of three nucleotide letters in genetics. However, unlike codons, the arrangement of the structural elements within baryons is not fixed; there is symmetry with respect to permutations of quarks. Therefore, constructing an analogue of Table 1 for baryons is not relevant. Instead, baryons are categorized into multiplets based on their quantum numbers, similar to the presentation of amino acids in Table 2. This multiplet classification reveals that baryons exhibit a natural organization, where all members of the same multiplet interact strongly in the same way. This approach provides a coherent explanation for the observed baryon spectrum as bound states of three quarks (Griffiths [18]).

Given the facts, that the nature of excited baryons is still not properly understood and that they would be highly unstable, here we focus on ground state baryons (states of minimal energy), typically containing three quarks and exhibiting zero orbital angular momentum. In this context, the total angular momentum $J$ is formed solely by the spin values of the constituent quarks. Baryons composed of a single type of quark can exist in a $J = 3/2$ configuration, as $J = 1/2$ is prohibited by the Pauli exclusion principle. On the other hand, baryons composed of two types of quarks can exist in both $J = 1/2$ and $J = 3/2$ configurations. Additionally, baryons composed of three different types of quarks can also exist in both $J = 1/2$ and $J = 3/2$ configurations. Moreover, for these baryons, two distinct $J = 1/2$ configurations, differing in isospin, are possible.

There are six distinct types, or flavors, of quarks: $u$, $d$, $s$, $c$, $t$, and $b$, each characterized by unique mass and charge properties. While the composition of elementary fermions, whether they consist of three sub-components (preons) akin to nucleotides that are consisted of three elements (a sugar, nitrogenous base, and phosphate group), remains unknown, in the framework of quantum chromodynamics, each quark flavor is associated with three color charges. This property ensures the formation of baryons, analogous to quark-codons. However, it's important to note that $t$ and $b$ quarks are exceptionally heavy, and particles containing them are relatively rare. Baryons composed of $t$ quarks are not expected to exist due to the extremely short lifetime of this quark.

In the realm of genetic code, it has been discovered that there are also at least six nucleotide bases. In addition to the four standard bases used in Table 1, nonstandard P and Z nucleotides have been identified. To draw a parallel with the genetic code, we can present a table of baryons composed of the four lightest quarks (Table 3). These baryons fall into six distinct groups: nucleon ($N$), Delta ($\Delta$), Lambda ($\Lambda$), Sigma ($\Sigma$), Xi ($\Xi$), and Omega ($\Omega$) particles. Hyperons ($\Lambda$, $\Sigma$, $\Xi$ and $\Omega$ particles) contain one or more quarks from the second generation are heavier and shorter-lived compared to nucleons and are typically not present in atomic nuclei. However, they can be observed in short-lived hypernuclei.

