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## **Symmetry Groups for the Rumer–Konopel’chenko– Shcherbak “Bisections” of the Genetic Code and Applications**

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# Symmetry Groups for the Rumer–Konopel’chenko–Shcherbak “Bisections” of the Genetic Code and Applications<sup>#</sup>

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## Abstract

We derive, in a new way, the discrete symmetry groups for (i) the 4–base set {U, C, A, G}, (ii) the 16–doublet set and (iii) the 64–codon set, as collections of adjacency matrices of selected graphs on the Wittmann sub–sets of the above respective sets. In the case of the genetic code 64 codons system, we re–derive the chain of groups  $D_8 \supset V \supset C_2$  and show that the last member of the chain,  $C_2$ , leaves 16 codons of type GNN invariant and this invariance is maintained across all species with respect to their “non–standard” use of the genetic code, including nuclear genomes as well as mitochondrial genomes. Moreover, we show that this symmetry is suited, in fact it fits, the “bisections” of the set of 64 codons, used by Shcherbak to derive many striking arithmetical regularities and balances, involving the nucleon numbers in the amino acids. Besides the symmetry aspects, our next new result concerns the derivation, using only the concept of matrix–norms in traditional linear algebra, of some (striking) numbers which appear to be characteristic of the genetic code. Finally, by using only the RNA–components, *i.e.*, the four nitrogenous bases mentioned above, we introduce matrices encoding the hydrogen–bond attribute and other matrices encoding a certain “molecular size index” for the bases and derive the ratio of their trace, and of their norms, which appear to be equal in both cases to Shcherbak’s “*Prime Quantum*” 037.

**Keywords.** Genetic code; symmetry; Rumer transformation; invariant codons; Wittmann multipliers; matrix–norms; autopoietic numbers.

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## 1 INTRODUCTION

When the writing of the results, corresponding to part of this work, was made the first cut in, we were focusing on symmetry aspects of the genetic code (Rumer symmetry), and were far from imagining that the final aspect of this invited paper, dedicated to Professor Nenad Trinajstić on the occasion of his 65<sup>th</sup> birthday, was going to become richer by the addition of a new section. The reason is the recent publishing in *Biosystems* of an important paper by Shcherbak, summing up some fifteen years of published research leading to the mentioned paper entitled “*Arithmetic inside the universal genetic code*” [1], in which the author describes striking arithmetical regularities in the genetic code, revealed when certain partitions of the 64–codon set are made. We shall, in section 4,

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<sup>#</sup> Dedicated to Professor Nenad Trinajstić on the occasion of the 65<sup>th</sup> birthday.

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return to the work of Shcherbak but let us say only that Rumer’s symmetry plays an important role in revealing these regularities. Moreover, we take the opportunity given by the added section to (i) present the derivation of some (no less striking) numbers we have found, appearing to be characteristic of the genetic code, which results *would* have been presented elsewhere<sup>1</sup> and (ii) to propose a simple derivation of Shcherbak’s “*Prime Quantum*” 037, a distinguished (decimal) number which plays an important role in the work of Shcherbak where it is associated to a *Prime Quantum Divisibility* feature.

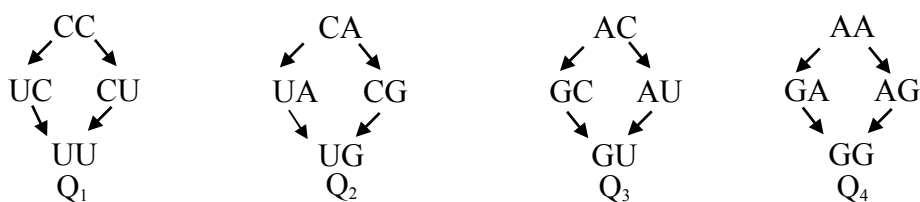
In this paper, which is a continuation of recent works [2,3,4], we shall present, in a new way, the symmetries associated to the four fundamental nitrogenous bases, uracil, cytosine, adenine and guanine, the building blocks of RNA, and to the  $k$ -plet sets constructed out of them: the set of 16 doublets ( $k = 2$ ) and the set of 64 triplets or codons ( $k = 3$ ). (A  $k$ -plet set is also called, in the computing science community, the  $k^{\text{th}}$  extension of the quaternary alphabet {U/T, C, A, G} (Yockey [20]). Our construction, which was introduced in [2], starts with the constituents of the bases themselves: the atoms, written as  $2 \times 2$  matrices and, as will be shown in section 2, these sets (for  $k = 1, 2, 3$ ) are obtained as matrices of dimension  $2^k \times 2^k$ . They constitute our *classification* matrices. There exist also an “experimental” manner to construct all the members of these  $k$ -plet sets which goes back to Wittmann who, in the heroic days of the deciphering of the genetic code in the early sixties, used mutagens like nitrous acid to investigate the genetic code. In particular, in [5], he studied the genetic code in Tobacco Mosaic Virus and deduced the *Octet Model* in which the 64 possible codons are partitioned into eight Octets of eight triplet–codons each (see section 3).

As this is important for what follows, let us say some words on this construction. Wittmann, considering the phenomenon of deamination induced by nitrous acid, formulated the conversions of the bases as follows: U, unchanged,  $C \rightarrow U$ ,  $G \rightarrow (X) \rightarrow G$  and  $A \rightarrow (H) \rightarrow G$ . X (xantine) and H (hypoxantine), are two minor bases both with very similar hydrogen bonding properties to guanine. Using these rules, one could start with sub–sets containing *only* A and/or C, *i.e.*, bases whose deamination can produce a mutation and, for each member of these sub–sets, construct the other co–members by following the rules.

As a simple example, in the case of the four–base set ( $k = 1$ ), the sub–set is constituted by C and A. C will give U and A will give G so that the two Wittmann Doublets are  $C \rightarrow U$  and  $A \rightarrow G$ . For  $k = 2$ , the sub–set has  $2^2 = 4$  base–doublets containing C and/or A: CC, CA, AC and AA. Take CA, for example. It produces UA and CG. UA could give only UG and CG could give only UG and, the process stops. The four Wittmann Quartets  $Q_i$  ( $i = 1, 2, 3, 4$ ) are shown below (Figure 1).

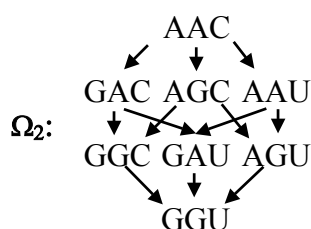
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<sup>1</sup> In the Congress “Festival Symmetry” 2003 (Budapest, August, 16–22, 2003) or in the “Third International Symposium on Quantum Theory and Symmetries”, Cincinnati, Sept. 10 – 14, 2003). These two invitations, and another one didn’t go, unfortunately, to an end because of the blindness of local rulers.



**Figure 1.** The four Wittmann Quartets  $Q_i$ .

Finally, in the case  $k = 3$ , the starting sub-set contains eight ( $2^3$ ) combinations of A and C: AAA, AAC, ACA, CAA, ACC, CAC, CCA and CCC. As above, each one of these triplets will be the first top member of a descending cascade governed by the Wittmann rules. One such Octet ( $\Omega_2$ , top member AAC), as an example, could be visualized as presented in Figure 2.



**Figure 2.** One of the eight Wittmann Octets ( $\Omega_2$ ), see text.

In this way, a total of eight Wittmann Octets ( $\Omega_i$ ,  $i = 1, \dots, 8$ ) are constructed comprising all 64 codons; we have shown only one of them,  $\Omega_2$ . Now, our own way to construct these objects, which relies on a matrix representation of the base, doublet and codon sets, is linked to the Wittmann Doublets, Quartets and Octets in a very simple manner: the latter are the *rows* of our classification matrices, respectively for  $k = 1, 2, 3$ . This very fact will let us realize two objectives in this work: (i) a guided search of the symmetries, through the use of permutation graphs between the Wittmann multiplets, and the use of the adjacency matrices of these graphs as transformation operators on our classification matrices (sections 2 and 3) and (ii) a mathematically correct establishment of certain striking numbers (mentioned briefly above), all relevant for (and characteristic of) the genetic code, which appear to be attached to certain matrices coding either the *hydrogen bond attribute* or a *molecular-size-index* relying on the total number of atoms in the bases, either as “norms”, sizing the matrices and, at the same time, sizing the Wittmann Doublets and Octets, or as invariants (traces). This will be done in section 4. Shcherbak [1], besides using the Rumer symmetry, has chosen another attribute, the number of nucleons of the amino acids and, in fact in his work, everything seems to be associated with a special number, he calls the “*Quantum Prime*” 037, which divides almost everything. We propose, briefly in the fourth section, a possible *raison d’être* for this number, which is not transparent in the above work. In particular, we show that it is independent of the amino acids.

In the second section, we sum up the construction of our classification matrices. In the third, we

construct the symmetry groups which will act on the classification matrices. These matrix groups are obtained as collections of adjacency matrices for selected graphs on the Wittmann sets. In the fourth section, we use some tools supplied by linear algebra (matrix–norms and traces) to establish some interesting numbers.

