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The 24 Possible Algebraic Representations of the Standard Genetic Code in Six or in Three Dimensions

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Abstract

Herein, we analyze the 24 different ways of constructing a 6-dimensional binary vector space, or a 3-dimensional $\mathrm{GF}(4)-$vector space of the 64 triplets of the Standard Genetic

Code (SGC), where $\mathrm{GF}(4)$ is the Galois Field of four elements. We also analyze the transformations that lead any model into each of the remaining ones. In all the cases the definition of a given ordering begins with a matching of the set $\mathrm{N}=\{\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G}\}$ of the four nucleotide RNA bases with the set $\mathbb{Z}_2\times\mathbb{Z}_2=\{00,01,10,11\}$ of the four binary duplets. Since the set N can be endowed with the structure of the Galois Field $\mathrm{GF}(4)$, which is an algebraic extension of degree two of the binary field $\mathbb{Z}_2$, the 6-dimensional $\mathbb{Z}_2-$hypercube NNN becomes a 3-dimensional $\mathrm{GF}(4)-$vector space, which can be inserted in the Euclidean $\mathbb{R}-$space $\mathbb{R}^3$ as a multicube. The set N may be partitioned into two disjoint binary classes in three different ways, according to chemical criteria: strong-weak, amino-keto and pyrimidine-purine. Here, we show that for each of these classifications, there are eight different associated orderings and each of them leads to a different 6-dimensional binary hypercube or to a different 3-dimensional multicube over the field $\mathrm{GF}(4)$. We use the Hamming distance, $\mathrm{H},$ in the 6-dimensional vector space and the Manhattan distance, $\mathrm{M},$ in the 3-dimensional $\mathrm{GF}(4)$-vector space. The SGC is found to exhibit an exact symmetry under a Galois field of 4 elements $\mathrm{GF}(4),$ which is the so-called Klein four-group. The Klein four-group emerges naturally from the simplest model for the prebiotic evolution that has led to the SGC. Then the hypothesis that this symmetry has been selected since the origin and during the evolution of the genetic code is strengthened.

Keywords: Standard Genetic Code, Algebraic representations, Group Theory, Galois Group, Klein 4-group, Symmetry breaking, Evolution

1. Introduction

The genetic material of living organisms is stored in DNA or RNA molecules. Linear sequences of DNA or RNA called protein coding regions contain information about protein synthesis. The Standard Genetic Code (SGC) is used by cellular mechanisms to decode this information. The SGC is almost universal and the correspondence of codons (words of three nucleotides) with amino acids was deciphered almost 5 decades ago [1]. The SGC possesses punctuation signals: one start codon and three stop codons. Traditionally, the SGC has been represented as a table of three entries in two dimensions [4]. However, a spatial representation of the triplet code includes the information about vicinity of the codons [6-7, 9], and it facilitates the study of symmetries. A 3-dimensional spatial structure of the triplets code was used to describe the smoothest energy gradient relating it to mutational pathways [14]; also, the genetic code was related to a gray code to study the development of the SGC [23]; the binary structure of a gray code led to the idea of a 6-dimensional hypercube which has been used to study the molecular evolution of the SGC

[7], the relationship between codon assignment and physicochemical characteristics of amino acids [18, 20] and how the primeval RNA code could have evolved to generate the SGC [10-12]. In a previous work [10], 3-dimensional algebraic models were rigorously derived in order to represent the Standard Genetic Code (SGC). They were dubbed Genetic Hotels of codons and the Phenotypic Hotel of amino acids. These models were used to test hypothesis about the evolution of the SGC. A model for topological coding of chain polymers was applied to investigate the nature of triplet-amino acid assignment [13]. The search for symmetries led to the Lie group theory [7], and a Lie algebra was associated with the physicochemical properties of amino acids, codon assignments and single point mutation in genes [19].

Different ways in which an algebraic structure of a binary 6-dimensional vector space in the set of the 64 triplets of the SGC can be constructed have been used [7, 10-14,18-,20,22] (see Table I).

Table I

Orderings				**Partition**	**References**
00	01	10	11		
U	C	A	G	$\wp_2$	Swanson [23]
A	G	U	C	$\wp_2$	Jiménez-Montaño *et al.* [9]; Klump [14]
C	U	G	A	$\wp_2$	Karasev and Soronkin [13]
U	C	G	A	$\wp_1$	Stambuk [22]
C	A	U	G	$\wp_1$	Stambuk *et al* [22]*;* José *et al.* [10]
C	U	A	G	$\wp_1$	Sánchez *et al*. [18-20]; José *et al.* [11-12]
G	A	U	C	$\wp_1$	Sánchez *et al.* [18-20]
G	U	A	C	$\wp_1$	Sánchez *et al.* [19]
A	U	C	G	$\wp_3$	Jiménez-Montaño *et al.* [8]

In all the cases, the definition begins with a matching of the set N of the four nucleotide RNA bases with the set $\{00, 01, 10, 11\}$ of the four binary duplets. The 3-dimensional geometrical representation that naturally emerges from the interpretation of the duplets $00, 01, 10,$ and 11 as the binary representation of the integers $0, 1, 2,$ and 3 in the base -4 numerical system, and its matching with the set N, has been recently exploited [11, 19]. Potentially these matchings can be performed in $4! = 24$ different ways. Although some authors explain their reasoning for choosing a specific match, it has been tacitly assumed that any ordering can lead to the same results. Actually, all the possible hypercubes are isomorphic and isometric with the hypercube $(\mathbb{Z}_2)^6$, and all the possible multicubes are isomorphic and isometric with the multicube $(\mathrm{GF}(4))^3$ and, both isomorphism and isometry are transitive relations. Therefore, we can assert that all the obtained hypercubes and multicubes are, respectively, not only pairwise isomorphic but also pairwise isometric.

Herein, we analyze the 24 different ways of carrying out these constructions, in six dimensions as well as in three dimensions, together with the transformations that lead from any model into each of the remaining ones. In this work, we pose the following questions**:** Do the 24 permutations of an arbitrarily chosen primary order induce isometric transformations of the original hypercube, with respect to its Hamming (6-dimensional) or Manhattan distance (3-dimensional)? Do they induce isomorphic affine transformation of that hypercube? Are there different subsets of the 6-dimensional or of the 3-dimensional representations of the 64 triplets, isometric and isomorphic to themselves when the transformations are performed?

The article is organized as follows. First, we present how the SGC can be viewed as an additive group and as a binary vector space. We also provide the mathematical basis for examining the effect of a permutation of the set $\mathrm{N}=\{\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G}\}$ over the algebraic representations of the Cartesian product $\mathrm{N}\times\mathrm{N}\times\mathrm{N}$ of the 64 codons. Secondly, we describe the three binary partitions of the set N according to chemical criteria. We depict how the mutations can be represented by translations. We show how to transform a given ordering into another, and we examine the isometries and isomorphisms. We found that the 24 algebraic representations of the SGC can be divided into 6 families of 4 pairwise isometric 6-dimensional hypercubes. We also examine the lattice structure of both models in six and three dimensions. The symmetry groups of both models are indicated. Finally, the results are discussed in terms of their potential use in order to understand the fundamental properties of the SGC.

2. Theoretical Background

2.1. *The SGC viewed as an additive group and as a binary vector space*

The bitwise modulo two addition, or XOR operation, in the set $\{00,01,10,11\}$ of the four binary duplets, induces in the set $\mathrm{N}=\{\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G}\}$ a structure of Abelian group. Consequently, the addition in N induces an addition in the Cartesian set $\mathrm{N}\times\mathrm{N}\times\mathrm{N}=\mathrm{NNN}$ of the 64 triplets, which, together with the obvious definition of the product of the scalars 0 and 1 by the triplets, conforms a structure of a 6-dimensional vector space over the binary field $\mathbb{Z}_2=\{0,1\}$, isomorphic to the $\mathbb{Z}_2$ - vector space $(\mathbb{Z}_2)^6$, also called the 6-dimensional hypercube. As it is well-known, it has also a structure of a Boolean lattice or Boolean algebra [8, 9].

Different hypercubes are determined by the initial matching between nucleotides and duplets. Depending on which element of N is assigned to the duplet 00 it is possible to obtain four families of different Abelian group $(\mathrm{N},+)$, although they are isomorphic one to each other. Each family of six tables with the same neutral element, define in essence, the same Abelian group. The $6=3!$ permutations of the set $\mathbb{Z}_2\times\mathbb{Z}_2=\{(0,0),(0,1),(1,0),(1,1)\}$, which fix the null element, can be envisaged as linear automorphisms of it as a $\mathbb{Z}_2-$vector space. These automorphisms can be represented by the six 2×2 binary matrices: $\mathrm{I}_2=\begin{pmatrix}1&0\\0&1\end{pmatrix}$, $\mathrm{A}_{12}=\begin{pmatrix}1&1\\0&1\end{pmatrix}$, $\mathrm{A}_{21}=\begin{pmatrix}1&0\\1&1\end{pmatrix}$, $\mathbf{P}_{12}=\begin{pmatrix}0&1\\1&0\end{pmatrix}$, $\mathrm{A}_{12}\,\mathrm{A}_{21}=\begin{pmatrix}0&1\\1&1\end{pmatrix}$, and $\mathrm{A}_{12}\mathrm{P}_{12}=\begin{pmatrix}1&1\\1&0\end{pmatrix}$. They comprise the so-called linear group $\mathrm{GL}_2(\mathbb{Z}_2)$, that is, the group of all the invertible 2×2 binary matrices. From them, only I_2 and P_{12} represent linear isometries with respect to the Hamming distance. Hence, they form the orthogonal linear group $\mathrm{O}_2(\mathbb{Z}_2)$, which consists of the orthogonal matrices, that is, the matrices whose inverses are their transposes. Compositions of the six automorphisms with the four translations: T_{00}, T_{01}, T_{10}, and T_{11}, give rise to the 24 affine transformations of the vector space $\mathbb{Z}_2\times\mathbb{Z}_2$. Curiously, in this particular case, the $4!=24$ permutations of the set $\mathbb{Z}_2\times\mathbb{Z}_2$, are affine transformations. This means that the affine group $\mathrm{Aff}(\mathbb{Z}_2\times\mathbb{Z}_2)$, coincides with the whole symmetric group, $\mathrm{Sym}(\mathbb{Z}_2\times\mathbb{Z}_2)$ of all the bijections.

The Klein four-group emerges naturally on the set of the four bases (see Table II). This is an Abelian group in which every element, different of the neutral, has order 2 [1, 21]. It means that every element is its own inverse, and that the sums of complementary DNA bases, the so-called Watson-Crick base pairs, are constant. That is, $X\oplus X=\mathrm{C}$, for all $X\in\{\mathrm{C,G,U,A}\}$, and $\mathrm{C}\oplus\mathrm{G}=\mathrm{A}\oplus\mathrm{U}=\mathrm{G}$. All the Klein four-groups are pairwise isomorphic. Actually, the Klein four-group is the smallest finite group that is not cyclic, but it arises from the direct product of 2 binary cyclic groups. Then, the direct product $(\mathbb{Z}_2)^2=\mathbb{Z}_2\times\mathbb{Z}_2$, with addition operation modulo 2, is its canonical group theoretical representation. The Klein four-group has the property that every binary set that contains the null element, defines a binary subgroup. It means that the two classes of any of the three binary partitions (see below) are the member classes of the factor group over the binary subgroup that contains the null element. The Klein four-group can also be visualized as a 2-dimensional binary vector space, which is isomorphic to $(\mathbb{Z}_2)^2=\mathbb{Z}_2\times\mathbb{Z}_2$ as a $\mathbb{Z}_2-$vector space**.** It also has the property that any permutation of its three non-null elements behaves as an automorphism, that is, a bijective endomorphism. It is equivalent to the fact that any ordered pair of non-null elements is a basis of the vector space, two of them being the only orthonormal basis in regard to the Hamming inner product.

The question about isometry is related to the type of distance or metric we are dealing with. In the 6-dimensional structure of the $\mathbb{Z}_2-$vector space the Hamming distance H is used. This distance, provides to the hypercube $(\mathbb{Z}_2)^6$ a structure of metric space, and it induces a distance in the $\mathbb{Z}_2-$vector space NNN. The Hamming distance induces in $(\mathbb{Z}_2)^6$ an $\mathbb{R}-$valued inner product, $\mathbb{R}$ being the field of real numbers, and hence it carries over the property of orthogonality or perpendicularity.