**Table 3.** Baryons made up of the four lighter quarks

| # | Particle name and mass (GeV) | Quark content | Total angular momentum | Degeneracy |
|---|---|---|---|---|
| 1 | $N(0.94)$ | $\mathbf{p} = \mathbf{uud},\ \mathbf{n} = \mathbf{udd}$ | 1/2 | Doublet |
| 2 | $\Delta(1.23)$ | $\Delta^{++} = \mathbf{uuu},\ \Delta^{+} = \mathbf{uud},\ \Delta^{\mathbf{0}} = \mathbf{udd},\ \Delta^{-} = \mathbf{ddd}$ | 3/2 | Quartet |
| 3 | $\Sigma(1.19)$ | $\Sigma^{+} = \mathbf{uus},\ \Sigma^{\mathbf{0}} = \mathbf{uds},\ \Sigma^{-} = \mathbf{dds}$ | 1/2 | Triplet |
| 4 | $\Sigma^{*}(1.38)$ | $\Sigma^{*+} = \mathbf{uus},\ \Sigma^{*\mathbf{0}} = \mathbf{uds},\ \Sigma^{*-} = \mathbf{dds}$ | 3/2 | Triplet |
| 5 | $\Lambda^{0}(1.12)$ | $\Lambda^{\mathbf{0}} = \mathbf{uds}$ | $(1/2)'$ | Singlet |
| 6 | $\Sigma_c(2.45)$ | $\Sigma_{\mathbf{c}}^{++} = \mathbf{uuc},\ \Sigma_{\mathbf{c}}^{+} = \mathbf{udc},\ \Sigma_{\mathbf{c}}^{\mathbf{0}} = \mathbf{ddc}$ | 1/2 | Triplet |
| 7 | $\Sigma_c^{*}(2.52)$ | $\Sigma_{\mathbf{c}}^{*++} = \mathbf{uuc},\ \Sigma_{\mathbf{c}}^{*+} = \mathbf{udc},\ \Sigma_{\mathbf{c}}^{*\mathbf{0}} = \mathbf{ddc}$ | 3/2 | Triplet |
| 8 | $\Lambda_c(2.29)$ | $\Lambda_{\mathbf{c}}^{+} = \mathbf{udc}$ | $(1/2)'$ | Singlet |
| 9 | $\Xi(1.32)$ | $\Xi^{\mathbf{0}} = \mathbf{uss},\ \Xi^{-} = \mathbf{dss}$ | 1/2 | Doublet |
| 10 | $\Xi^{*}(1.53)$ | $\Xi^{*\mathbf{0}} = \mathbf{uss},\ \Xi^{-} = \mathbf{dss}$ | 3/2 | Doublet |
| 11 | $\Xi_c(2.47)$ | $\Xi_{\mathbf{c}}^{+} = \mathbf{usc},\ \Xi_{\mathbf{c}}^{\mathbf{0}} = \mathbf{dsc}$ | 1/2 | Doublet |
| 12 | $\Xi_c'(2.58)$ | $\Xi_{\mathbf{c}}'^{+} = \mathbf{usc},\ \Xi_{\mathbf{c}}'^{\mathbf{0}} = \mathbf{dsc}$ | $(1/2)'$ | Doublet |
| 13 | $\Xi_c^{*}(2.65)$ | $\Xi_{\mathbf{c}}^{*\mathbf{0}} = \mathbf{usc},\ \Xi_{\mathbf{c}}^{*\mathbf{0}} = \mathbf{dsc}$ | 3/2 | Doublet |
| 14 | $\Xi_{cc}(3.62)$ | $\Xi_{\mathbf{cc}}^{++} = \mathbf{ucc},\ \Xi_{\mathbf{cc}}^{+} = \mathbf{dcc}$ | 1/2 | Doublet |
| 15 | $\Xi_{cc}^{*}$ | $\Xi_{\mathbf{cc}}^{*++} = \mathbf{ucc},\ \Xi_{\mathbf{cc}}^{*+} = \mathbf{dcc}$ | 3/2 | Doublet |
| 16 | $\Omega(1.67)$ | $\Omega^{-} = \mathbf{sss}$ | 3/2 | Singlet |
| 17 | $\Omega_c(2.70)$ | $\Omega_{\mathbf{c}}^{\mathbf{0}} = \mathbf{ssc}$ | 1/2 | Singlet |
| 18 | $\Omega_c^{*}(2.77)$ | $\Omega_{\mathbf{c}}^{*\mathbf{0}} = \mathbf{ssc}$ | 3/2 | Singlet |
| 19 | $\Omega_{cc}$ | $\Omega_{\mathbf{cc}}^{+} = \mathbf{scc}$ | 1/2 | Singlet |
| 20 | $\Omega_{cc}^{*}$ | $\Omega_{\mathbf{cc}}^{*+} = \mathbf{scc}$ | 3/2 | Singlet |
| 21 | $\Omega_{ccc}$ | $\Omega_{\mathbf{ccc}}^{++} = \mathbf{ccc}$ | 3/2 | Singlet |

From Table 3, it's evident that baryons composed of the four lightest quarks are categorized into 21 distinct classes based on their composition. Baryons in the $J = 3/2$ configuration that have the same symbols as their $J = 1/2$ counterparts are denoted by an asterisk ($^*$). Additionally, to distinguish baryons that are made of three different quarks in $J = 1/2$ configuration, the prime ($'$) is used.