## 2 BASES, DINUCLEOTIDES AND CODONS

### 2.1 The base–matrix

In [2], we have designed a 2×2 matrix representation of atoms and molecules, among them, the four nitrogenous bases U (uracil: C<sub>4</sub>N<sub>2</sub>H<sub>4</sub>O<sub>2</sub>), C (cytosine: C<sub>4</sub>N<sub>3</sub>H<sub>5</sub>O), A (adenine: C<sub>5</sub>N<sub>5</sub>H<sub>5</sub>) and G (guanine: C<sub>5</sub>N<sub>5</sub>H<sub>5</sub>O), the building blocks of RNA. Their particular (matrix) form, which is the consequence of their detailed atomic composition, is such that they could be easily united in the following base–matrix [2]

$$\mathbf{B} = \begin{pmatrix} \text{U} & \text{C} \\ \text{A} & \text{G} \end{pmatrix}, \quad (1)$$

where the numerical values are  $U = 6^4 7^2 8^2 = 4064256$ ,  $C = 6^4 7^3 8 = 3556224$ ,  $A = 6^5 7^5 = 130691232$ ,  $G = 6^5 7^5 8 = 1045529856$  and are the products of the atomic numbers of the constituent atoms: carbon ( $Z = 6$ ), nitrogen ( $Z = 7$ ), oxygen ( $Z = 8$ ) and hydrogen ( $Z = 1$ ). Eq. (1) is the basis of the next constructions.

### 2.2 The doublet–matrix

The matrix of the 16 possible base–doublets is constructed using the (recently introduced) Kronecker product with *concatenation*<sup>2</sup> [3], which incorporates the non–commutativity of the bases, unlike the ordinary Kronecker product. From Eq. (1), we have:

$$\mathbf{D} = \mathbf{B} \parallel \mathbf{B} = \begin{pmatrix} \text{UU} & \text{UC} & \text{CU} & \text{CC} \\ \text{UA} & \text{UG} & \text{CA} & \text{CG} \\ \text{AU} & \text{AC} & \text{GU} & \text{GC} \\ \text{AA} & \text{AG} & \text{GA} & \text{GG} \end{pmatrix}. \quad (2)$$

The numerical value of each one of the 16 base–doublets, the matrix elements in the form XY, is obtained by concatenating the corresponding values X and Y from the values given above in Eq. (1). For example  $UG = 40642561045529856$  is different from  $GU = 10455298564064256$ . In this

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<sup>2</sup> For two matrices M and N, with integer entries, this product is given by  $(M \parallel N)_{j_s, k_t} = M_{j_k} \parallel N_{s_t}$ , and the computation is the same as for the ordinary Kronecker product except that the product of matrix elements is replaced by the *concatenation* of these (see ref. [3]). The concatenation of any two integers a and b,  $a \parallel b$ , is just their juxtaposition ab.

way the 16 objects are all numerically distinct. Recall that the four Wittmann Doublets,  $Q_i$ , are respectively the four rows in Eq. (2). Also and importantly (see section 4), the doublets belonging to the same column have the same total number of hydrogen bonds (recall that U and A have both two hydrogen bonds while C and G have three each).

### 2.3 The Codon–Matrix

To obtain the matrix representing the 64 (triplet) codons of the genetic code, it is sufficient to repeat the operation on the base–doublet matrix in Eq. (2). One has:

$$\mathbf{C} = \mathbf{D} \parallel \mathbf{B} = \begin{pmatrix} \text{UUU} & \text{UUC} & \text{UCU} & \text{UCC} & \text{CUU} & \text{CUC} & \text{CCU} & \text{CCC} \\ \text{UUA} & \text{UUG} & \text{UCA} & \text{UCG} & \text{CUA} & \text{CUG} & \text{CCA} & \text{CAG} \\ \text{UAU} & \text{UAC} & \text{UGU} & \text{UGC} & \text{CAU} & \text{CAC} & \text{CGU} & \text{CGC} \\ \text{UAA} & \text{UAG} & \text{UGA} & \text{UGG} & \text{CAA} & \text{CAG} & \text{CGA} & \text{CGG} \\ \text{AUU} & \text{AUC} & \text{ACU} & \text{ACC} & \text{GUU} & \text{GUC} & \text{GCU} & \text{GCC} \\ \text{AUA} & \text{AUG} & \text{ACA} & \text{ACG} & \text{GUA} & \text{GUG} & \text{GCA} & \text{GCG} \\ \text{AAU} & \text{AAC} & \text{AGU} & \text{AGC} & \text{GAU} & \text{GAC} & \text{GGU} & \text{GGC} \\ \text{AAA} & \text{AAG} & \text{AGA} & \text{AGG} & \text{GAA} & \text{GAG} & \text{GGA} & \text{GGG} \end{pmatrix}. \quad (3)$$

Here also, each codon, as a matrix element, has an associated value obtained by concatenating three numbers. For example, UUC = 406425640642563556224, UCU = 406425635562244064256, CUU = 355622440642564064256, so that the non–commutativity of the bases, in the codons, is also implemented. Here also, the rows in Eq. (3) are the eight Wittmann Octets and the triplets belonging to the same column have a constant total number of hydrogen bonds (see Eq. (21)). As said above, these two properties will gain all their importance in section 4.

## 3 THE RUMER–KONOPEL’CHENKO SYMMETRY

Now, we turn to symmetry considerations. In 1966 [7], Rumer introduced an interesting partition of the 64–codon set into two equal sub–sets with 32 codons each, by “breaking” the degeneracy number six (see below). The two sets, we call them  $M_1$  and  $M_2$ , are exchanged under the Rumer transformation  $\text{UCAG} \leftrightarrow \text{GACU}$ . We shall, in the following three sub–sections, build a group theoretical framework for the Rumer symmetry and its extensions, following Konopel’chenko and Rumer [8] (Cf. [1]).

### 3.1 $C_2$ Rumer–symmetry for $\mathbf{B}$

This is the simplest case. In order to find a symmetry (matrix) transformation for  $\mathbf{B}$ , we consider the two Wittmann Doublets,  $\text{WD}_1$  and  $\text{WD}_2$  which, as we have said, are the rows in the matrix in Eq. (1). Alternatively, we can consider the columns of this matrix which contain complementary bases, with fixed number of hydrogen bonds, respectively two and three, and forming the sets  $\{\text{U}, \text{A}\}$  and  $\{\text{C}, \text{G}\}$ . Now with two objects, here the Wittmann Doublets,  $\text{WD}_1$  and  $\text{WD}_2$ , we can

consider the two graphs shown below (self-loops allowed), representing links, or transformations, between these two objects (see figure 3, below)



**Figure 3.** The two possible graphs representing transformations between the two Wittmann Doublets  $WD_1$  and  $WD_2$ .

In the first, we have the identity, while in the second,  $WD_1$  and  $WD_2$  are exchanged. The adjacency matrices for these two graphs are given respectively by:

$$\mathbf{e} = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}, \quad \boldsymbol{\eta} = \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}. \quad (4)$$

Recall the adjacency matrix for a graph  $(V, E)$  with  $n = |V|$  vertices is an  $n \times n$  matrix  $\mathbf{M}$  such that  $\mathbf{M}_{ij}$  is 1 if and only if there is an edge from vertex  $i$  to vertex  $j$ ; otherwise  $\mathbf{M}_{ij}$  is zero. The set  $\{\mathbf{e}, \boldsymbol{\eta}\}$  close under matrix multiplication ( $\boldsymbol{\eta}^2 = \mathbf{e}$ ) and constitutes the simplest group with two elements, the cyclic group  $C_2$ . From the point of view of graph theory, this set is also what is called a *cellular algebra* or Bose–Mesner algebra (in fact the simplest) verifying  $\mathbf{e} + \boldsymbol{\eta} = \mathbf{J}$ , with  $\mathbf{J}$  the all–1 matrix. Now, as we have explained in the introduction, these two matrices, obtained as adjacency matrices of graphs on the Wittmann multiplets (or, alternatively, graphs on the columns), will be used as symmetry transformations for the matrix  $\mathbf{B}$ . For  $\mathbf{e}$ , one has the identity and, for  $\boldsymbol{\eta}$  ( $\boldsymbol{\eta}^{-1} = \boldsymbol{\eta}$ ), one gets

$$\boldsymbol{\eta}^{-1} \mathbf{B} \boldsymbol{\eta} = \begin{pmatrix} G & A \\ C & U \end{pmatrix} \quad (5)$$

We see therefore that the transformation  $\boldsymbol{\eta}$ , which acts as a *similarity transformation*, exchanges pyrimidines and purines:  $U \leftrightarrow G$  and  $C \leftrightarrow A$ . It exchanges at the same time the rows (the two Wittmann Doublets  $WD_1$  and  $WD_2$ ) and the columns. This is the Rumer transformation, mentioned above and noted  $UCAG \leftrightarrow GACU$ . There exist also a *combined* transformation  $UCAG \leftrightarrow CUGA$  and  $UCAG \leftrightarrow AGUC$ , equivalent to the Rumer transformation  $UCAG \leftrightarrow GACU$ , [9, 10]. The latter two transformations do not really exist individually but, jointly, they reconstitute the Rumer transformation. (They are sometimes called secondary Rumer transformations.) This could be seen with the aid of the second graph, above. This graph means, as we have said, that the two rows and the two columns are exchanged (or permuted) which is just the result of applying one time the matrix  $\boldsymbol{\eta}$ , see Eq. (5). Below, we shall meet this kind of transformations and shall call them simply *transitions*, for  $UCAG \leftrightarrow CUGA$ , and *transversions*, for  $UCAG \leftrightarrow AGUC$ . Note that the Rumer transformation is a transversion.