Table II

Addition Cayley Table of N of the Klein four-group as determined by the ordering (CUAG).

+	C	U	A	G
C	C	U	A	G
U	U	C	G	A
A	A	G	C	U
G	G	A	U	C

2.2. *Three dimensional representation of the genetic code*

A 3-dimensional algebraic model of the SGC naturally emerges from the facts that $4^3 = 2^6 = 64$ and that there is a field of 4 elements which is an extension of the binary field $\mathbb{Z}_2$. A 3-dimensional representation of the SGC is easy to visualize and pedagogical for several purposes. The interpretation of the duplets 00, 01, 10 and 11 as the binary representation of the integers 0, 1, 2 and 3, in the base-4 numerical system, turns out into a bijection between the set N and the set $\{0,1,2,3\}$ and it allows us to insert the set $\mathrm{N}^3 = \mathrm{NNN}$ as a subset of the Euclidean 3-dimensional $\mathbb{R}-$space, $\mathbb{R}^3 = \mathbb{R}\times\mathbb{R}\times\mathbb{R}$ [19].

If the set of the 4 nucleotide bases of the Standard Genetic Code (SGC) is denoted by $\mathrm{N} = \{\mathrm{C}, \mathrm{A}, \mathrm{U}, \mathrm{G}\}$, then the set of the 64 codons or triplets can realized as the Cartesian power $\mathrm{N}^3 = \mathrm{N}\times\mathrm{N}\times\mathrm{N}$, which we will briefly represent as NNN. The ordered triple $(\mathrm{N},+,\times)$ is, up to isomorphisms, the so-called Galois Field $\mathrm{GF}(4)$, of 4 elements. In that way, the set NNN of the triplets of the SGC becomes a 3-dimensional vector space over the Galois Field $\mathrm{N} = \mathrm{GF}(4)$ and, at the same time, it remains to be a 6-dimensional vector space, over the binary field $\mathbb{Z}_2$, which is isomorphic to the prime subfield $(Y,+,*)$ of the Galois Field $(N,+,\times) \sim GF(4)$. We see that the set NNN of the 64 triplets, identified with the $\mathbb{Z}_2-$vector space $(\mathbb{Z}_2)^6$, is also an $N-$vector space over the Galois Field $N = GF(4)$, which is an algebraic extension of degree 2 of the binary field $\mathbb{Z}_2$.

In our work [11], the $\mathbb{Z}_2-$hypercube NNN was derived as a 3-dimensional vector space over the Galois Field GF(4) of 4 elements, and the obtained field was shown to be an algebraic extension of degree 2 of the binary field $\mathbb{Z}_2$ of 2 elements. It is, up to isomorphism, the so-called Galois Field GF(4) of four elements. Since the set N has the structure of the Galois Field GF(4), the 6-dimensional $\mathbb{Z}_2-$hypercube NNN becomes a GF(4) 3-dimensional vector space. Geometrically, we get a cube or regular hexahedron, with three of its edges lying over the coordinated axis. This cube has edges of length 3 and it is the union of 27 unitary cubes. For this reason it will be called the mutlicube NNN. The Manhattan distance [19] also known as Taxi-cab [15], distance provides to the cube a structure of metric space.

2.2.1. *A note about the hypercube* $(\mathbb{Z}_2)^6$ *and the multicube* $(GF(4))^3$

A convex set in the Euclidean vector space $\mathbb{R}^n$, is a set S such that, for any points A and B, the closed segment between A and B, that is, the set $\{P \in \mathbb{R}^n \mid P = (1-\alpha)A + \alpha B\}$, where α is a real number, such that $0 \le \alpha \le 1$, is entirely contained in S. The 6-dimensional hypercube is actually the convex hull, in the Euclidean vector space $\mathbb{R}^6$ of the finite set $(\mathbb{Z}_2)^6$ of its 2^6 vertexes. The convex hull of any set S is the least convex set that contains S, that is, the intersection of all the convex sets that contain S. Analogously, the actual 3-dimensional multicube is the convex hull, in the Euclidean vector space $\mathbb{R}^3$, of the finite set $(GF(4))^3$ of its 4^3 vertexes or triplets (X,Y,Z) where $(X,Y,Z) \in \{0,1,2,3\}$.

2.4. *Effect of a permutation of the set* N *over the algebraic representations of the set* NNN *of the 64 codons*

Let $f: N \to (\mathbb{Z}_2)^2$ a bijective function, that is, a matching between the sets N and $(\mathbb{Z}_2)^2$. This function induces a bijection $F: NNN \to ((\mathbb{Z}_2)^2)^3 \simeq (\mathbb{Z}_2)^6$ between the sets NNN and $(\mathbb{Z}_2)^6$, which is a representation of every codon or triplet XYZ of NNN as a sextuple $\alpha = (\alpha_1,\alpha_2,\alpha_3,\alpha_4,\alpha_5,\alpha_6)$, of zeros and ones, where $f(X) = (\alpha_1,\alpha_2)$, $f(Y) = (\alpha_3,\alpha_4)$ and $f(Z) = (\alpha_5,\alpha_6)$. The triplet XYZ can be envisaged as a literal label of the point $\alpha = (\alpha_1,\alpha_2,\alpha_3,\alpha_4,\alpha_5,\alpha_6)$ in the hypercube $(\mathbb{Z}_2)^6$, which we can be viewed as a subset of the 6-dimensional Euclidean vector space $\mathbb{R}^6$. The binary components α_i of the vector α are the coordinates of the triplet XYZ under the assignment F.

Let $\boldsymbol{\pi}$ be a permutation of the set N, that is, a member of the symmetric group S(N) of all the bijections of N with itself. In a natural way $\boldsymbol{\pi}$ induces a permutation Π of the set NNN. As Π and F are bijective functions, the composition $F \circ \Pi$ is a bijective function from NNN onto the hypercube $(\mathbb{Z}_2)^6$, which assigns to the triplet XYZ another sextuple of zeros and ones. Obviously, the composition $F \circ \Pi = \bar{\Pi} \circ F^{-1}$ is a permutation $\bar{\Pi}$ of the set $(\mathbb{Z}_2)^6$ of all the binary sextuples.

2.4.1 *Two possible interpretations for the transformation* $F \circ \Pi = \bar{\Pi} \circ F^{-1}$

The permutation Π can be envisaged as a motion inside the set NNN, that is, a change of position of every triplet that is converted into another element of the set, which has other coordinates. Then, the function $F \circ \Pi$ assigns to every triplet the coordinates of its images under the motion Π. On the other hand, the permutation $\bar{\Pi}$ performs a change of the coordinates F(XYZ) of every original triplet XYZ. The same happens in ordinary analytic geometry, where a transformation can be interpreted as a motion, a change of position of every point, or as a change of coordinates, referring it to another referential system. These two interpretations are known as “alibi” (change of place), or “alias” (change of name).

The bijections F and f, can be interpreted as identifications of the set NNN with the set $(\mathbb{Z}_2)^6$, and of the set N with the set $(\mathbb{Z}_2)^2$, respectively, as if they were their corresponding identity functions. Then Π and $\bar{\Pi}$ would be the same permutation, of the same set, and with this approach it is very clear the double interpretation of Π as a motion (alibi), or as a change of coordinates (alias).

As the 24 permutations $\boldsymbol{\pi}$ of the set N can be interpreted as affine transformations with respect to the $\mathbb{Z}_2$ – vector space structure, then the 24 permutations Π induced by them, would be affine transformations of the $\mathbb{Z}_2$ – vector space NNN, respectively, of the $\mathbb{Z}_2$ – vector space $(\mathbb{Z}_2)^6$.

In the same way, we can assert that only 12 out of the 24 permutations of the set N of the set GF(4), can be interpreted as affine transformations with respect to the GF(4) – vector space structure, namely, those of the form $X \to \alpha X + \beta$, with α and β elements of $\mathbb{Z}_4$ with $\alpha \neq 0$. Then, only the 12 permutations Π induced by them, would be affine transformations of the GF(4) – vector space NNN, of the GF(4) – vector space $(GF(4))^3$.

2.5. The three binary partitions of the set N

It is well known that a set of 4 elements has exactly three different partitions as union of two subsets, each of two elements. In the case of our set $\mathrm{N}=\{\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G}\}$ the only three partitions are: $\wp_1=\{\{\mathrm{C},\mathrm{G}\},\{\mathrm{U},\mathrm{A}\}\}$, $\wp_2=\{\{\mathrm{C},\mathrm{A}\},\{\mathrm{U},\mathrm{G}\}\}$ and, $\wp_3=\{\{\mathrm{C},\mathrm{U}\},\{\mathrm{A},\mathrm{G}\}\}$. For every selected ordering we will use the correspondence of a partition of N with the partition of the set $(\mathbb{Z}_2)^2=\{00,01,10,11\}$, as determined by algebraic complementarity. We understand by algebraic complementarity, the one that exists between 2 duplets of zeros and ones, when each is the bitwise Boolean negation of the other one. Then, the partition of $(\mathbb{Z}_2)^2=\mathbb{Z}_2\times\mathbb{Z}_2$ by algebraic complementarity is $\{\{00,11\},\{01,10\}\}$. The three partitions are related to chemical properties of the nucleotides. The partition $\wp_1$ corresponds to the biological classification of nucleotide bases in strong $\mathrm{S}=\{\mathrm{C},\mathrm{G}\}$ (those which form three hydrogen bonds between them), and weak $\mathrm{W}=\{\mathrm{U},\mathrm{A}\}$ (those which form two hydrogen bonds between them). In the case of $\wp_2$, algebraic complementarity is consistent with the chemical classification of nucleotides into amino nucleotides: $\mathrm{M}=\{\mathrm{C},\mathrm{A}\}$, and keto nucleotides: $\mathrm{K}=\{\mathrm{U},\mathrm{G}\}$. Finally, if $\wp_3$ is used, algebraic complementarity is assigned to nucleotide bases of the same chemical kind: pyrimidines $\mathrm{Y}=\{\mathrm{C},\mathrm{U}\}$ and purines $\mathrm{R}=\{\mathrm{A},\mathrm{G}\}$. A selected list of the different matchings that have been used according to this chemical categorization of the bases is provided in Table I. The matchings associated to $\wp_3$ have been used in [8].

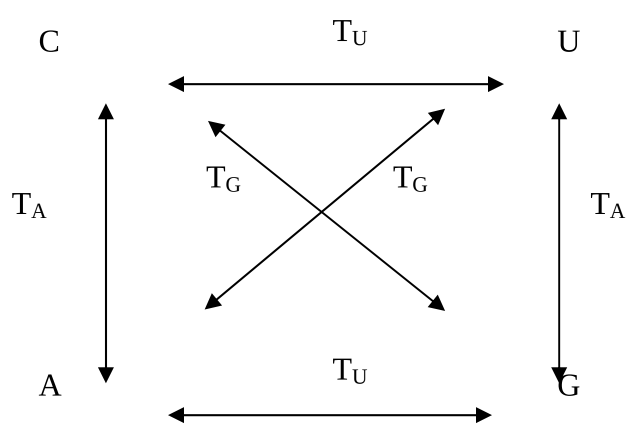
2.6. The role of translations as representative of mutations

In any additive group $(\mathbb{G},+)$ a translation is a transformation of the form: $\mathrm{T_X}:\mathrm{Y}\to\mathrm{Y}+\mathrm{X}$, X being a fixed element of $\mathbb{G}$. Obviously, the translation $\mathrm{T_0}$, associated to the neutral element is the identity function $\mathrm{I}_{\mathbb{G}}$ of $\mathbb{G}$. Every translation is a bijective function and the set $\mathrm{T}(\mathbb{G})$, of all the translations in $\mathbb{G}$, is closed under the composition. In fact, the ordered pair $(\mathrm{T}(\mathbb{G}),\circ)$, where $\circ$ denotes the composition of functions, is an Abelian subgroup of the symmetric group $(\mathrm{S}(\mathbb{G}),\circ)$, of all the bijective transformations of the set $\mathbb{G}$. The correspondence $\mathrm{X}\to\mathrm{T_X}$ is an injective homomorphism from $(\mathbb{G},+)$ into its symmetric group $(\mathrm{S}(\mathbb{G}),\circ)$, being the group $(\mathrm{T}(\mathbb{G}),\circ)$ of translations the image of this homomorphism. Then, every Abelian group is isomorphic to its own group of translations.