The degeneracy in the mass of these multiplets arises from the spin values of the quarks. This arrangement of particles bears resemblance to the DNA coding system depicted in Table 2, where 21 different amino acids found in the human body are encoded by triplets formed from the four standard nucleotides. In both cases 21 fundamental triplets are degenerate, but multiplets differ in numbers. Despite these similarities, there are notable differences between the two systems. In the genetic code, there are four nucleotide bases, and almost all combinations are utilized for coding. Additionally, there is no symmetry with respect to base transmissions within the codon. In contrast, for baryons, only the composition of quarks matters, rather than their arrangement. This means that baryons with different quark permutations, such as $uud$ and $duu$, are considered identical.

## 4.3 DNA Model for Atomic Nuclei

The best-known baryons are nucleons that make up all atomic nuclei from the Mendeleev periodic table, which are carriers of chemical information and can be considered as some kind of DNA molecules built with 'nucleon codons' (protons and neutrons). We hope that by comparing some general properties of DNA and nuclei one can find glues in unsolved problems of these structures.

DNA is generally double stranded so that, due to extra bonds between chains, it is more stable and less reactive. We have no evidence about possible pairings of protons and neutrons inside nuclei and forming of a chain, or 'nuclear polymer' (see the model [40]). At low energies (1-10 MeV), most of the approaches (Shell model, Interacting boson model, Mean field model, Collective models) assume that nucleons in a nucleus mostly behave like stable units, they do not melt together into a collection of quarks. Quarks forming the neutron are intermediary between the protons and this bonding (as in the case of DNA) is proposed as the reason for neutron stability within the nucleus, whereas free neutrons are unstable particles.

In nuclear physics there are so-called magic numbers of neutrons and protons which confer to the corresponding nuclei a particularly stable configuration [46]. To explain magic numbers usually the mean field approach of nucleon-nucleon two-particle interactions is used, but only the two smallest magic numbers (8 and 20) could be explained from solutions of simple potential wells. A fundamental understanding of magic numbers for protons and neutrons may be achieved if the underlying corresponding symmetry of the nuclear many body system is determined. For example, one can try to define some analogies of stop codons for nuclei.

In genetic code there are 3 special codons that mainly function as stop signals and therefore are called stop codons. These codons are the last ones of the long, protein defining codon sequences, so they basically mark the end of the information. Shifts in nucleotide bases can occur during the transcription or translation processes, potentially leading to incorrect sequences of codons and the production of undesirable proteins. The presence of multiple stop codons helps prevent such errors, ensuring that cells do not produce undesirable proteins and thereby conserve energy. Magic numbers can also be considered from the same point of view. Shell model suggests the structure of the nucleus in terms of energy levels and describes magic numbers as the numbers of nucleons in the nucleus corresponding to complete shells. Atomic nuclei consisting of such a magic number of nucleons (either protons, neutrons or in the most special case - both) are very stable and have much larger binding energy then neighboring nuclei, meaning, these particular combinations of quarks create the most desirable - minimal energy states for the nucleus.

Based on the similarities discussed above, one can consider the DNA model of nuclear, where the magic numbers could serve as the stop codons.

## 5. Conclusion

To summarize, in this paper we have suggested that algebraic language could be a fundamental way for describing the basic features of the universe, in particular, we have demonstrated the importance of 8-dimensional algebras in the fields of genetics and particle physics. In the structures of DNA and fundamental fermions we observed the resemblance between the coding systems, more precisely, three and four element divisions which is the manifestation of the symmetry of 8-dimensional normed split-algebra having (3+4)-signature for its hypercomplex units. Some comparisons between the genetic code and classification of all possible baryons are made. In both cases, we are able to specify 21 basic triplets (codons and baryons) with corresponding degeneracies that encode information. Finally, the possible use of those observed analogies for various problems in particle physics and genetics is emphasized.

### Competing Interests

The authors declare that they have no competing interests.

### Authors' Contributions

All the authors contributed significantly in writing this article. The authors read and approved the final manuscript.

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