### 3.2 Rumer and Rumer–Konopel’chenko Symmetry for D

Since the seminal work by Rumer, many people have studied (and still do today) the structure of the genetic code in terms of the 16–doublet set (see, only but a few examples [11,12,13]). This corresponds to what Shcherbak calls the “compressed” representation of the genetic code at scale 1 with known symmetries. In this sub–section, we shall describe these symmetries in terms of a small discrete group, known as the Klein group V. Danckwert and Neubert [11], already in 1975, used this group but in a formal way, *i.e.*, without a concrete representation. Here, we shall define *concretely* two Klein groups with different actions on the set of doublets.

We take, as a starting set, the four Wittmann Quartets which are the four rows in matrix (2); four is the required number of objects to get 4×4 adjacency matrices able to act on our 4×4 matrix **D**. Now, we have found two different graph–sets of four graphs each. The first one is given by the following four graphs (Figure 4), symbolizing the transformations (the nodes represent the Wittmann Quartets numbered from 1 to 4 from left to right and from top to bottom)

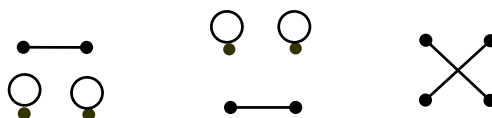


**Figure 4.** The first graph–set for the four Wittmann’s Quartets (see text).

The adjacency matrices for these graphs are given respectively by:

$$V_1: \mathbf{T}_1 = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}, \mathbf{T}_2 = \begin{pmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{pmatrix}, \mathbf{T}_3 = \begin{pmatrix} 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix}, \mathbf{T}_4 = \begin{pmatrix} 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{pmatrix}. \quad (6)$$

Note that these matrices are also permutation matrices. It has been shown in [3] that the set  $\{\mathbf{T}_1, \mathbf{T}_2, \mathbf{T}_3, \mathbf{T}_4\}$  close under matrix multiplication and constitute a commutative group, the four group V, also known as Klein’s 4–group<sup>3</sup>; call it  $V_1$ . The second set of graphs, comprising the same identity transformation (the first graph above) which we do not duplicate below, is the following (Figure 5):



**Figure 5.** The second graph–set for the four Wittmann’s Quartets.

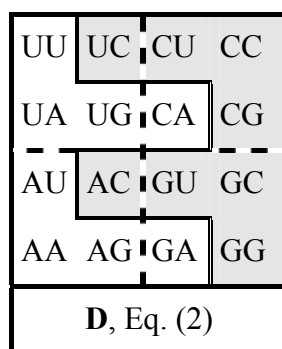
Here, the adjacency matrices are the following:

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<sup>3</sup> The Klein group V could be defined, for example, via the following permutations on four objects,  $\{1, (12)(34), (13)(24), (14)(23)\}$  or simply by its Cayley table (elements e, a, b, c):  $a^2 = b^2 = c^2 = e$ ,  $ab = ba = c$ ,  $ac = ca = b$ ,  $bc = cb = a$ .

$$V_2 : S_1 = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}, S_2 = \begin{pmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}, S_3 = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{pmatrix}, S_4 = \begin{pmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{pmatrix}. \quad (7)$$

In this case, the set  $\{S_1, S_2, S_3, S_4\}$  also close under matrix multiplication and constitute a second Klein’s 4–group,  $V_2$ , as it could be easily verified from (7). Note that the first set,  $\{T_1, T_2, T_3, T_4\}$  is a cellular algebra while it is not the case for the set  $\{S_1, S_2, S_3, S_4\}$ . We reproduce for ease of comparison Eq. (2) as the following representation:



We also add, before continuing, some comments on **D** which prepare us for the next sub–section. First, the set of 16 elements is partitioned in two sub–sets  $M_1$  (UC, CU, CC, CG, AC, GU, GC, GG) and  $M_2$  (UU, UA, UG, CA, AU, AA, AG, GA) the elements of which are exchanged by the Rumer transformation  $UCAG \leftrightarrow GACU$  and separated by the double lines. When going to the codon level (see below), all the codons from  $M_1$  will correspond to amino acids for which the third base is irrelevant (the quartets and the quartet part of the sextets), while those of  $M_2$ , except for the singlets, will necessitate a third base (doublets, triplet). The idea to “break” the 64 codons set into two equal parts  $M_1$  and  $M_2$ , by invoking the partition of the greatest degeneracy 6 as 4+2, goes back to Yuriĭ Borisovich Rumer, in 1966 [7]. (As a short historical note, Ginzburg, Mikhaĭlov (Rumer) and Pokrovskii have written an entire paper, in 2001, on his life as a physicist and an untiring teacher and also on his contribution to biology, in *Physics Uspekhi* **2001**, 44, 1075–1081. They say, for example, “He wrote a paper on the classification of codons in the genetic code using the symmetry principles and some linguistic arguments”.) Second, viewing otherwise, **D** could be partitioned into four sub–sets, of four doublets each, harboring the same *first* base. We shall call these sub–sets  $U^{(1)}$ ,  $C^{(1)}$ ,  $A^{(1)}$  and  $G^{(1)}$ . Each of these sub–sets (one of the four quadrants) have doublets belonging to codons sharing the same *first* base and, therefore, are related by *biosynthetic pathways* [14], (see also [4,6]). There exist another partitioning where these sub–sets correspond to doublets (codons) sharing the same *second* base and being related by similar physico–chemical properties [14] (see below, Eq. (8), and in the sequel for the codon set). We shall return later to these various “views”.

Let us now consider the action of our groups. For the first set, the transformations act as follows:

<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 2px;">UG</td><td style="padding: 2px;">UA</td><td style="padding: 2px;">CG</td><td style="padding: 2px;">CA</td></tr> <tr><td style="padding: 2px;">UC</td><td style="padding: 2px;">UU</td><td style="padding: 2px;">CC</td><td style="padding: 2px;">CU</td></tr> <tr><td style="padding: 2px;">AG</td><td style="padding: 2px;">AA</td><td style="padding: 2px;">GG</td><td style="padding: 2px;">GA</td></tr> <tr><td style="padding: 2px;">AC</td><td style="padding: 2px;">AU</td><td style="padding: 2px;">GC</td><td style="padding: 2px;">GG</td></tr> </table>	UG	UA	CG	CA	UC	UU	CC	CU	AG	AA	GG	GA	AC	AU	GC	GG	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 2px;">GU</td><td style="padding: 2px;">GC</td><td style="padding: 2px;">AU</td><td style="padding: 2px;">AC</td></tr> <tr><td style="padding: 2px;">GA</td><td style="padding: 2px;">GG</td><td style="padding: 2px;">AA</td><td style="padding: 2px;">AG</td></tr> <tr><td style="padding: 2px;">CU</td><td style="padding: 2px;">CC</td><td style="padding: 2px;">UU</td><td style="padding: 2px;">UC</td></tr> <tr><td style="padding: 2px;">CA</td><td style="padding: 2px;">CG</td><td style="padding: 2px;">UA</td><td style="padding: 2px;">UG</td></tr> </table>	GU	GC	AU	AC	GA	GG	AA	AG	CU	CC	UU	UC	CA	CG	UA	UG	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 2px;">GG</td><td style="padding: 2px;">GA</td><td style="padding: 2px;">AG</td><td style="padding: 2px;">AA</td></tr> <tr><td style="padding: 2px;">GC</td><td style="padding: 2px;">GU</td><td style="padding: 2px;">AC</td><td style="padding: 2px;">AU</td></tr> <tr><td style="padding: 2px;">CG</td><td style="padding: 2px;">CA</td><td style="padding: 2px;">UG</td><td style="padding: 2px;">UA</td></tr> <tr><td style="padding: 2px;">CC</td><td style="padding: 2px;">CU</td><td style="padding: 2px;">UC</td><td style="padding: 2px;">UU</td></tr> </table>	GG	GA	AG	AA	GC	GU	AC	AU	CG	CA	UG	UA	CC	CU	UC	UU
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CG	CA	UG	UA																																															
CC	CU	UC	UU																																															
$V_1 : (T_2)^{-1}T_2D$	$(T_3)^{-1}T_3D$	$(T_4)^{-1}T_4D$																																																

In this case, the Rumer transformation is implemented in all cases by  $V_1$ .  $T_2$  leaves  $U^{(1)}$ ,  $C^{(1)}$ ,  $A^{(1)}$  and  $G^{(1)}$  globally invariant by implementing the Rumer transformation at the *second* position.  $T_3$  at the same time exchanges  $U^{(1)}$ ,  $C^{(1)}$ ,  $A^{(1)}$  and  $G^{(1)}$ , according to the Rumer transformation, and implements this latter only at the *first* position.  $T_4$  acts as  $T_3$  but, here, the two positions are concerned. Importantly,  $T_4$  exchanges  $M_1$  and  $M_2$  and the Rumer transformation acts on both positions. Now, let us consider the action of the second group  $V_2$ . We have in this case:

<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 2px;">UG</td><td style="padding: 2px;">UA</td><td style="padding: 2px;">CA</td><td style="padding: 2px;">CG</td></tr> <tr><td style="padding: 2px;">UC</td><td style="padding: 2px;">UU</td><td style="padding: 2px;">CU</td><td style="padding: 2px;">CC</td></tr> <tr><td style="padding: 2px;">AC</td><td style="padding: 2px;">AU</td><td style="padding: 2px;">GU</td><td style="padding: 2px;">GC</td></tr> <tr><td style="padding: 2px;">AG</td><td style="padding: 2px;">AA</td><td style="padding: 2px;">GA</td><td style="padding: 2px;">GG</td></tr> </table>	UG	UA	CA	CG	UC	UU	CU	CC	AC	AU	GU	GC	AG	AA	GA	GG	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 2px;">UU</td><td style="padding: 2px;">UC</td><td style="padding: 2px;">CC</td><td style="padding: 2px;">CU</td></tr> <tr><td style="padding: 2px;">UA</td><td style="padding: 2px;">UG</td><td style="padding: 2px;">CG</td><td style="padding: 2px;">CA</td></tr> <tr><td style="padding: 2px;">AA</td><td style="padding: 2px;">AG</td><td style="padding: 2px;">GG</td><td style="padding: 2px;">GA</td></tr> <tr><td style="padding: 2px;">AU</td><td style="padding: 2px;">AC</td><td style="padding: 2px;">GC</td><td style="padding: 2px;">GU</td></tr> </table>	UU	UC	CC	CU	UA	UG	CG	CA	AA	AG	GG	GA	AU	AC	GC	GU	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 2px;">UG</td><td style="padding: 2px;">UA</td><td style="padding: 2px;">CG</td><td style="padding: 2px;">CA</td></tr> <tr><td style="padding: 2px;">UC</td><td style="padding: 2px;">UU</td><td style="padding: 2px;">CC</td><td style="padding: 2px;">CU</td></tr> <tr><td style="padding: 2px;">AG</td><td style="padding: 2px;">AA</td><td style="padding: 2px;">GG</td><td style="padding: 2px;">GA</td></tr> <tr><td style="padding: 2px;">AC</td><td style="padding: 2px;">AU</td><td style="padding: 2px;">GC</td><td style="padding: 2px;">GU</td></tr> </table>	UG	UA	CG	CA	UC	UU	CC	CU	AG	AA	GG	GA	AC	AU	GC	GU
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AC	AU	GC	GU																																															
$V_2 : (S_2)^{-1}DS_2$	$(S_3)^{-1}DS_3$	$(S_4)^{-1}DS_4$																																																

Here, the situation is different from the preceding one. In all three cases,  $U^{(1)}$ ,  $C^{(1)}$ ,  $A^{(1)}$  and  $G^{(1)}$  are globally conserved (*first* base invariant) with a specific action on each one of them at the *second* base position:

$S_2$ : conserves *strictly*  $G^{(1)}$ , implements  $UCAG \leftrightarrow CUGA$  in  $A^{(1)}$  and  $UCAG \leftrightarrow AGUC$  in  $C^{(1)}$  and the Rumer transformation in  $U^{(1)}$ .

$S_3$ : conserve *strictly*  $U^{(1)}$ , implements  $UCAG \leftrightarrow CUGA$  in  $C^{(1)}$  and  $UCAG \leftrightarrow AGUC$  in  $A^{(1)}$  and the Rumer transformation in  $G^{(1)}$ .

$S_4$ : implements the Rumer transformation in all cases.

Finally, and for later use, we consider the action of  $V_2$  on the following transformed form of  $D$ ,  $D'$ , which classifies together the doublets sharing the same second base:

$$\mathbf{D}' = \mathbf{X}_1^{-1} \mathbf{D} \mathbf{X}_1 = \begin{pmatrix} \text{UU} & \text{CU} & \text{UC} & \text{CC} \\ \text{AU} & \text{GU} & \text{AC} & \text{GC} \\ \text{UA} & \text{CA} & \text{UG} & \text{CG} \\ \text{AA} & \text{GA} & \text{AG} & \text{GG} \end{pmatrix}, \quad \mathbf{X}_1 = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}. \quad (8)$$

The group  $V_2$  act as follows on  $\mathbf{D}'$ :

GU AU AC GC	UU CU CC UC	GU AU GC AC
CU UU UC CC	AU GU GC AC	CU UU CC UC
CA UA <b>UG CG</b>	AA GA GG AG	GA AA GG AG
GA AA <b>AG GG</b>	UA CA CG UG	CA UA CG UG
$V_2 : (\mathbf{S}_2)^{-1} \mathbf{D}' \mathbf{U}_2$	$(\mathbf{S}_3)^{-1} \mathbf{D}' \mathbf{S}_3$	$(\mathbf{S}_4)^{-1} \mathbf{D}' \mathbf{S}_4$

Here, the situation is analogous to the preceding one, but the roles of the base–position are exchanged, *i.e.*,  $U^{(2)}$ ,  $C^{(2)}$ ,  $A^{(2)}$  and  $G^{(2)}$  are globally conserved (*second* base invariant) with a specific action on each one of them at the *first* base position. We have in the detail

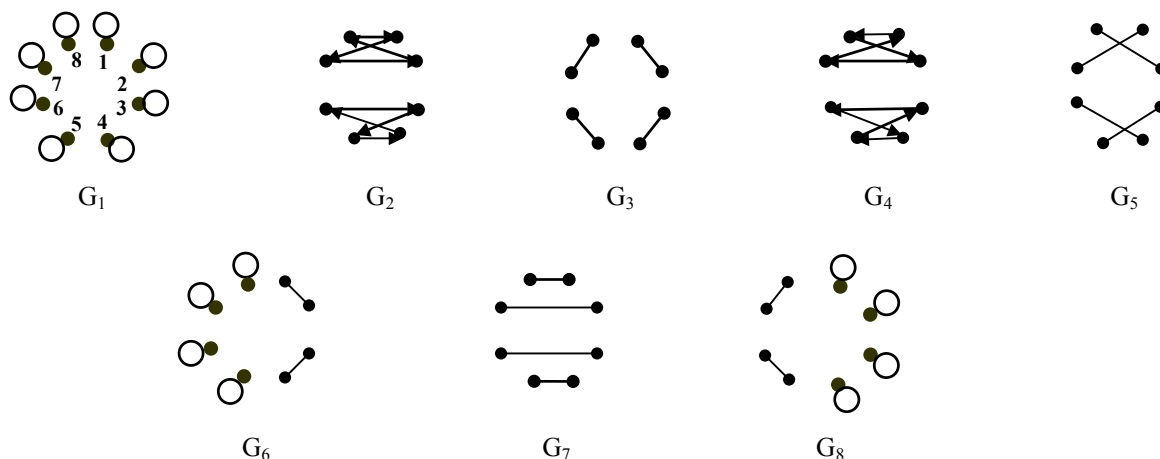
$\mathbf{S}_2$ : conserves *strictly*  $G^{(2)}$ , implements  $\text{UCAG} \leftrightarrow \text{CUGA}$  in  $A^{(2)}$  and  $\text{UCAG} \leftrightarrow \text{AGUC}$  in  $C^{(2)}$  and the Rumer transformation in  $U^{(2)}$ .

$\mathbf{S}_3$ : conserve *strictly*  $U^{(2)}$ , implements  $\text{UCAG} \leftrightarrow \text{CUGA}$  in  $C^{(2)}$  and  $\text{UCAG} \leftrightarrow \text{AGUC}$  in  $A^{(2)}$  and the Rumer transformation in  $G^{(2)}$ .

$\mathbf{S}_4$ : implements the Rumer transformation in all cases.

### 3.3 Rumer and Rumer–Konopel’chenko symmetry for C

Now, we turn to the 64 codons matrix in Eq. (3), and study its symmetries. As for the set of doublets, we consider the eight Wittmann Octets (WO), which are the eight rows in Eq. (3) numbered from 1 to 8, from top to bottom. From the many ways to define graphs between these WOs, we have retained the ones below because first, the eight graphs contain one, the adjacency matrix of which corresponds to the Rumer transformation, a basic transformation. Second, the adjacency matrices of these graphs constitute a symmetry group which is a dihedral group  $D_8$  with eight elements containing, as symmetry sub–groups, a Klein group  $V$  and a cyclic group with two elements  $C_2$ . We find again, in a new way, a result [6] that this end–of–the–chain group  $C_2$  could describe an invariant part of the 64–codon set, more exactly 16 codons, which appear to be invariant across all species with respect to their use, in their respective genetic codes (see the end of this section). Third, these symmetry groups seem to fit nicely into the Rumer–division and the “5’–bisections” of the 64–codon set used by Shcherbak, (see [1] and the references therein), to establish the many arithmetical regularities inside the genetic code. We shall return to this latter point in section 4. Consider now the following eight graphs,  $G_i$  ( $i = 1, 2, \dots, 8$ ):



**Figure 6.** Graph-set for the eight Wittmann's Octets (see text).

These are permutation graphs on the eight Wittmann Octets. For example  $G_2$  corresponds to the permutation  $(7\ 8\ 2\ 1)(5\ 6\ 4\ 3)$  and  $G_6$  to the permutation  $(2\ 1)(4\ 3)(5\ 6\ 7\ 8)$ . It is immediate to write down the adjacency matrices for these graphs. They are:

$$\mathbf{R}_1 = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}, \quad \mathbf{R}_2 = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}, \quad \mathbf{R}_3 = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix}, \quad (9.1)$$

$$\mathbf{R}_4 = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}, \quad \mathbf{R}_5 = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}, \quad \mathbf{R}_6 = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix}, \quad (9.2)$$

$$\mathbf{R}_7 = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}, \quad \mathbf{R}_8 = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix}.$$

With respect to the ordinary matrix product, we obtain the following multiplication table (Table 1) of these matrices, or the Cayley table, as it is called in group theory.