One of the mechanisms leading to biological evolution involves punctual mutations which consist in the substitution of any nucleotide base by another one from the set N. When a pyrimidine is replaced by the other pyrimidine, or a purine by the other purine, the mutation is called *transition*. When a pyrimidine is changed to a purine, or vice versa, the mutation is called a *transversion*. There are two different kinds of transversions: first, those that convert a nucleotide to another of the same class according to the partition $\wp_2$ (the amino-keto classification), and second, those that convert a nucleotide to another of the same class according to the partition $\wp_1$ (the strong–weak classification). Then, the latter are transformations that convert nucleotides into their complementaries.

The 4 possible translations may represent each one of these mutations. Different matching between N and the set $\{00, 01, 10, 11\}$ will generate different notations for the respective translations. The identity $\mathrm{I_N}$, the translation corresponding to the null element, preserves pointwise the structure of the three partitions $\wp_1$, $\wp_2$ and $\wp_3$ of N. Diagram I illustrates the three non-trivial translations corresponding to the Klein Group Cayley table (see Table II). The translation $\mathrm{T_U}$, represented by horizontal lines performs transitions, that preserve the members of the partition $\wp_3$, of the pyrimidine-purine classification, but interchanges the members of the other two partitions $\wp_1$ and $\wp_2$. Translations $\mathrm{T_A}$, represented by vertical lines, perform transversions, which preserve the members of the partition $\wp_2$, of the amino–keto classification, and interchange the members of the other two partitions $\wp_1$ and $\wp_3$. The translations $\mathrm{T_G}$, represented by diagonal lines, perform also transversions but they preserve the members of the partition $\wp_1$, of the strong-weak classification, and interchanges the members of the other two partitions $\wp_2$ and $\wp_3$. Note that, the four translations preserve the set $\{\wp_1, \wp_2, \wp_3\}$ of the three partitions $\wp_1$, $\wp_2$, and $\wp_3$. In Diagram I, the actions of the three non-trivial translations are pointed out. Note that one of them, $\mathrm{T_U}$, performs a transition and the other two perform transversions.

Diagram I



__2.7.__ The concept of orbit in Group Theory

When a group $\mathbf{G}$ is operating over a set E, as a group of transformations of E, we call orbit of an element x of E, the set of all the elements that are images of x under the action of $\mathbf{G}$. The set of orbits is a partition of E associated to the equivalence relations determined by the action of $\mathbf{G}$. Two elements are equivalent under this action if each is the image of the other under a transformation determined by $\mathbf{G}$.

__2.8.__ A comment about the lattice structure of both models

A lattice is a partially ordered set where every binary subset $\{x,y\}$ has a least upper bound, denoted as $x\vee y$, and a greatest lower bound, denoted as $x\wedge y$. When the two binary operations $\vee$ and $\wedge$ are distributive, each one with respect to the other, the lattice is called a distributive lattice.

If a lattice has a maximum M and a minimum m, it is said that some element x' is a complement of the element x if $x\vee x'=\mathrm{M}$ and $x\wedge x'=\mathrm{m}$. If, in a lattice, with maximum and minimum, every element has a complement, it is called a complemented lattice. A distributive and complemented lattice is called a Boolean lattice.

A very well known fact is that every hypercube $(\mathbb{Z}_2)^n$ is also a Boolean lattice, where the partial order amongst vectors is the component-wise partial order induced by the numerical order $0<1$. The lattice operations are the bitwise logic operations $\vee$, $\wedge$ which in Logic are known as disjunction (the <u>or</u>), and conjunction (the <u>and</u>) operations. Then, $x\vee y$, and $x\wedge y$ are, respectively, the supremum and infimun of the unitary or binary set $\{x,y\}$. In other words, $x\vee y$ and $x\wedge y$ are, respectively, the least upper bound and the greatest lower bound of the set $\{x,y\}$. In particular, the set $\mathrm{N}=(\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G})$ of the four nucleotides is a Boolean lattice, where G and C are the maximum and the minimum, respectively, while U and A are not comparable, in regard to the partial order.

On the other hand, in the 3-dimensional model, that is, the $\mathrm{GF}(4)-$vector space $(\mathrm{GF}(4))^3$, the partial order is the one induced by the linear order $\mathrm{C}<\mathrm{U}<\mathrm{A}<\mathrm{G}$, associated to its numerical order $0<1<2<3$, under the choice of CUAG as the starting order of the four nucleotides. In this case, the lattice operations in the set $\mathrm{N}=(\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G})$ would be $x\vee y=\max\{x,y\}$ and $x\wedge y=\min\{x,y\}$. Then, the ordered pair $\left((\mathrm{GF}(4))^3,\leq\right)$ as a partially ordered set is a distributive, but not a complemented lattice. Then, it is not a Boolean lattice. But in $\mathrm{N}=(\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G})$ we have another kind of complement. It is induced by the complementation defined in the set $(\mathbb{Z}_2)^2=\{00,01,10,11\}=\{0,1,2,3\}$, and is defined as $x'=3-x$. It follows that 0 with 3, and 1 with 2 are complements, one to each other. This coincides with the above definition of algebraic complementation. We observe that this complementation coincides with the operation of bitwise of bitwise logic negation in $(\mathbb{Z}_2)^2$, and it is also logic negation in the set $\{0,1,2,3\}$, if we see it as a Four-valued logic [2]. For this kind of logic model, 0 represents falsity, 3 represents absolute veracity, while 1 and 2 represent relative veracity, with degrees of certainty 1/3 and 2/3, respectively. This kind of complementation, which is not a Boolean complementation, induces a non-Boolean complementation in the distributive lattice $((\mathrm{GF}(4)^3,\leq)$. We also observe that in the multicubes NNN, obtained from the orderings associated to partition $\wp_1$, complementation in the distributive lattice coincides with biological complementation, that is, the relation codon-anticodon. The distributive lattice $((\mathrm{GF}(4)^3,\leq)$ contains a sub-lattice which is homomorphic image of the Boolean lattice $((\mathbb{Z}_2)^6,\leq)$, where the number of vertexes is the same but it is not so with respect to the number of arcs, having the lattice $((\mathrm{GF}(4)^3,\leq)$ a greater number.

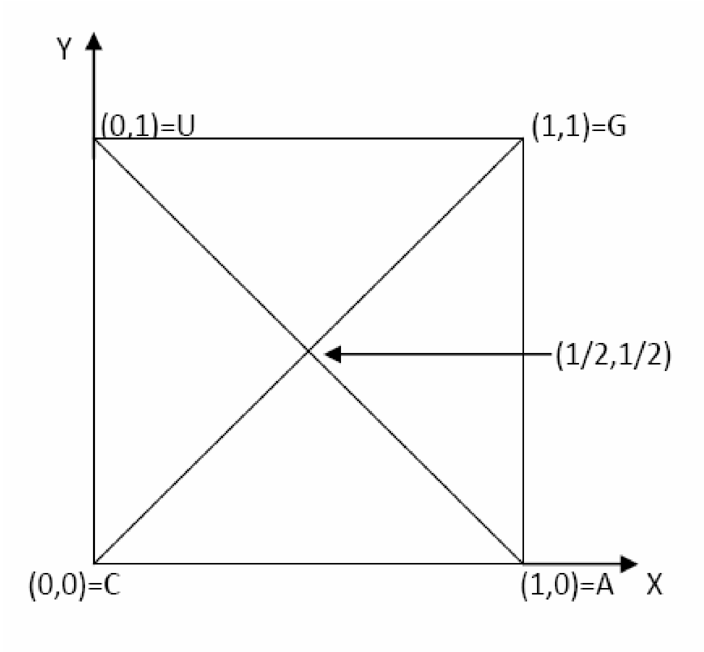
3. Results

3.1. Transforming one ordering into another, isometries and isomorphisms

In this work, our initial matching is $\mathrm{C}\leftrightarrow 00,\ \mathrm{U}\leftrightarrow 01,\ \mathrm{A}\leftrightarrow 10,,\ \mathrm{G}\leftrightarrow 11.$ It means that we select the primary ordering as CUAG. The matching of the Abelian group $(\mathrm{N},+)$ with the 2-dimensional $\mathbb{Z}_2-$vector space $(\mathbb{Z}_2)^2=\mathbb{Z}_2\times\mathbb{Z}_2$ allows us to use 2×2 elementary matrices, for representing the bijections which transform one ordering into another, when they are linear transformations. Based upon these transformations, isomorphic and isometric models in six and three dimensions are here identified.

The Abelian group $(\mathrm{N},+)$ can also be regarded as a bidimensional vector space over the binary field $\mathbb{Z}_2=\{0,1\}$, where the only orthonormal basis, according to the inner product, induced by the Hamming distance, are (U,A) and (A,U). If we identify these elements $\mathrm{A}=10$ and $\mathrm{U}=01$, with the canonical unitary vectors $\mathrm{e}_1=(1,0)$ and $\mathrm{e}_2=(0,1)$ in the Euclidean coordinated plane $\mathbb{R}^2=\mathbb{R}\times\mathbb{R}$, the $\mathbb{Z}_2-$vector space N is embedded in the plane, not as a subspace, but as a subset of the plane. The 4 elements, $\mathrm{C},\mathrm{U},\mathrm{A},$ and $\mathrm{G},$ correspond, respectively, to the vertexes of a unit square situated in the first quadrant of the plane. See Figure 1.

Figure 1



3.1.1. *Orderings associated to partition* $\wp_1$

Our initial ordering CUAG is associated to partition $\wp_1$, in which algebraic complementarity corresponds to the strong-weak classification of nucleotides. The orderings $(U, C, G, A), (A, G, C, U)$ and (G, A, U, C) are obtained from the initial by applying the translations T_U, T_A and T_G, respectively (see Table III). The only isometric linear transformations, or orthogonal transformation, are those with matrices $I_2 = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$ and $\mathbf{P}_{12} = \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}$. In the plane $\mathbb{R}^2$, the matrix $\mathbf{P}_{12}$ represents a reflexion, or axial symmetry, with respect to the line of equation $y = x$, the angle bisector of the first and the third quadrants. As it is well known, the isometric transformations of any metric vector space are the compositions of its linear isometric transformation with all the isometric translations. Then, in the 2-dimensional case, the isometric transformations of any metric vector space are the compositions of its linear isometric transformation with all the vector space $(\mathbb{Z}_2)^2$, the group of isometric transformation would have $2 \times 4 = 8$ elements. These eight isometries correspond to the permutations associated to partition $\wp_1$ (Table III). Notice that the linear transformation I_2 is the same as the translation T_C. Hence the linear transformation $\mathbf{P}_{12}$ is the same as the composition $\mathrm{T}_\mathrm{C} \circ \mathbf{P}_{12}$.

We recall the fact that the insertion of the $\mathbb{Z}_2-$vector space $\mathrm{N}^3 = \mathrm{NNN}$ into the $\mathbb{R}-$vector space $\mathbb{R}^6$, does not mean that it is a vector subspace, since the operations are different, as the scalar fields are also different. Now, observe that the odd permutation: $\mathrm{C} \leftrightarrow \mathrm{C}, \mathrm{U} \leftrightarrow \mathrm{A}, \mathrm{A} \leftrightarrow \mathrm{U}, \mathrm{G} \leftrightarrow \mathrm{G}$, that is, the transformation $(\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G}) \leftrightarrow (\mathrm{C},\mathrm{A},\mathrm{U},\mathrm{G})$, induced by the linear transformation of matrix $\mathbf{P}_{12}$ of the $\mathbb{Z}_2-$vector space N, then a group homomorphism of the additive group $(\mathrm{N},+)$, is not homomorphic for the product $\times$ of the Galois Field $\mathrm{GF}(4)$. In fact, it transforms the neutral element U of N into the element A, which is not the neutral. Hence, it does not induce a linear transformation of the cube NNN, regarded as a $\mathrm{GF}(4)-$vector space. Accordingly, the odd permutation $(\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G}) \leftrightarrow (\mathrm{C},\mathrm{A},\mathrm{U},\mathrm{G})$, that is isometric with respect to the Hamming distance, it is not an isometry with respect to the Taxi-cab distance. In fact, it converts the unitary vectors UCC, CUC, and CCU into the vectors ACC, CAC, and CCA, that have length 2 (see Figures 2 and 3).

In Figure 2, three non-symmetric permutations of the type SW in 3 dimensions are shown. It is illustrated how the initial order CUAG associated to partition $\wp_1$ in the 3-dimensional model is converted to orderings associated to the same partition $\wp_1$. It is shown how a subset as the prism YNY can change its size and position. Likewise, in Figure 3, permutations that convert the initial order CUAG into orderings associated to the same partition $\wp_1$ in the 6-dimensional model are indicated as examples. They illustrate how a subset, as the 4-dimensional hypercube YNY, do not change neither its size nor its form, because the transformations are Hamming isometric.

The elements $\mathbf{P}_{12}, \mathrm{T}_\mathrm{U}, \mathrm{T}_\mathrm{A}$ generate the group $\mathrm{E}_2(\mathbb{Z}_2)$ of all the Hamming isometries of $\left(\mathbb{Z}_2\right)^2$, that we will call the Euclidean group of that vector space, which is isomorphic to the dihedral group D_4 of all the symmetries of a square. When this group operates over the set of the 24 orderings of the set $\mathrm{N} = \{\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G}\}$, then the subset, $\{\mathrm{CUAG}, \mathrm{UCGA}, \mathrm{AGCU}, \mathrm{GAUC}, \mathrm{CAUG}, \mathrm{UGCA}, \mathrm{ACGU}, \mathrm{GUAC}\}$ of the eight orderings, associated to partition $\wp_1$, is the orbit of the initial ordering CUAG, under the action of the group $\mathrm{E}_2(\mathbb{Z}_2)$. We can also say that the four binary subsets $\{\mathrm{CUAG}, \mathrm{GAUC}\}, \{\mathrm{UCGA}, \mathrm{AGCU}\}, \{\mathrm{CAUG}, \mathrm{GUAC}\}, \{\mathrm{UGCA}, \mathrm{ACGU}\}$, of the set $\{\mathrm{CUAG}, \mathrm{UCGA}, \mathrm{AGCU}, \mathrm{GAUC}, \mathrm{CAUG}, \mathrm{UGCA}, \mathrm{ACGU}, \mathrm{GUAC}\}$ of the eight orderings associated to partition $\wp_1$, are the orbits of the group $\{\mathrm{I}_2, \mathrm{T}_\mathrm{G}\}$, the isometries of the set N, under Manhattan distance when group $\{I_2, T_G\}$ operates over that set of the eight orderings.

Figure 2

First partition SW 3D: Three non-symmetric permutations that belong to the Strong-Weak classification in 3 dimensions. See text for explanation.

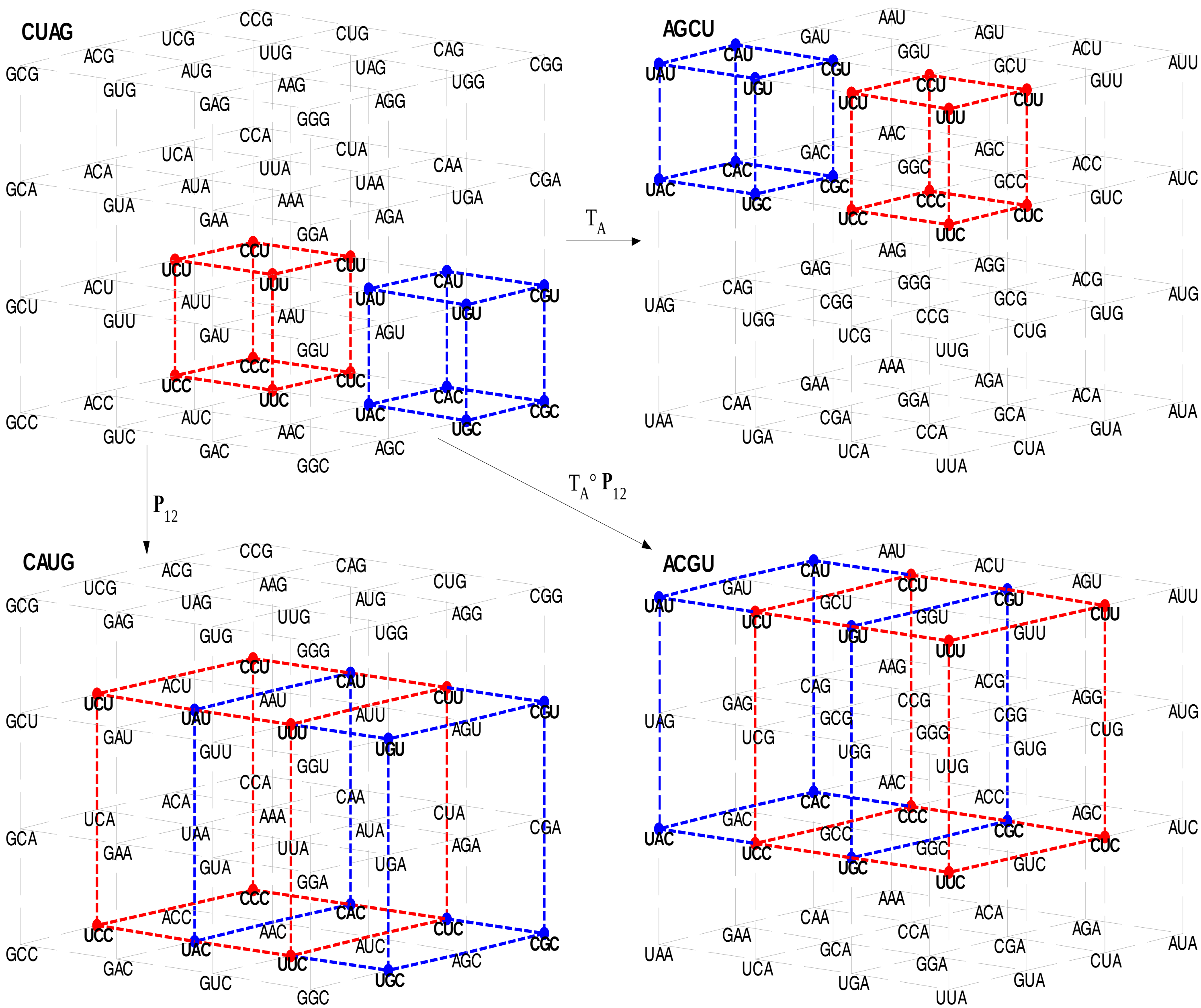
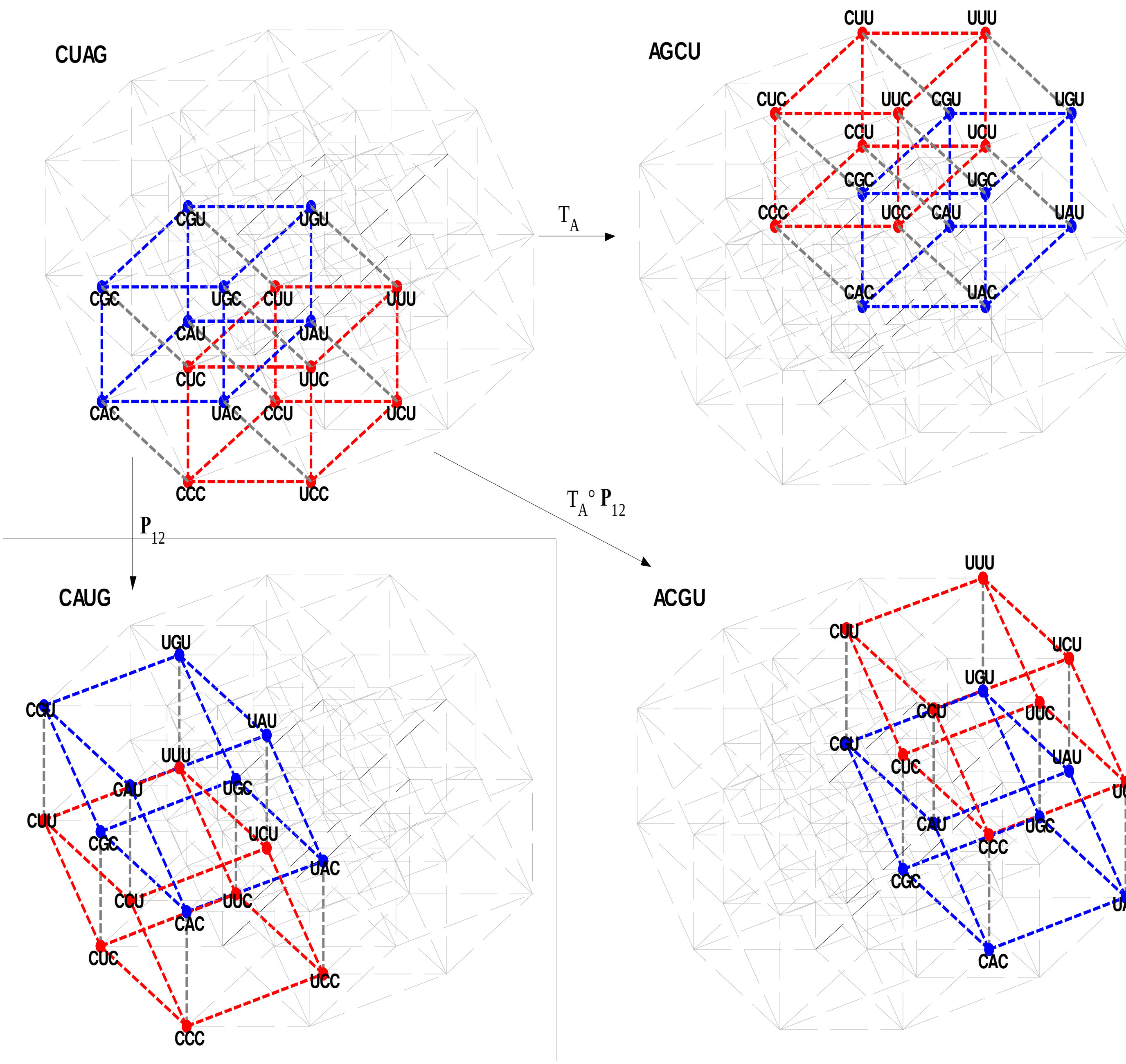


Figure 3

First partition SW in 6D: Three non-symmetric permutations that belong to the Strong-Weak classification in 6 dimensions. See text for explanation.



3.1.2. *Orderings associated to partition* $\wp_2$

In order to transform (CUAG), into the elements associated to partition $\wp_2$, in which algebraic complementarity corresponds to the amino-keto classification of nucleotides, we first consider the bijection that transforms the initial ordering CUAG into the ordering (CUGA), and notice that, in the $\mathbb{Z}_2$ – vector space N, it is the linear transformation defined by the matrix $\mathbf{A_{21}} = \begin{pmatrix} 1 & 0 \\ 1 & 1 \end{pmatrix}$ that fixes the vectors C and U, and interchanges the vectors A and G. In the present case the linear transformation represented by $\mathbf{A_{21}}$ is not isometric with respect to the Hamming distance, since it interchanges the vector A of length 1 with the vector G of length 2. Analogously, we can say that it is not an isometry with respect to the Taxi-cab distance, because it interchanges A of length 2 with G of length 3. It is easy to prove that this transformation is not linear with respect to the structure of GF(4) – vector space of the set NNN. Applying the compositions of $\mathbf{A_{21}}$ with the translations T_C, T_U, T_A, and T_G converts (CUAG) into the orderings (C,U,G,A), (U,C,A,G), (A,G,U,C) and (G,A,C,U), respectively. The linear isometry, which interchanges U and G, and fixes C and A, is the one represented by the matrix $\mathbf{A}_{12} = \begin{pmatrix} 1 & 1 \\ 0 & 1 \end{pmatrix}$. It converts the ordering (C,U,G,A), into the ordering (C,G,U,A). Applying the compositions of $\mathbf{A_{12}}$ with T_C, T_U, T_A, and T_G converts (C,U,G,A) into the orderings $(C,G,U,A),(U,A,C,G),(A,U,G,C)$ and (G,C,A,U), respectively (Table III). The group $\mathbf{A}_{21}(E_2(\mathbb{Z}_2))(\mathbf{A}_{21})^{-1}$, conjugated, then isomorphic, of the group $E_2(\mathbb{Z}_2)$, leaves invariant the set $\{CUGA, UCAG, AGUC, GACU, CGUA, UACG, AUGC, GCAU\}$ of the orderings associated to partition $\wp_2$. Notice that $\mathbf{A_{21}}$ is of order 2, then, its own inverse is $(\mathbf{A_{21}})^{-1}$. Actually, this set is the orbit of the ordering CUGA under the action of that group over the set of the 24 different orderings of the set N. The elements $\mathbf{A_{21}}$, T_U, and T_A generate the group $\mathbf{A}_{21}(E_2(\mathbb{Z}_2))(\mathbf{A}_{21})^{-1}$, which leaves invariant the set $(\mathbb{Z}_2)^2$, but not all of its elements are symmetries of the square of vertexes C, U, A, G. We can also say that the four binary subsets

$\{CUGA, GACU\}, \{UCAG, AGUC\}, \{CGUA, GCAU\}, \{UACG, AUGC\}$, of the set $\{CUGA, UCAG, AGUC, GACU, CGUA, UACG, AUGC, GCAU\}$ of the eight orderings, associated to partition $\wp_2$, are the orbits of the group $\{I_2, T_G\}$, of the Manhattan isometries of N when it operates over that set of the eight orderings.