**Table 1.** Multiplication table for the eight matrices  $R_i$

	$R_1$	$R_2$	$R_3$	$R_4$	$R_5$	$R_6$	$R_7$	$R_8$
$R_1$	$R_1$	$R_2$	$R_3$	$R_4$	$R_5$	$R_6$	$R_7$	$R_8$
$R_2$	$R_2$	$R_3$	$R_4$	$R_1$	$R_8$	$R_5$	$R_6$	$R_7$
$R_3$	$R_3$	$R_4$	$R_1$	$R_2$	$R_7$	$R_8$	$R_5$	$R_6$
$R_4$	$R_4$	$R_1$	$R_2$	$R_3$	$R_6$	$R_7$	$R_8$	$R_5$
$R_5$	$R_5$	$R_6$	$R_7$	$R_8$	$R_1$	$R_2$	$R_3$	$R_4$
$R_6$	$R_6$	$R_7$	$R_8$	$R_5$	$R_4$	$R_1$	$R_2$	$R_3$
$R_7$	$R_7$	$R_8$	$R_5$	$R_6$	$R_3$	$R_4$	$R_1$	$R_2$
$R_8$	$R_8$	$R_5$	$R_6$	$R_7$	$R_2$	$R_3$	$R_4$	$R_1$

This is the Cayley table of the dihedral group with eight elements  $D_8$ . Consider now the codon-matrix  $C$ , in Eq. (3), which we reproduce below (for ease of comparison) as table  $C$  ( $R_1$  is the identity so it corresponds to  $C$ ). In the other seven tableaux, we show the action of the remaining seven transformation matrices. They are the following:

UUU UUC	UCU UCC	CUU CUC	CCU CCC	UUG UUA	UCG UCA	CUA CUG	CCA CCG
UUA UUG	UCA UCG	CUA CUG	CCA CCG	UUC UUU	UCC UCU	CUU CUC	CCU CCC
UAU UAC	UGU UGC	CAU CAC	CGU CGC	UAG UAA	UGG UGA	CAA CAG	CGA CGG
UAA UAG	UGA UGG	CAA CAG	CGA CGG	UAC UAU	UGC UGU	CAU CAC	CGU CGC
AUU AUC	ACU ACC	GUU GUC	GCU GCC	AUC AUU	ACC ACU	GUU GUC	GCU GCC
AUA AUG	ACA ACG	GUA GUG	GCA GCG	AUG AUA	ACG ACA	GUA GUG	GCA GCG
AAU AAC	AGU AGC	GAU GAC	GGU GGC	AAC AAU	AGC AGU	GAU GAC	GGU GGC
AAA AAG	AGA AGG	GAA GAG	GGA GGG	AAG AAA	AGG AGA	GAA GAG	GGA GGG
$C$				$(R_6)^{-1} C R_6$			

UUU UUC	UCU UCC	CUC CUU	CCC CCU	UUG UUA	UCG UCA	CUG CUA	CCG CCA
UUA UUG	UCA UCG	CUG CUA	CCG CCA	UUC UUU	UCC UCU	CUC CUU	CCC CCU
UAU UAC	UGU UGC	CAC CAU	CGC CGU	UAG UAA	UGG UGA	CAG CAA	CGG CGA
UAA UAG	UGA UGG	CAG CAA	CGG CGA	UAC UAU	UGC UGU	CAC CAU	CGC CGU
AUA AUG	ACA ACG	GUG GUA	GCG GCA	AUG AUA	ACG ACA	GUG GUA	GCG GCA
AUU AUC	ACU ACC	GUC GUU	GCC GCU	AUC AUU	ACC ACU	GUC GUU	GCC GCU
AAA AAG	AGA AGG	GAG GAA	GGG GGA	AAG AAA	AGG AGA	GAG GAA	GGG GGA
AAU AAC	AGU AGC	GAC GAU	GGC GGU	AAC AAU	AGC AGU	GAC GAU	GGC GGU
$(R_8)^{-1} C R_8$				$(R_3)^{-1} C R_3$			

GGG	GGA	GAG	GAA	AGG	AGA	AAG	AAA		GGG	GGA	GAG	GAA	AGA	AGG	AAA	AAG
GGC	GGU	GAC	GAU	AGC	AGU	AAC	AAU		GGC	GGU	GAC	GAU	AGU	AGC	AAU	AAC
GCG	GCA	GUG	GUA	ACG	ACA	AUG	AUA		GCG	GCA	GUG	GUA	ACA	ACG	AUA	AUG
GCC	GCU	GUC	GUU	ACC	ACU	AUC	AAU		GCC	GCU	GUC	GUU	ACU	ACC	AAU	AUC
CGG	CGA	CAG	CAA	UGG	UGA	UAG	UAA		CGC	CGU	CAC	CAU	UGU	UGC	UAU	UAC
CGC	CGU	CAC	CAU	UGC	UGU	UAC	UAU		CGG	CGA	CAG	CAA	UGA	UGG	UAA	UAG
CCG	CCA	CUG	CUA	UCG	UCA	UUG	UUA		CCC	CCU	CUC	CUU	UCU	UCC	UUU	UUC
CCC	CCU	CUC	CUU	UCC	UCU	UUC	UUU		CCG	CCA	CUG	CUA	UCA	UCG	UUA	UUG
$(\mathbf{R}_7)^{-1}\mathbf{CR}_7$								$(\mathbf{R}_2)^{-1}\mathbf{CR}_2$								
GGU	GGC	GAU	GAC	AGC	AGU	AAC	AAU		GGU	GGC	GAU	GAC	AGU	AGC	AAU	AAC
GGA	GGG	GAA	GAG	AGG	AGA	AAG	AAA		GGA	GGG	GAA	GAG	AGA	AGG	AAA	AAG
GCU	GCC	GUU	GUC	ACC	ACU	AUC	AAU		GCU	GCC	GUU	GUC	ACU	ACC	AAU	AUC
GCA	GCG	GUA	GUG	ACG	ACA	AUG	AUA		GCA	GCG	GUA	GUG	ACA	ACG	AUA	AUG
CGA	CGG	CAA	CAG	UGG	UGA	UAG	UAA		CGU	CGC	CAU	CAC	UGU	UGC	UAU	UAC
CGU	CGC	CAU	CAC	UGC	UGU	UAC	UAU		CGA	CGG	CAA	CAG	UGA	UGG	UAA	UAG
CCA	CCG	CUA	CUG	UCG	UCA	UUG	UUA		CCC	CCU	CUC	CUU	UCU	UCC	UUU	UUC
CCU	CCC	CUU	CUC	UCC	UCU	UUC	UUU		CCG	CCA	CUG	CUA	UCA	UCG	UUA	UUG
$(\mathbf{R}_4)^{-1}\mathbf{CR}_4$								$(\mathbf{R}_5)^{-1}\mathbf{CR}_5$								