In Figure 4, examples of permutations that convert the initial order (CUAG) associated to partition $\wp_1$ into orderings associated to partition $\wp_2$ (Amino-Keto) in the 3-dimensional model are illustrated. They show how a subset as the prism YNY, can change under permutations that are not Taxi-cab isometries. In Figure 5, examples of permutations that convert the initial order (CUAG) into orderings associated to partition $\wp_2$ in the 6-dimensional model are portrayed. They illustrate how a subset as the prism YNY, can change its form under permutations that are not Hamming isometries.

Figure 4

Second Partition MK in 3D: Three non-symmetric permutations that belong to the Amino-Keto classification in 3 dimensions. See text for explanation.

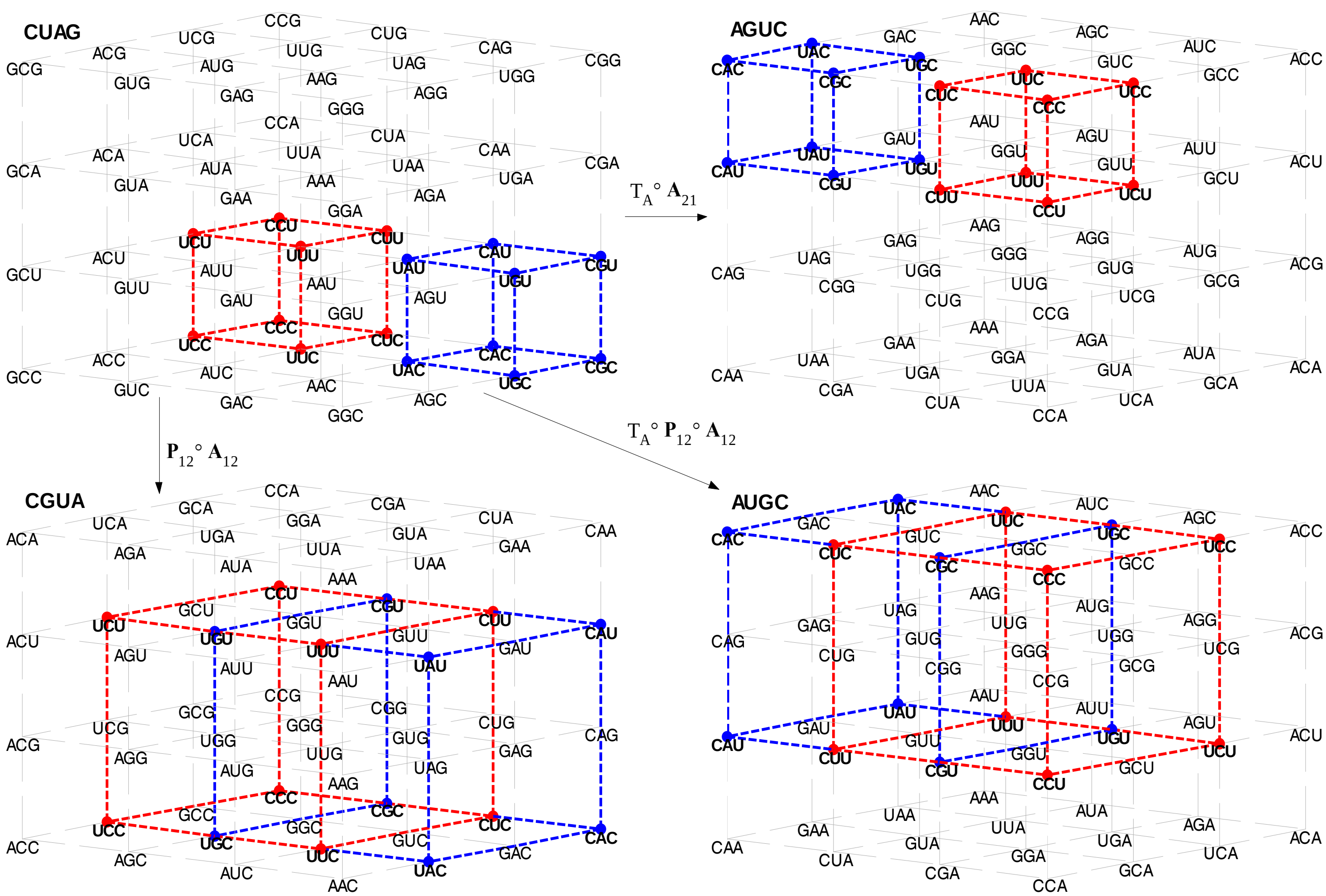
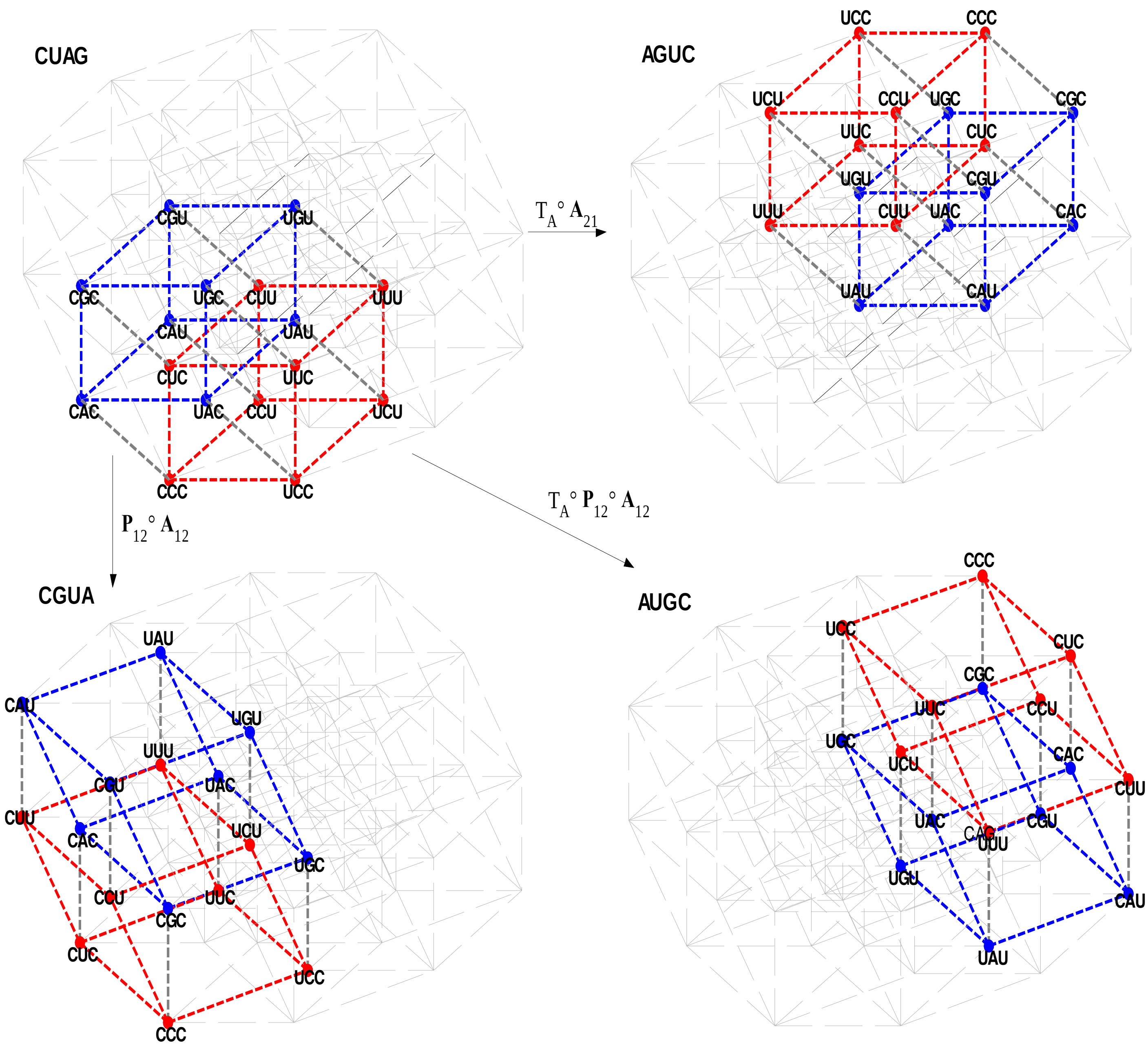


Figure 5
Second partition MK in 6D: Three non-symmetric permutations that belong to the Amino-Keto classification in 6 dimensions. See text for explanation.



In order to transform $(\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G})$ into the orderings associated to partition $\wp_3$, in which algebraic complementarity corresponds to the purine-pyrimidine classification of nucleotides, we examine the bijection that transforms the initial ordering into the ordering $(\mathrm{C},\mathrm{A},\mathrm{G},\mathrm{U})$, and note that it is the linear transformation with matrix $\mathbf{P}_{12}\mathbf{A}_{21}=\begin{pmatrix}1&1\\1&0\end{pmatrix}$ in the $\mathbb{Z}_2-$vector space N, which performs a cyclic permutation over the vectors U, A and G. In the present case the linear transformation represented by $\mathbf{P}_{12}\mathrm{A}_{21}$ is not isometric with respect to the Hamming distance, since it converts A of length 1 into G of length 2, and G of length 2 into U of length 1. Analogously, we can say that it is not an isometry with respect to the Taxi-cab distance, because it converts U of norm 1 into A of norm 2, A of norm 2 into G of norm 3, and G of norm 3 into U of norm 1. Applying the compositions of $\mathbf{P}_{12}\mathrm{A}_{21}$ with $\mathrm{T}_\mathrm{C},\mathrm{T}_\mathrm{U},\mathrm{T}_\mathrm{A}$, and T_G, converts $(\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G})$ into the orderings $(\mathrm{C},\mathrm{A},\mathrm{G},\mathrm{U})$, $(\mathrm{U},\mathrm{G},\mathrm{A},\mathrm{C})$, $(\mathrm{A},\mathrm{C},\mathrm{U},\mathrm{G})$ and $(\mathrm{G},\mathrm{U},\mathrm{C},\mathrm{A})$, respectively. The linear isometry, which interchanges A and G and fixes C and U is the one represented by the matrix $\mathbf{A}_{21}=\begin{pmatrix}1&0\\1&1\end{pmatrix}$. It converts the ordering $(\mathrm{C},\mathrm{A},\mathrm{G},\mathrm{U})$, into the ordering $(\mathrm{C},\mathrm{G},\mathrm{A},\mathrm{U})$. Applying the compositions of $\mathbf{A}_{21}$ with $\mathrm{T}_\mathrm{C},\mathrm{T}_\mathrm{U},\mathrm{T}_\mathrm{A}$, and T_G converts $(\mathrm{C},\mathrm{A},\mathrm{G},\mathrm{U})$, into the orderings $(\mathrm{C},\mathrm{G},\mathrm{A},\mathrm{U})$, $(\mathrm{U},\mathrm{A},\mathrm{G},\mathrm{C})$, $(\mathrm{A},\mathrm{U},\mathrm{C},\mathrm{G})$, and $(\mathrm{G},\mathrm{C},\mathrm{U},\mathrm{A})$, respectively (Table III). The group $\mathbf{P}_{12}\mathbf{A}_{21}(\mathrm{E}_2(\mathbb{Z}_2))(\mathbf{P}_{12}\mathbf{A}_{21})^{-1}$, conjugated, then isomorphic to the group $\mathrm{E}_2(\mathbb{Z}_2)$, leaves invariant the set $\{\mathrm{CAGU},\mathrm{UGAC},\mathrm{ACUG},\mathrm{GUCA},\mathrm{CGAU},\mathrm{UAGC},\mathrm{AUCG},\mathrm{GCUA}\}$ of the orderings associated to partition $\wp_3$. Actually, this set is the orbit of the ordering $(\mathrm{C},\mathrm{A},\mathrm{G},\mathrm{U})$, under the action of that group, over the set of the 24 different orderings of the set N. The elements $\mathrm{A}_{21},\mathrm{T}_\mathrm{U},\mathrm{T}_\mathrm{A}$ generate the group $\mathbf{P}_{12}\mathbf{A}_{21}(\mathrm{E}_2(\mathbb{Z}_2))(\mathbf{P}_{12}\mathbf{A}_{21})^{-1}$, which leaves invariant the set $(\mathbb{Z}_2)^2$, but not all of its elements are symmetries of the square of vertexes $\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G}$. We can also say that the four binary subsets $\{\mathrm{CAGU},\mathrm{GUCA}\}$, $\{\mathrm{UGAC},\mathrm{ACUG}\}$, $\{\mathrm{CGAU},\mathrm{GCUA}\}$, and $\{\mathrm{UAGC},\mathrm{AUCG}\}$, of the set $\{\mathrm{CAGU},\mathrm{UGAC},\mathrm{ACUG},\mathrm{GUCA},\mathrm{CGAU},\mathrm{UAGC},\mathrm{AUCG},\mathrm{GCUA}\}$ of the eight orderings, associated to partition $\wp_3$ are the orbits of the group $\{\mathrm{I}_2,\mathrm{T}_\mathrm{G}\}$, of the Manhattan isometries of N, when it operates over that set of those eight orderings.

In Figure 6, three non-symmetric permutations of the type RY in 3 dimensions are shown. Examples of permutations that convert the initial order (CUAG) associated to partition $\wp_1$ into orderings associated to partition $\wp_3$ in the 3-dimensional model are illustrated. They show how a subset as the prism YNY, can change under permutations that are not Taxi-cab isometries. In Figure 7, examples of permutations that convert the initial order (CUAG) into orderings associated to partition $\wp_3$ in the 6-dimensional model are portrayed. They illustrate how a subset as the prism YNY, can change its form under permutations that are not Hamming isometries.

Figure 6
Third partition RY in 3D: Three non-symmetric permutations that belong to the Purine-Pyrimidine classification in 3 dimensions. See text for explanation.

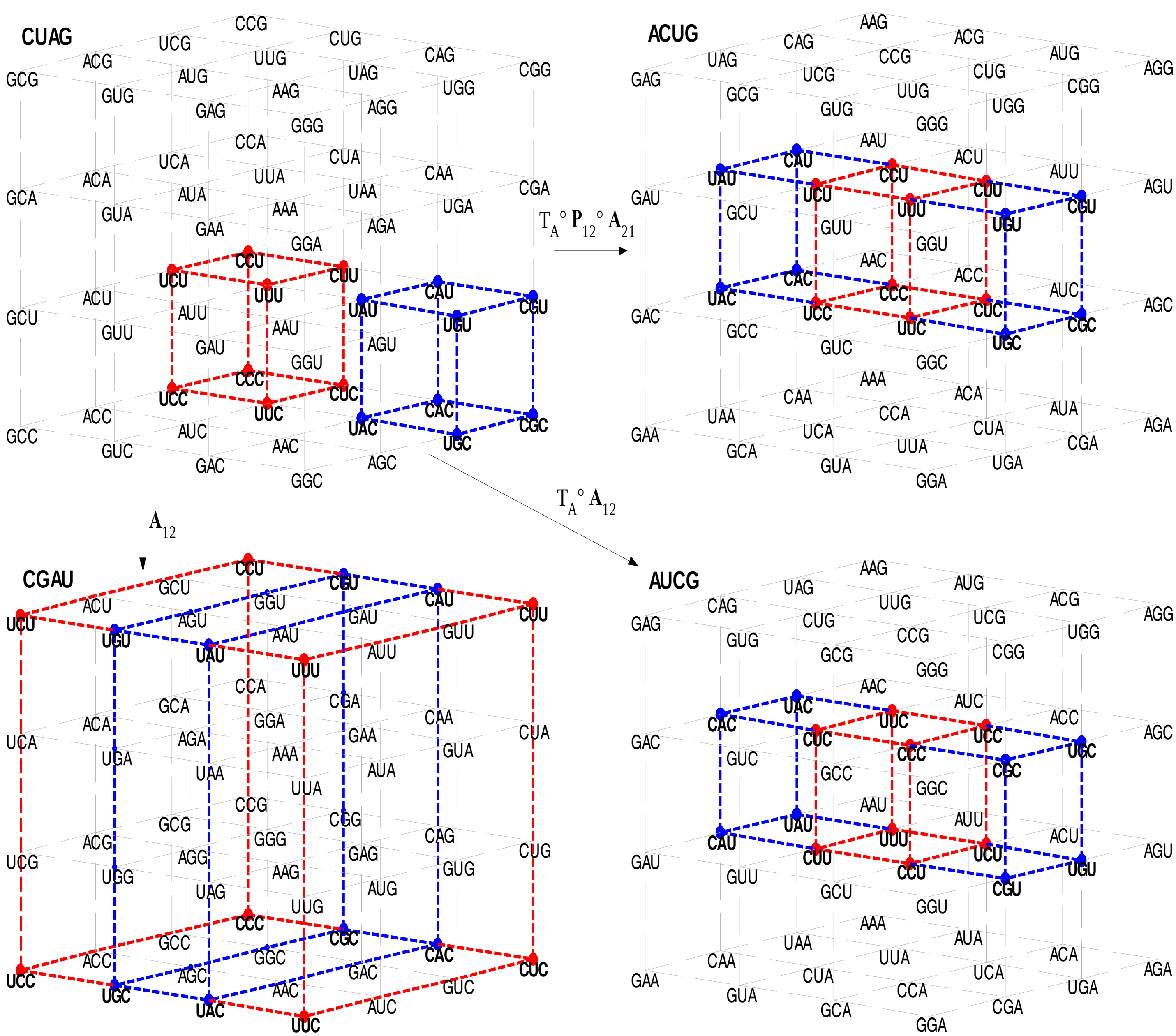


Figure 7

Third partition RY in 6D: Three non-symmetric permutations that belong to the Purine-Pyrimidine classification in 6 dimensions. See text for explanation.

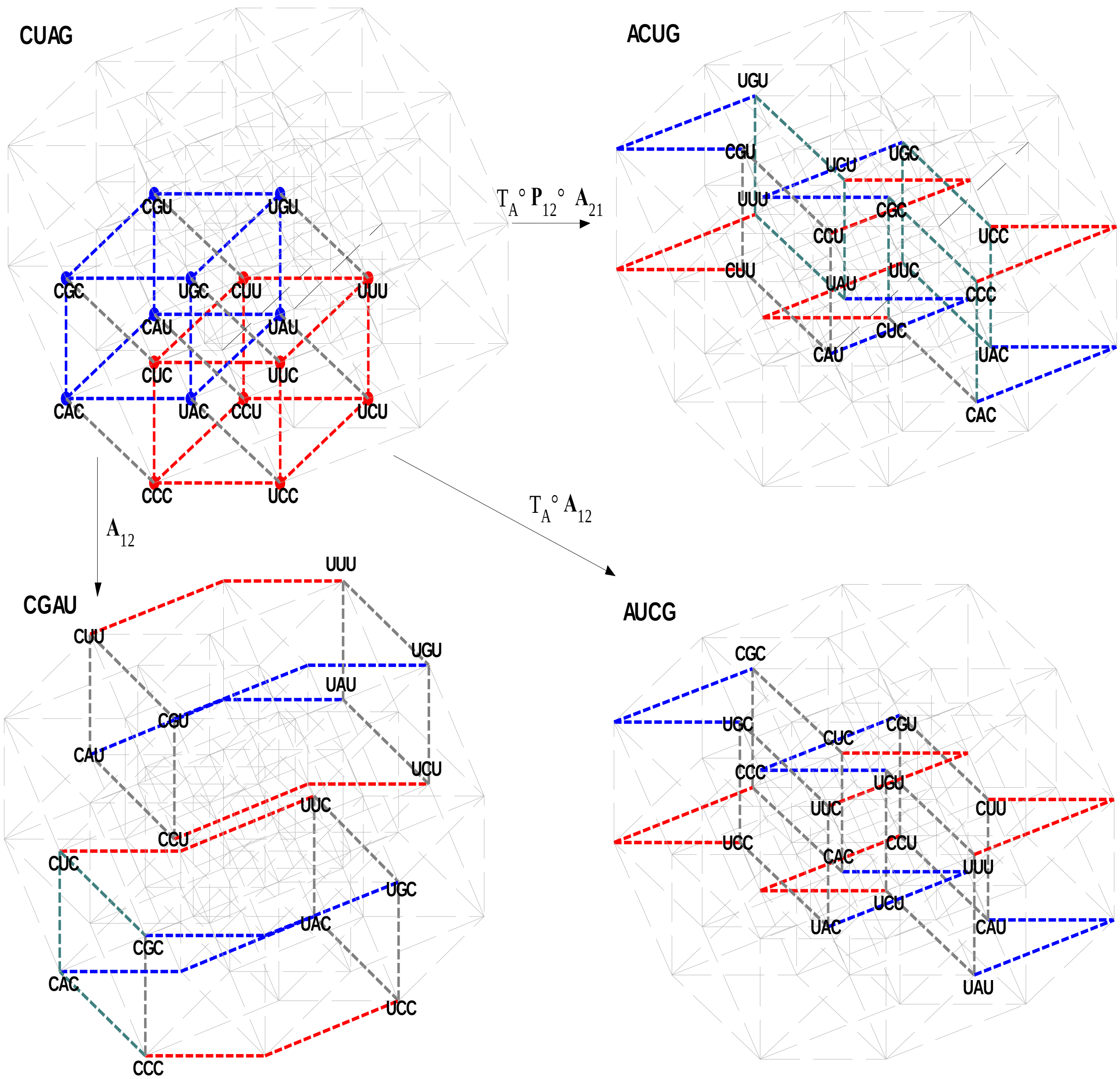


Table III

Partition	Type of transformation	Symbol	Action over N	Parity as permutation of the set N
$\wp_1$	Linear and translation	$I_2 = T_C$	$(C,U,A,G) \leftrightarrow (C,U,A,G)$	Even
	Translation	T_U	$(C,U,A,G) \leftrightarrow (U,C,G,A)$	Even
	Translation	T_A	$(C,U,A,G) \leftrightarrow (A,G,C,U)$	Even
	Translation	T_G	$(C,U,A,G) \leftrightarrow (G,A,U,C)$	Even
	Linear	$\mathbf{P}_{12}$	$(C,U,A,G) \leftrightarrow (C,A,U,G)$	Odd
	Affine	$T_U \circ \mathbf{P}_{12}$	$(C,U,A,G) \leftrightarrow (U,G,C,A)$	Odd
	Affine	$T_A \circ \mathbf{P}_{12}$	$(C,U,A,G) \leftrightarrow (A,C,G,U)$	Odd
	Affine	$T_G \circ \mathbf{P}_{12}$	$(C,U,A,G) \leftrightarrow (G,U,A,C)$	Odd
$\wp_2$	Linear and translation	$\mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (C,U,G,A)$	Odd
	Translation	$T_U \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (U,C,A,G)$	Odd
	Translation	$T_A \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (A,G,U,C)$	Odd
	Translation	$T_G \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (G,A,C,U)$	Odd
	Linear	$A_{12} \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (C,G,U,A)$	Even
	Affine	$T_U \circ A_{12} \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (U,A,C,G)$	Even
	Affine	$T_A \circ A_{12} \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (A,U,G,C)$	Even
	Affine	$T_G \circ A_{12} \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (G,C,A,U)$	Even
$\wp_3$	Linear	$\mathbf{P}_{12} \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (C,A,G,U)$	Even
	Affine	$T_U \circ \mathbf{P}_{12} \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (U,G,A,C)$	Even
	Affine	$T_A \circ \mathbf{P}_{12} \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (A,C,U,G)$	Even
	Affine	$T_G \circ \mathbf{P}_{12} \circ \mathbf{A}_{21}$	$(C,U,A,G) \leftrightarrow (G,U,C,A)$	Even
	Linear	$\mathbf{A}_{12}$	$(C,U,A,G) \leftrightarrow (C,G,A,U)$	Odd
	Affine	$T_U \circ \mathbf{A}_{12}$	$(C,U,A,G) \leftrightarrow (U,A,G,C)$	Odd
	Affine	$T_A \circ \mathbf{A}_{12}$	$(C,U,A,G) \leftrightarrow (A,U,C,G)$	Odd
	Affine	$T_G \circ \mathbf{A}_{12}$	$(C,U,A,G) \leftrightarrow (G,C,U,A)$	Odd