In this sub-section, we shall continue to use  $M_1$  and  $M_2$  to name the two members of the Rumer bisection, see section 3, ( $M_1$  is in gray). Now, from the above tables, we see that the general action is concentrated mainly at the third base-position, and the Rumer transformation, acting exclusively, concerns only the first and second base-positions. The group  $D_8$  has, as an interesting sub-group, the Klein group  $V$  with elements  $\{\mathbf{R}_1, \mathbf{R}_3, \mathbf{R}_6, \mathbf{R}_8\}$ . This latter group leaves  $M_1$  and  $M_2$  invariant and, consequently, leaves also invariant all 16 “family boxes”, *i.e.*, all quartets of (four) codons sharing the same first two bases (separated from each other by small dashed lines in the tableaux). Thus, this means that, possibly, only the third base will be altered. Next, the transformation  $\mathbf{R}_7$  implements the Rumer transformation  $UCAG \leftrightarrow GACU$  at all *three* base-positions. As for the other three transformations,  $\mathbf{R}_2$ ,  $\mathbf{R}_4$  and  $\mathbf{R}_5$  of  $D_8$ , they alter the first two base-positions according to the Rumer transformation with, possibly, full invariance or alteration by the (secondary Rumer

transformations mentioned in section 3.1) at the third base–position, see the tableaux. As in section 3.2, we could consider either the Bio–Synthetic Classes or Physico–Chemical Classes, using the same notation as for the doublets in the last section:  $U^{(1)}$ ,  $C^{(1)}$ ,  $A^{(1)}$  and  $G^{(1)}$  and  $U^{(2)}$ ,  $C^{(2)}$ ,  $A^{(2)}$  and  $G^{(2)}$ , respectively. For the former, we shall unit the four Bio–Synthetic Classes into two big ones, the Pyrimidine Bio–Synthetic Class (Pyr–BC), made of  $U^{(1)}$  and  $C^{(1)}$ , and the Purine Bio–Synthetic Class (Pur–BC), made of  $A^{(1)}$  and  $G^{(1)}$ . The first class occupies the four top rows, in matrix (3), and the second class occupy the last four. In this way, the transformations induced by the matrices  $R_i$  act as follows:  $R_1$ ,  $R_3$ ,  $R_6$ ,  $R_8$ , the sub–group  $V$ , conserve (globally) Pyr–BC and Pur–BC while  $R_2$ ,  $R_4$  and  $R_5$  exchange them. Moreover,  $R_6$  conserves *strictly* the 16 codons of  $G^{(1)}$  and  $R_8$  conserves *strictly* the 16 codons of  $U^{(1)}$ . For the latter, it is interesting to transform the codon–matrix  $C$  as follows:

$$C' = X^{-1} C X = \begin{pmatrix} UUU & UUC & CUU & CUC & UCU & UCC & CCU & CCC \\ UUA & UUG & CUA & CUG & UCA & UCG & CCA & CCG \\ AUU & AUC & GUU & GUC & ACU & ACC & GCU & GCC \\ AUA & AUG & GUA & GUG & ACA & ACG & GCA & GCG \\ UAU & UAC & CAU & CAC & UGU & UGC & CGU & CGC \\ UAA & UAG & CAA & CAG & UGA & UGG & CGA & CGG \\ AAU & AAC & GAU & GAC & AGU & AGC & GGU & GGC \\ AAA & AAG & GAA & GAG & AGA & AGG & GGA & GGG \end{pmatrix} \quad (10)$$

where  $X$  is given by (see Eq. (8)):

$$X = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \otimes \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \quad (11)$$

Here, the symbol  $\otimes$  is for the usual Kronecker product of matrices. In (10),  $U^{(2)}$ ,  $C^{(2)}$ ,  $A^{(2)}$  and  $G^{(2)}$  occupy the four quadrants and we could apply the transformations  $R_i$ , as for  $C$ . The transformation patterns are the same. Proceeding as before, we have that the Physico–Chemical Classes Pyr–PC and Pur–PC, which are invariant under the action of  $R_3$ ,  $R_6$ ,  $R_8$ , are exchanged by  $R_7$ ,  $R_2$ ,  $R_4$  and  $R_5$ . (Alternatively, we could let the transformations defined recently in reference [6] act directly on the matrix  $C$  and we obtain the same results.) Concerning the physico–chemical properties, Pelc, in 1965 ([22], see also [23]), analyzed the correlation between the triplets codons and the structure of the amino acids and found that codons with U or C, as a *second* base, correspond mainly to hydrophobic and weakly polar amino acids, whereas those containing A or G, as a *second* base, involve strongly polar amino acids. To close this section, let us give a last example of a symmetry group for  $C$  in which the family boxes of a given Bio–Synthetic Class are mixed. Consider the transformations corresponding to the permutations (1)(23)(45678), (123458)(67) and (their product) (1458)(23)(67) of the Wittmann Octets. As adjacency matrices of the corresponding graphs (not drawn here) they read, respectively (without the identity  $W_1$ ):

$$\mathbf{W}_2 = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}, \quad \mathbf{W}_3 = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}, \quad \mathbf{W}_4 = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}. \quad (12)$$

The set  $\{\mathbf{W}_1, \mathbf{W}_2, \mathbf{W}_3, \mathbf{W}_4\}$  constitutes also a Klein group V. This group acts analogously to  $\mathbf{R}_3, \mathbf{R}_6, \mathbf{R}_8$  but, here,  $\mathbf{W}_2, \mathbf{W}_3$  leave invariant 36 codons and  $\mathbf{W}_4$  only 16. The Rumer sets become mixed but the Bio-Synthetic Classes  $U^{(1)}, C^{(1)}, A^{(1)}$  and  $G^{(1)}$  are globally conserved with possible mixing between family boxes. The group above acts as follows (compare to the action of the first group V, in Eq. (9.2)):

<table border="1" style="width: 100%; border-collapse: collapse; text-align: left;"> <tbody> <tr><td>UUU</td><td>UUC</td><td>UCU</td><td>UCC</td><td>CUU</td><td>CUC</td><td>CCU</td><td>CCC</td></tr> <tr><td>UUA</td><td>UUG</td><td>UCA</td><td>UCG</td><td>CUA</td><td>CUG</td><td>CCA</td><td>CCG</td></tr> <tr><td>UAU</td><td>UAC</td><td>UGU</td><td>UGC</td><td>CAU</td><td>CAC</td><td>CGU</td><td>CGC</td></tr> <tr><td>UAA</td><td>UAG</td><td>UGA</td><td>UGG</td><td>CAA</td><td>CAG</td><td>CGA</td><td>CGG</td></tr> <tr><td>AAU</td><td>AUC</td><td>ACU</td><td>ACC</td><td>GUU</td><td>GUC</td><td>GCU</td><td>GCC</td></tr> <tr><td>AUA</td><td>AUG</td><td>ACA</td><td>ACG</td><td>GUA</td><td>GUG</td><td>GCA</td><td>GCG</td></tr> <tr><td>AAU</td><td>AAC</td><td>AGU</td><td>AGC</td><td>GAU</td><td>GAC</td><td>GGU</td><td>GGC</td></tr> <tr><td>AAA</td><td>AAG</td><td>AGA</td><td>AGG</td><td>GAA</td><td>GAG</td><td>GGA</td><td>GGG</td></tr> </tbody> </table>	UUU	UUC	UCU	UCC	CUU	CUC	CCU	CCC	UUA	UUG	UCA	UCG	CUA	CUG	CCA	CCG	UAU	UAC	UGU	UGC	CAU	CAC	CGU	CGC	UAA	UAG	UGA	UGG	CAA	CAG	CGA	CGG	AAU	AUC	ACU	ACC	GUU	GUC	GCU	GCC	AUA	AUG	ACA	ACG	GUA	GUG	GCA	GCG	AAU	AAC	AGU	AGC	GAU	GAC	GGU	GGC	AAA	AAG	AGA	AGG	GAA	GAG	GGA	GGG	<table border="1" style="width: 100%; border-collapse: collapse; text-align: left;"> <tbody> <tr><td>UUU</td><td>UCU</td><td>UUC</td><td>UCC</td><td>CUU</td><td>CUC</td><td>CCU</td><td>CCC</td></tr> <tr><td>UAU</td><td>UGU</td><td>UAC</td><td>UGC</td><td>CAU</td><td>CAC</td><td>CGU</td><td>CGC</td></tr> <tr><td>UUA</td><td>UCA</td><td>UUG</td><td>UCG</td><td>CUA</td><td>CUG</td><td>CCA</td><td>CCG</td></tr> <tr><td>UAA</td><td>UGA</td><td>UAG</td><td>UGG</td><td>CAA</td><td>CAG</td><td>CGA</td><td>CGG</td></tr> <tr><td>AAU</td><td>ACU</td><td>AUC</td><td>ACC</td><td>GUU</td><td>GUC</td><td>GCU</td><td>GCC</td></tr> <tr><td>AUA</td><td>ACA</td><td>AUG</td><td>ACG</td><td>GUA</td><td>GUG</td><td>GCA</td><td>GCG</td></tr> <tr><td>AAU</td><td>AGU</td><td>AAC</td><td>AGC</td><td>GAU</td><td>GAC</td><td>GGU</td><td>GGC</td></tr> <tr><td>AAA</td><td>AGA</td><td>AAG</td><td>AGG</td><td>GAA</td><td>GAG</td><td>GGA</td><td>GGG</td></tr> </tbody> </table>	UUU	UCU	UUC	UCC	CUU	CUC	CCU	CCC	UAU	UGU	UAC	UGC	CAU	CAC	CGU	CGC	UUA	UCA	UUG	UCG	CUA	CUG	CCA	CCG	UAA	UGA	UAG	UGG	CAA	CAG	CGA	CGG	AAU	ACU	AUC	ACC	GUU	GUC	GCU	GCC	AUA	ACA	AUG	ACG	GUA	GUG	GCA	GCG	AAU	AGU	AAC	AGC	GAU	GAC	GGU	GGC	AAA	AGA	AAG	AGG	GAA	GAG	GGA	GGG
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We see that the Bio–Synthetic Classes keep their individuality (globally invariant) and the codons of the amino acids of a given class get exchanged in various manners. Take  $W_2$  for example. It acts in  $U^{(1)}$  in such a way that it reproduce the action of  $X_1$  in Eq. (8): the exchanges are vertical, horizontal and diagonal. The exchanges in  $C^{(1)}$  are only vertical and in  $A^{(1)}$  only horizontal. As for  $G^{(1)}$ , its 16 codons are strictly conserved, as with the action of  $R_6$  (see above). A similar analysis could be made with  $W_3$  and  $W_4$ . Before closing this section, let us return to our first Klein group  $V$ :  $\{R_1, R_3, R_6, R_8\}$ . As we have mentioned in the introduction, the manner we have built these transformations is guided. In reference [6], we were motivated by the search of transformation groups that lead to invariance of groups of codons across all species. It is well known that some living species use differently the genetic code. They use a variant form of the “standard” genetic code where, in general and in each case, only few codons are concerned and there are several known variants, see [15,16]. These variant codons code evidently for a different amino acid, other than the one in the above table which is the standard form. The table below (Table 2), represents Eq. (3) of section 2.3 with the additional information about the amino acids and their molecular weights or total number of nucleons. The codons which are subject to variations, considering all (known) genomes, nuclear and mitochondrial, and taken from [16], are underlined. Examining the above table reveals that the Bio–Synthetic Class  $G^{(1)}$ , and only this class among the four, has 16 codons which are never subject to variations, [6]. The authors of reference [15] explain that there are several reasons why the codons in the form GNN (N: any base, U, C, A and G) are thought to be the most primitive. Loomis, [17], in the beautiful article entitled “Origin of life” mentions also the five amino acids glycine, valine, alanine, aspartic acid and glutamic acid (those of class  $G^{(1)}$ ) when discussing the appearance of the hypercycles in the pre–biotic soup.