3.1.4. *Orbits of the 24 different orderings*

Now we will make some remarks about the orbits of the group $T(N) = \{T_C, T_U, T_A, T_G\}$ of all the translations of the group $(N,+)$, when it operates over the set of the 24 different orderings of the set N. In the foregoing sections *3.1.1., 3.1.2, and 3.1.3.*, we have compared the initial ordering (C,U,A,G) with the remaining 23 orderings, and pointed out which of the hypercubes and multicubes are isometric to the ones obtained from the ordering (C,U,A,G). But a more general picture can be obtained by noticing that choosing the ordering (C,U,G,A) for $\wp_2$, or the ordering (C,A,G,U) for partition $\wp_3$ as the initial ones, we can derive the other 7 elements associated to each partition by applying the translations T_C, T_U, T_A, and T_G and the compositions of these translations with the linear transformation of matrix $\mathbf{A}_{12}$ in partition $\wp_2$, and with the linear transformation of matrix $\mathbf{A}_{21}$ in the case of partition $\wp_3$.

3.2. *Classification of the 24 representations of the SGC*

We have seen that the 8 hypercubes of only the partition $\wp_1$ are pairwise isometric with respect to the Hamming distance. In all cases, odd and even permutations divide the family associated to each partition, into two subfamilies. Choosing the orderings (C,U,A,G) and (C,A,U,G) for $\wp_1$, or the orderings (C,U,G,A) and (C,G,U,A) for $\wp_2$, or the orderings (C,A,G,U) and (C,G,A,U) for partition $\wp_3$, as the initial ones, only translations are needed in order to get the 3 remaining elements of each subfamily. As a result we get 6 families of 4 pairwise isometric 6-dimensional hypercubes:

Subfamilies of partition $\wp_1$:

$\mathfrak{I}_1$: The 4 cubes obtained from the orderings: (C,U,A,G), (U,C,G,A), (A,G,C,U) and (G,A,U,C), that are even permutations of the initial ordering (C,U,A,G).

$\mathfrak{I}_2$: The 4 cubes obtained from the orderings: (C,A,U,G), (U,G,C,A), (A,C,G,U) and (G,U,A,C), that are odd permutations of the initial ordering (C,U,A,G).

Subfamilies of partition $\wp_2$:

$\mathfrak{I}_3$: The 4 cubes obtained from the orderings: (C,U,G,A), (U,C,A,G), (A,G,U,C) and (G,A,C,U), that are odd permutations of the initial ordering (C,U,A,G).

$\mathfrak{I}_4$: The 4 cubes obtained from the orderings: (C,G,U,A), (U,A,C,G), (A,U,G,C) and (G,C,A,U), that are even permutations of the initial ordering (C,U,A,G).

Subfamilies of partition $\wp_3$:

$\Im_5$: The 4 cubes obtained from the orderings (C, A, G, U), (U, G, A, C), (A, C, U, G) and (G, U, C, A), that are even permutations of the initial ordering (C, U, A, G).

$\Im_6$: The 4 cubes obtained from the orderings (C, G, A, U), (U, A, G, C), (A, U, C, G) and (G, C, U, A), that are odd permutations of the initial ordering (C, U, A, G).

In fact, every subfamily is an orbit of the group $T(N)$ when it operates over the set of the 24 different orderings of the set N.

If the parity of a permutation $\boldsymbol{\pi}$ is defined as the number of inversions it has, then the first 4 permutations associated to partition $\wp_1$, are even permutations of the primary ordering (C, U, A, G), while the other four are odd permutations (Table III). This produces a partition of the set into 2 classes: the class of those obtained by translations (even permutations), and the class obtained by the linear transformation $\mathbf{P}_{12}$ or the composition of $\mathbf{P}_{12}$ with a translation (odd permutations).

It is straightforward to notice that every Hamming isometry of the vector space N, induces exactly an isometry of the 6-dimensional hypercube $(\mathbb{Z}_2)^6$, and also that every Manhattan isometry of N, induces exactly an isometry of the 3-dimensional multicube $(GF(4))^3$. Then, the 8 selected permutations of the set $N = (C, U, A, G)$, induce isometries of the metric space $N \times N \times N$ of all the triplets, with respect to its Hamming distance. However, as a remarkable result, we have that the only permutation that induces an isometry of the ordered set (C, U, A, G) with respect to the Taxi-cab distance, is the translation T_G.

In the above paragraphs we have compared the initial ordering (C, U, A, G) with the remaining 23 orderings, and pointed out which of the hypercubes and cubes are isometric to the ones obtained with the ordering (C, U, A, G).

3.3. *Examples*

3.3.1. *The cube on the ordering* (C, U, A, G)

The eight triplets CCC, CCU, CUC, CUU, UCC, UCU, UUC, and UUU, that we denote according to their chemical composition as the set YYY, are the vertexes of a unitary cube in the ordering (C, U, A, G). The set YYY is a 3-dimensional $\mathbb{Z}_2$ – vector subspace of NNN, if we consider it as a 6-dimensional $\mathbb{Z}_2$ – vector space. The cube YYY is a subgroup of the additive group $(NNN, +)$ of the $N-$vector space

NNN, but it is not an N−subspace, since it is not closed under multiplication of the scalars A or G of the field N by vectors of YYY.

In the 6-dimensional hypercube, YYY is a unitary cube with three of its edges lying over the coordinated axes e_2, e_4 and e_6 (see Table IVa). Application of the linear transformation of matrix $\mathbf{P}_{12}$, transforms this cube isometrically, and now three of its edges lie over the coordinated axes e_1, e_3 and e_5 (Table IVb). Under the permutation $(C,U,A,G) \to (C,A,U,G)$, if it is visualized in the 3-dimensional NNN, the cube YYY is converted into the cube $\{C,A\}^3$ whose edges are of length 2 (Table IVb).

Table IV

The assignment of binary sextuples to the triplets of the set YYY, for six different orderings of the nucleotides C, U, A, G.

a) (C,U,A,G)

Codon	Associated Sextuple					
CCC	0	0	0	0	0	0
UCC	0	1	0	0	0	0
CUC	0	0	0	1	0	0
UUC	0	1	0	1	0	0
CCU	0	0	0	0	0	1
UCU	0	1	0	0	0	1
CUU	0	0	0	1	0	1
UUU	0	1	0	1	0	1

b) (C,A,U,G)

Associated Sextuple					
0	0	0	0	0	0
1	0	0	0	0	0
0	0	1	0	0	0
1	0	1	0	0	0
0	0	0	0	1	0
1	0	0	0	1	0
0	0	1	0	1	0
1	0	1	0	1	0

c) (C,U,G,A)

Codon	Associated Sextuple					
CCC	0	0	0	0	0	0
UCC	0	1	0	0	0	0
CUC	0	0	0	1	0	0
UUC	0	1	0	1	0	0
CCU	0	0	0	0	0	1
UCU	0	1	0	0	0	1
CUU	0	0	0	1	0	1
UUU	0	1	0	1	0	1

d) (C,G,U,A)

Associated Sextuple					
0	0	0	0	0	0
1	0	0	0	0	0
0	0	1	0	0	0
1	0	1	0	0	0
0	0	0	0	1	0
1	0	0	0	1	0
0	0	1	0	1	0
1	0	1	0	1	0

e) (C,A,G,U)

Codon	Associated Sextuple					
CCC	0	0	0	0	0	0
UCC	1	1	0	0	0	0
CUC	0	0	1	1	0	0
UUC	1	1	1	1	0	0
CCU	0	0	0	0	1	1
UCU	1	1	0	0	1	1
CUU	0	0	1	1	1	1
UUU	1	1	1	1	1	1

f) (C,G,A,U)

Associated Sextuple					
0	0	0	0	0	0
1	1	0	0	0	0
0	0	1	1	0	0
1	1	1	1	0	0
0	0	0	0	1	1
1	1	0	0	1	1
0	0	1	1	1	1
1	1	1	1	1	1

3.3.2. *Distance between a codon and its anticodon*

We call the anticodon of a triplet or codon the reverse of its complementary, according to the YR classification. For example, the complementary of AUG is UAC and the anticodon is the codon CAU.

In Table V the Hamming (or Taxi-cab) distance between every codon and its anticodon is illustrated. It is shown in which cases the distances are equal to 1, that is, when a codon is adjacent to its anticodon.

Table V

Codon	**Anti-codon**	**Distance in the 6-dimensional hypercube**						**Distance in the 3-dimensional cube**					
		CUAG	CAUG	CUGA	CGUA	CAGU	CGAU	CUAG	CAUG	CUGA	CGUA	CAGU	CGAU
CCC	GGG	6	6	3	3	3	3	9	9	6	3	6	3
CCU	AGG	4	4	5	5	3	3	7	5	6	5	4	5
CCA	UGG	4	4	3	3	5	5	5	7	4	5	6	5
CCG	CGG	2	2	1	1	1	1	3	3	2	1	2	1
CUC	GAG	6	6	3	3	3	3	7	7	6	3	6	3
CUU	AAG	4	4	5	5	3	3	5	3	6	5	4	5

CUA	UAG	4	4	3	3	5	5	3	5	4	5	6	5
CUG	CAG	2	2	1	1	1	1	1	1	2	1	2	1
CAC	GUG	6	6	3	3	3	3	7	7	6	3	6	3
CAU	AUG	4	4	5	5	3	3	5	3	6	5	4	5
CAA	UUG	4	4	3	3	5	5	3	5	4	5	6	5
CGC	GCG	6	6	3	3	3	3	9	9	6	3	6	3
CGU	ACG	4	4	5	5	3	3	7	5	6	5	4	5
CGA	UCG	4	4	3	3	5	5	5	7	4	5	6	5
UCC	GGA	4	4	5	5	3	3	7	5	6	5	4	5
UCU	AGA	6	6	3	3	3	3	5	5	6	3	6	3
UCA	UGA	2	2	1	1	1	1	3	3	2	1	2	1
UUC	GAA	4	4	5	5	3	3	5	3	6	5	4	5
UUU	AAA	6	6	3	3	3	3	3	3	6	3	6	3
UUA	UAA	2	2	1	1	1	1	1	1	2	1	2	1
UAC	GUA	4	4	5	5	3	3	5	3	6	5	4	5
UAU	AUA	6	6	3	3	3	3	3	3	6	3	6	3
UGC	GCA	4	4	5	5	3	3	7	5	6	5	4	5
UGU	ACA	6	6	3	3	3	3	5	5	6	3	6	3
ACC	GGU	4	4	3	3	5	5	5	7	4	5	6	5
ACU	AGU	2	2	1	1	1	1	3	3	2	1	2	1
AUC	GAU	4	4	3	3	5	5	3	5	4	5	6	5
AUU	AAU	2	2	1	1	1	1	1	1	2	1	2	1
AAC	GUU	4	4	3	3	5	5	3	5	4	5	6	5
AGC	GCU	4	4	3	3	5	5	5	7	4	5	6	5
GCC	GGC	2	2	1	1	1	1	3	3	2	1	2	1
GUC	GAC	2	2	1	1	1	1	1	1	2	1	2	1

Actually, positions of codons and their respective complements are symmetric with respect to the center $(3/2, 3/2, 3/2)$ of the multicube, not only for the ordering $(\mathrm{C}, \mathrm{U}, \mathrm{A}, \mathrm{G})$ but also for the other 7 orderings, associated to partition $\wp_1$. The same holds for the cases of hypercubes in which their Hamming distances, where symmetries are taken with respect to the center $(1/2, 1/2, 1/2, 1/2, 1/2, 1/2)$.