**Table 2.** The standard genetic code table

UUU Phe	UUC 165	UCU	UCC	<u>CUU</u>	<u>CUC</u>	CCU	CCC
Leu	131	Ser	105	Leu	131	Pro	115
<u>UUA</u>	<u>UUG</u>	<u>UCA</u>	<u>UCG</u>	<u>CUA</u>	<u>CUG</u>	<u>CCA</u>	<u>CCG</u>
<u>UAU</u>	<u>UAC</u>	<u>UGU</u>	<u>UGC</u>	<u>CAU</u>	<u>CAC</u>	<u>CGU</u>	<u>CGC</u>
Tyr	181	Cys	121	His	155		
Stop1	Stop2	Stop3	Trp <sub>204</sub>	Gln	146	Arg	174
<u>UAA</u>	<u>UAG</u>	<u>UGA</u>	<u>UGG</u>	<u>CAA</u>	<u>CAG</u>	<u>CGA</u>	<u>CGG</u>
<u>AUU</u>	<u>AUC</u>	<u>ACU</u>	<u>ACC</u>	<u>GUU</u>	<u>GUC</u>	<u>GCU</u>	<u>GCC</u>
Ile	131	Thr	119	Val	117	Ala	89
<u>AUA</u>	Met <sub>149</sub> <u>AUG</u>	<u>ACA</u>	<u>ACG</u>	<u>GUA</u>	<u>GUG</u>	<u>GCA</u>	<u>GCG</u>
<u>AAU</u>	<u>AAC</u>	<u>AGU</u>	<u>AGC</u>	<u>GAU</u>	<u>GAC</u>	<u>GGU</u>	<u>GGC</u>
Asn	132	Ser	105	Asp	133		
Lys	146	Arg	174	Glu	147	Gly	75
<u>AAA</u>	<u>AAG</u>	<u>AGA</u>	<u>AGG</u>	<u>GAA</u>	<u>GAG</u>	<u>GGA</u>	<u>GGG</u>

As a result, we have [6], that the cyclic group  $C_2$ , a sub-group of a certain Klein group, itself sub-group of a dihedral group  $D_8$  according to the chain  $D_8 \subset V \subset C_2$ , as an end-of-chain group implements the invariance of the above mentioned 16 codons of  $G^{(1)}$ . In the context of the present work, the group  $C_2$  corresponds to the set  $\{\mathbf{R}_1, \mathbf{R}_6\}$ , sub-group of  $V$  ( $\mathbf{R}_1, \mathbf{R}_3, \mathbf{R}_6, \mathbf{R}_8$ ), itself sub-group of  $D_8$  ( $\mathbf{R}_i, i = 1, 2, \dots, 8$ ).

The guiding idea, in considering this problem, was to define graphs with a maximum of four invariant rows, and their variations. For example, in the graph  $G_6$ , of section 3.3, the nodes 5, 6, 7 and 8 are connected only to themselves (the self-loops) while the nodes 1, 2, 3 and 4 are subject to permutations with an edge between the nodes 1 and 2, in the one hand and 3 and 4, on the other. Furthermore, as we explained in section 2, these transformations between nodes concern at the same time the rows and the columns. In this way, we constructed the corresponding adjacency matrix,  $\mathbf{R}_6$ , which gives us, in this case, strict invariance in  $G^{(1)}$  and transitions in  $A^{(1)}$ , both belonging to the four last rows and only transversions in  $U^{(1)}$  and  $C^{(1)}$ , both belonging to the first four rows. For all other transformations in this work, we proceeded analogously.

#### 4 MATRIX-NORMS, TRACES, AND SHCHERBAK'S QUANTUM PRIME 037

As mentioned in the introduction, we end this article by presenting some (striking) numbers which arise by “sizing” our classification matrices for the 16 doublets and the 64 codons. Before giving these results let us, first, recall some numbers pertaining to the genetic code functioning. Besides the (ubiquitous) existence of 64 codons and 20 (canonical) amino acids, there is a total of 44 *degenerate* codons (64–20) of which 24 are in  $M_1$  and 20 in  $M_2$  (counting the three stop codons). Note that not including the latter reduces this number to 41, see below.

Another (complementary) manner to reckon, which goes back to the physicist Georges Gamow (1954) see [1], is based on the division of the 64 triplet codons set into three sub-sets, depending on their composition (identical and unique base) regardless of their types and positions in the codons. This partitioning is shown in Tables 3–5 (in the first three rows in each table)

**Table 3.** The “36” Family (two identical bases)

CUU	UUA	UUG	CUC	CCA	CCG	AAU	AAC	AGA	GGU	GGC	AGG
UCU	AUU	GUU	CCU	ACC	GCC	UAA	CAA	AAG	UGG	CGG	GAG
UUC	UAU	UGU	UCC	CAC	CGC	AUA	ACA	GAA	GUG	GCG	GGA
444	555	666	555	777	888	777	888	1110	999	1110	1221

**Table 4.** The “24” Family (one unique base)

CAU	CUA	CUG	GUC	UGA	AGU	AGC	ACG
UCA	ACU	GCU	CGU	AUG	UAG	CAG	GAC
AUC	UAC	UGC	UCG	GAU	GUA	GCA	CGA
666	666	777	777	888	888	999	999

**Table 5.** The “4” Family (three identical bases)

UUU	CCC	AAA	GGG
111	222	333	444

There are therefore 36 codons in the “36” Family (Table 3), 24 codons in the “24” Family (Table 4) and 4 codons in the “4” Family (Table 5). Note that 60 (36 + 24) is also an important number which arise in the combinatorial necklace model of the genetic code [18], where the structure consists of 64 beads (the codons) of four colors (the bases) and the colored beads form hanging vertical decorations or chains of three ( $x = 3$ ) beads. In this model, there are  $y = 4^3$  distinct vertical chains. The total number of possible vertical decorations containing at least two colors each is  $y^x - y = 60$  and  $y = 4$  decorations are of the same color.

Now, we turn to our results. We have found interesting to assign *attributes* to the bases and *norms* to the (classification) matrices. Let us begin by the norms, more exactly the matrix–norms. (The latter, are widely used in many applications of linear algebra, and have been termed the “yardsticks”. Also, they are often used in matrix–based algorithms.) These norms capture the essential notions of size and distance in vector spaces. The matrix–norms of a matrix  $A$ , we shall use in this paper, are the 1–norm,  $\|A\|_1$ , which is equal to the *maximum column sum* and the  $\infty$ –norm,  $\|A\|_\infty$ , which is equal to the *maximum row sum*. They are defined as follows

$$\|N\|_1 = \max_{1 \leq j \leq n} \sum_{i=1}^n |a_{ij}| \quad \|N\|_\infty = \max_{1 \leq i \leq n} \sum_{j=1}^n |a_{ij}| \quad (13)$$

where the modules in the sums are vector norms. We have therefore a mean to compare the rows between themselves and the columns between themselves. Now, concerning the attributes of the bases, we shall concentrate on their “molecular size” and also on their hydrogen bonding properties. We shall take as the “molecular size index” of a given base the following expression

$$\mu = 2(n_N - n_C) + n_O + 2 \quad (14)$$

Where the numbers refer to the number of nitrogen, carbon and oxygen atoms, respectively, in a given base (U, C, A and G). This formula has been introduced in 1991 by Rosen [19], (see also [2]). The size index,  $\mu$ , captures the monotonic size gradation of the four bases: U = 0, C = 1, A = 2, G = 3 (see section 2.1). This ordering, among others, is often considered (see [13] for a recent example). As for the hydrogen bond attribute, it is unambiguous: U = A = 2 and C = G = 3. Now, let us gather these numbers into the two following simple 2×2 matrices, respectively  $\mu$  and  $\mathbf{h}$ .