3.4. *Symmetries of the hypercube* $(\mathbb{Z}_2)^6$ *and of the multicube* $(\mathrm{GF}(4))^3$

First we analyze the symmetries of the hypercube. The linear isometric transformations in regard to the Hamming distance are those canonically defined by the permutations of the canonical basis $(e_1, e_2, e_3, e_4, e_5, e_6)$. They are the orthogonal transformations of the hypercube and conform a group, isomorphic to the group $\mathbf{P}_6(\mathbb{Z}_2)$ of the binary permutation 6×6 matrices. On the other hand, all the translations are Hamming isometries. Then, the group $T((\mathbb{Z}_2)^6)$ of the $2^6 = 64$ translations, is a group of isometric transformations of the hypercube. All the symmetries are the compositions of linear permutations with the translations. Then, the total number of symmetries is the product $6!\times 2^6 = 46,080$.

If we identify the hypercube with the set $N\times N\times N = NNN$ of the 64 triplets, using the matching of the set $N = \{C, U, A, G\}$ of the 4 nucleotide RNA bases with the set $\{00, 01, 10, 11\}$ of the 4 binary duplets, taking the ordering (C, U, A, G), we have seen that, from the 24 different orderings of the set N, only the eight associated to the strong-weak partition $\wp_1$, determine isometric transformations of the original hypercube.

Now, we analyze the symmetries of the multicube. The linear isometric transformations in regard to the Manhattan distance are those canonically defined by the $3! = 6$ permutations of the canonical basis (e_1, e_2, e_3). They are the orthogonal linear transformations of the multicube and conform a group $\mathbf{P}_3(\mathbb{Z}_2)$ of the 3×3 binary permutation matrices. On the other hand, only the eight translations determined by the translations T_0 and T_3 in the field $GF(4)$ are Manhattan isometric. Then, the order 8 group $\{T_{000}, T_{003}, T_{030}, T_{033}, T_{300}, T_{303}, T_{330}, T_{333}\}$ is the group of all the Manhattan isometric translations of the multi-cube. All the symmetries are the compositions of linear permutations with isometric translations. Then, the total number of symmetries is the product $3!\times 2^3 = 48$. Here we recall that the number of symmetries of any cube is precisely 48, which are rotations and reflections or roto-reflections around its center.

If we identify the multicube with the set $N\times N\times N = NNN$ of the 64 triplets, using the matching of the set $N = \{C, U, A, G\}$ of the 4 nucleotide bases with the set $\{00, 01, 10, 11\}$ of the 4 binary duplets, taking the ordering (C, U, A, G), we have seen that, from the 24 different orderings of the set N only three, among the eight associated to the strong-weak partition $\wp_1$, determine isometric transformations of the original multicube. These are the permutations $(C, U, A, G) \leftrightarrow (C, U, A, G)$ and $(C, U, A, G) \leftrightarrow (G, A, U, C)$, determined by the additive translation T_G, the linear transformations $\mathbf{P}_{12}$, and the composition $T_G \circ P_{12}$, respectively, in the set N.

4. Discussion

For the sake of completeness and generality, in this work we have examined the 24 possible matchings of the set of the 4 nucleotides with the set of the 4 duplets of zeros and ones. The set N may be partitioned into two disjoint binary classes in three different ways, according to chemical criteria: strong-weak, amino-keto and pyrimidine-purine. For each of these classifications, there are eight different associated orderings and each of them leads to a different 6-dimensional binary hypercube or to a different 3-dimensional multicube over the field $\mathrm{GF}(4)$. We use the Hamming distance, H, in the 6-dimensional vector space and the Manhattan distance, M, in the 3-dimensional $\mathrm{GF}(4)$-vector space NNN. As the permutations that convert elements of a family into elements of another one, are not always isometries with respect to the distance H in the 6-dimensional vector space, or the distance M in the 3-dimensional multicube, respectively, the corresponding transformations may change the shape and the size of a subset of the set NNN.

From the 24 possible transformations, the parity of twelve is even and the parity of the other twelve is odd. Four out of the twelve which are even are the translations $(\mathrm{T_C}, \mathrm{T_U}, \mathrm{T_A}, \mathrm{T_G})$ and the remaining eight are affine transformations. The twelve that are odd are linear transformations or compositions of a linear transformation with translations. The matrices $\mathbf{P}_{12}$ and $\mathbf{A}_{21}$, which perform the interchanges $\mathrm{U} \leftrightarrow \mathrm{A}$ and $\mathrm{A} \leftrightarrow \mathrm{G}$, respectively, are odd permutations. The cube $\mathrm{N\,NN}$ has been christened as The Hotel of Triplets, or Genetic Hotel, because of its resemblance with a three-floor building [11]. As the permutations that convert elements of a family into elements of the other one are not necessarily isometries, with respect to the taxi-cab distance in the 3-dimensional $\mathrm{N}-$cube, the corresponding transformation may change the shape and the size of a condominium of the Hotel. The prism RNY adopts different shapes in the set NNN depending upon the selected ordering.

A priori there is any biological reason to prefer one ordering over others. Assuming a primeval genetic code, such as the RNY code, different evolutionary mechanisms can lead to the same Standard Genetic Code [6]. Different orderings could be better than others in terms of the properties (e.g. physicochemical, evolutionary, and symmetrical) that are under study and that one finds convenient to be highlighted.

From the above results, we conclude that there are eight different ways of defining a structure of a 6-dimensional hypercube, or 6-dimensional vector space over the binary field $\mathbb{Z}_2$ in such a way that biological complementarity of nucleotides is consistent with the algebraic complementarity of the associated duplets of zeros and ones. They also lead to the eight ways up to isomorphisms, of defining a structure of $\mathrm{N}-$vector space, being N the set of RNA nucleotides, endowed with the structure of the Galois Field $\mathrm{GF}(4)$ of 4 elements.

4.1. The symmetries of the genetic code

The idea of "symmetry" is familiar to any educated person [3]. Basically, symmetry of a geometrical figure is an undetectable motion, and an object is symmetric if it has symmetries [5]. The nature of the codon-anticodon interactions allows us to explain the symmetry of the genetic code table [20]. This means that the algebraic symmetries in the 6-

dimensional hypercube $(\mathbb{Z}_2)^6$, and the 3-dimensional cube $(\mathrm{GF}(4))^3$ should be the result of the physicochemical properties of four DNA bases included in the group definition. Consequently, the algebraic symmetries in these cubes have to be closely connected to the physicochemical properties of amino acids [16]. In both algebraic-geometric models, the 6-dimensional $(\mathbb{Z}_2)^6$, and the 3-dimensional $(\mathrm{GF}(4))^3$ for the eight orderings associated to partition $\wp_1$, the positions of the codons and their respective complements are symmetric with respect to the center or barycenter of the figure in the corresponding $\mathbb{Z}_2-$vector space. The center in the 6-dimensional case is the sextuple $(1/2,1/2,1/2,1/2,1/2,1/2)$, and in the 3-dimensional case is the triple $(3/2,3/2,3/2)$. The same happens with the smoothest energy gradients, where codons with the same coefficient are symmetrically situated with respect to the center [14]. The distributive lattice $((\mathrm{GF}(4))^3,\le)$ contains a sublattice which is a homomorphic image of the Boolean lattice $((\mathbb{Z}_2)^6,\le)$, where the number of vertexes is the same but it is not so with respect to the number of arcs, having the lattice $((\mathrm{GF}(4))^3,\le)$ a greater number.

We can also assert that, regarding to the reference subset $(\mathrm{C},\mathrm{U},\mathrm{A},\mathrm{G})$, the additive translation $\mathrm{T_G}$, the linear transformations P_{12} and the composition $\mathrm{T_G}\circ\mathrm{P}_{12}$, respectively, induce isometries of the original 3-dimensional cube NNN, which are also bijective affine transformations. These symmetries are consequence of the Klein four-group structure defined on the set of DNA bases, for which the sums of complementary Watson-Crick base pairs are constant. That is, for every strong-weak base order the following holds: $\mathrm{C}\oplus\mathrm{G}=\mathrm{A}\oplus\mathrm{U}=Constant\in\{\mathrm{C,U,A,G}\}$. This implies $\mathrm{T_G}(\mathrm{C})=\mathrm{G}$, $\mathrm{T_G}(\mathrm{U})=\mathrm{A}$, $\mathrm{T_G}(\mathrm{A})=\mathrm{U}$, and $\mathrm{T_G}(\mathrm{G})=\mathrm{C}$. As a result, if the complementary bases of X_1, X_2, X_3 are the bases $X_{1'}, X_{2'}, X_{3'}$, respectively, $(X_i\in(\mathrm{C,U,A,G}), X_{i'}\in(\mathrm{G,A,U,C}), i=1,2,3)$ then the image of the codon ${}^{5'}X_1X_2X_3^{3'}$ is the codon ${}^{5'}X_{1'}X_{2'}X_{3'}^{3'}$. For example, the symmetric image of codon GUG is codon CAC. From the last observation the symmetric image of a codon that encodes for a hydrophilic amino acid, which has codons with A in the second position, is always a codon that encodes for a hydrophobic amino acid (codons with U in the second position). This is in correspondence with the observed in Boolean lattice of the genetic code [8]. In this algebraic structure the symmetry induced by complementary Watson-Crick base pairs is determined by the Boolean function NOT. However, observe that mutations described by translation $\mathrm{T_G}$ correspond to transversions, which are the most dangerous mutations. The biological impact of a single mutation depends on the magnitude in the physicochemical properties of amino acids encoded by the codons involved in such event. For a given gene, the mutation of a codon that encodes for hydrophilic amino acid into a codon that encodes for hydrophobic amino acid could lead to the lost of the biological function of the protein encoded by such gene.

The mutational events observed in gene populations can be represented as jumps from the 3-dimensional genetic code cube defined on the reference base order (C, U, A, G) to any other defined on a different strong-weak base order. According to the above discussion, under such cube representation, the mutational events described by the symmetric transformation T_G should be observed with very low frequency in gene populations. The other 7 permutations, induced by translations T_U, T_A, or compositions of the translations with the odd permutation $CUAG \to CAUG$, neither induce isometric transformations with respect to the Taxi-cab distance, nor affine transformations with respect to the $GF(4)-$vector space structure. Notwithstanding, the eight permutations induce isometric transformation of the binary 6-dimensional vector space NNN, with respect to its Hamming distance, and they are also affine transformations with respect to the $\mathbb{Z}_2$ – vector space structure. However, the mutational events described by the non-symmetric transformations T_A, T_C, and T_U should be observed in gene populations with larger frequencies than T_G. In particular, the non-symmetric transformations T_C and T_U, describe transitions of bases and, even when the non-symmetric transformation T_A describe transversions, these kinds of mutational events are, in general, less dangerous for protein function than T_G. For example, the mutational event: $T_A(CAG) = ACU$ transforms a codon that encode for an hydrophilic amino acid with electrically-charged side-chain (glutamine) into a codon that encode for an amino acid with a non-charged polar side-chain group (threonine), whilst the mutant codon $T_G(CAG) = GUA$ encodes for the hydrophobic amino acid valine. Analogous situation is found for the isometries P_{12} and $T_G \circ P_{12}$. As a result, the most frequent mutational events observed in gene populations should correspond to breakings of the symmetries given on the 3-dimensional $GF(4)$-vector space NNN.

As the permutations that convert elements of a family into elements of the other one are not necessarily isometries with respect to the Taxi-cab distance in the 3-dimensional $N-$cube, the corresponding transformation may change the shape and the size of a subset or condominium of the Hotel. Thus, for example, the set RNY that is a prism in the cube NNN, with edges of length 3, 1, 1, is transformed, under the permutation $(C, U, A, G) \leftrightarrow (C, A, U, G)$, into a bigger prism of lengths 3, 2, 2 (not shown). The prism

RNY, which is an additive coset subgroup in the multicube NNN, corresponds to an affine 4-dimensional vector subspace of the 6-dimensional $\mathbb{Z}_2$ – vector space.

The six-dimensional representation of a categorical phenomenon has the advantage of having a geometry in which the members of N are closer one to another (the maximum distance between two elements is 2), and every codon has six neighbors, whereas in three dimensions codons have 3 or 4 neighbors. Three dimensional representations have the obvious advantage of a clearer representation than on a plane.

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