$$\mu = \begin{pmatrix} 0 & 1 \\ 2 & 3 \end{pmatrix} + \mathbf{J} = \begin{pmatrix} 1 & 2 \\ 3 & 4 \end{pmatrix}, \quad \mathbf{h} = \begin{pmatrix} 2 & 3 \\ 2 & 3 \end{pmatrix}. \quad (15)$$

We have slightly translated the (would-be) matrix  $\mu$  by one unit by adding the matrix  $\mathbf{J}$ , the all-1 2×2 matrix, mentioned in section 3.1, just to avoid the zero. This is justified because this “attribute” is certainly rough but, as we shall see, it has interesting consequences. Let us begin by considering the set of 16 doublets, in Eq. (2). In this case, the rows which are sized by  $\|\mathbf{A}\|_\infty$ , are the Wittmann Doublets and the columns which are compared by  $\|\mathbf{A}\|_1$  are the sub-sets of doublets sharing the same total number of hydrogen bonds. The matrix encoding the sizes of the doublets is computed as follows:

$$\Pi^{(\text{ms})} = \mu \otimes \mathbf{J} + \mathbf{J} \otimes \mu = \begin{pmatrix} 2 & 3 & 3 & 4 \\ 4 & 5 & 5 & 6 \\ 4 & 5 & 5 & 6 \\ 6 & 7 & 7 & 8 \end{pmatrix}. \quad (16)$$

Were  $\mathbf{J}$  is the 2×2 all-1 matrix mentioned above. For the second attribute, the following matrix gives the total number of hydrogen bonds in each doublet.

$$\Pi^{(\text{hb})} = \mathbf{h} \otimes \mathbf{J} + \mathbf{J} \otimes \mathbf{h} = \begin{pmatrix} 4 & 5 & 5 & 6 \\ 4 & 5 & 5 & 6 \\ 4 & 5 & 5 & 6 \\ 4 & 5 & 5 & 6 \end{pmatrix}. \quad (17)$$

For these matrices we have:

$$\|\Pi^{(\text{ms})}\|_1 = 24, \quad \|\Pi^{(\text{ms})}\|_\infty = 28, \quad \|\Pi^{(\text{hb})}\|_1 = 24, \quad \|\Pi^{(\text{hb})}\|_\infty = 20, \quad \|\Pi^{(\text{hb})}\|_1 + \|\Pi^{(\text{hb})}\|_\infty = 44. \quad (18)$$

Note that the traces of the matrices (16) and (17) are both equal to 20. It is also interesting to compute the sum of the (hydrogen bond) attribute over the sets  $M_1$  and  $M_2$  (see the above sections). We have:

$$\sum_{M_1}^{(\text{hb})} = 44, \quad \sum_{M_2}^{(\text{hb})} = 36. \quad (19)$$

Now, for the codons, we have:

$$\Theta^{(ms)} = \mu \otimes J \otimes J + J \otimes \mu \otimes J + J \otimes J \otimes \mu = \begin{pmatrix} 3 & 4 & 4 & 5 & 4 & 5 & 5 & 6 \\ 5 & 6 & 6 & 7 & 6 & 7 & 7 & 8 \\ 5 & 6 & 6 & 7 & 6 & 7 & 7 & 8 \\ 7 & 8 & 8 & 9 & 8 & 9 & 9 & 10 \\ 5 & 6 & 6 & 7 & 6 & 7 & 7 & 8 \\ 7 & 8 & 8 & 9 & 8 & 9 & 9 & 10 \\ 7 & 8 & 8 & 9 & 8 & 9 & 9 & 10 \\ 9 & 10 & 10 & 11 & 10 & 11 & 11 & 12 \end{pmatrix} \quad (20)$$

and

$$\Theta^{(hb)} = h \otimes J \otimes J + J \otimes h \otimes J + J \otimes J \otimes h = \begin{pmatrix} 6 & 7 & 7 & 8 & 7 & 8 & 8 & 9 \\ 6 & 7 & 7 & 8 & 7 & 8 & 8 & 9 \\ 6 & 7 & 7 & 8 & 7 & 8 & 8 & 9 \\ 6 & 7 & 7 & 8 & 7 & 8 & 8 & 9 \\ 6 & 7 & 7 & 8 & 7 & 8 & 8 & 9 \\ 6 & 7 & 7 & 8 & 7 & 8 & 8 & 9 \\ 6 & 7 & 7 & 8 & 7 & 8 & 8 & 9 \\ 6 & 7 & 7 & 8 & 7 & 8 & 8 & 9 \end{pmatrix}. \quad (21)$$

It is important to carry out the products in the order displayed, to reproduce the correct number of the sum of the molecular indices or the total number of hydrogen bonds in all the 64 codons. In both definitions (20) and (21), the first term gives the contribution of the first base, the second that of the second base and finally the third term adds the contribution of the third base. This is also true for the doublet matrices in Eqs. (16) and (17) with only two bases. For the matrix in (20), we have  $\|\Theta^{(ms)}\|_1 = 72$ ,  $\|\Theta^{(ms)}\|_\infty = 84$ , and  $\text{Tr}(\Theta^{(ms)}) = 60$ . For the one in Eq. (21), we obtain  $\|\Theta^{(hb)}\|_1 = 72$ ,  $\|\Theta^{(hb)}\|_\infty = 60$ , and  $\text{Tr}(\Theta^{(hb)}) = 60$ . It is interesting to note that the last number, 60, plays also an important role in the work on the genetic code by Petoukhov [25], who constructed a similar matrix to matrix (21). We could also use, in place of the Kronecker product, the Kronecker product with *concatenation* (see section 2.2 and footnote 2) to obtain the interesting matrix (the double vertical bars are for concatenation):

$$\Theta_c^{(ms)} = \mu \parallel \mu \parallel \mu = \begin{pmatrix} 111 & 112 & 121 & 122 & 211 & 212 & 221 & 222 \\ 113 & 114 & 123 & 124 & 213 & 214 & 223 & 224 \\ 131 & 132 & 141 & 142 & 231 & 232 & 241 & 242 \\ 133 & 134 & 143 & 144 & 233 & 234 & 243 & 244 \\ 311 & 312 & 321 & 322 & 411 & 412 & 421 & 422 \\ 313 & 314 & 323 & 324 & 413 & 414 & 423 & 424 \\ 331 & 332 & 341 & 342 & 431 & 432 & 441 & 442 \\ 333 & 334 & 343 & 344 & 433 & 434 & 443 & 444 \end{pmatrix} \quad (22)$$

This operation, using the concatenation of matrix elements, has been introduced in [3] to make

sure that the non-commutativity of the bases in the triplets is respected. For example, in the above matrix the triplets UUC, UCU and CUU (see Table 2) are assigned the numbers 112, 121 and 211, respectively, which are all different, as we want. In fact, all the 64 triplets are numerically distinct. Had we taken only the ordinary Kronecker product, these assignments would have been 2 in all three cases, because the latter product involves ordinary multiplication of numbers. Moreover, the codon–numbers, generated by concatenation are interesting because when they are grouped into 20 triplets (of triplets codons) that is 12 triplets in the “**36**” Family and 8 triplets in the “**24**” Family, they show regular numerical patterns, see Tables 3–5 and below. Now, we have for the norms and the trace, in this case:

$$\|\Theta_c^{(ms)}\|_1 = 2664, \|\Theta_c^{(ms)}\|_\infty = 3108, \text{Tr}(\Theta_c^{(ms)}) = 2220.$$

The comparison of the numbers in Eqs. (18) and (19) and those described at the beginning of this section is, at least, striking. Even the number 28, which was not yet mentioned, could possibly find its place in the quasi 28–gon (or *Icosikaioctagon*) recent theory of the genetic code by Yang, which is based solely on the set of the 16 doublets [13]. What is really amazing is that if one permutes the two numbers, 3 and 4, in the second row of the first matrix ( $\mu$ ) in Eq. (15), which corresponds to another ordering of the bases (U = 0, C = 1, G = 2, A = 3, see above) chosen by Yang, and relying on another attribute, the  $sp^2$  N–atom number, where N is for nitrogen, then the obtained doublet–matrix as in Eq. (16) has for its trace and norms  $\text{Tr}(\Pi^{(ms)}) = 16, \|\Pi^{(ms)}\|_1 = 20$ , by  $\|\Pi^{(ms)}\|_\infty = 28$ , *i.e.*, just the right three numbers in Yang’s theory, which we recall, is based solely on the set of 16 doublets. Also the numbers 60 and 72 are interesting. From Eq. (21), we see that all the Wittmann Octets, the rows, have the same total number of hydrogen bonds which is 60. We have already shown the relevance of this number to the combinatorial necklace model [18]. As for the second, 72, interestingly, we have found in the recent literature connected with the use of graph theory to study the structural properties of the metabolic pathways (Fell and Wagner, [21]), that 72 happens to be the total number of reactions in the nucleotide and nucleoside biosynthesis. At least, this could happen to be just a happy coincidence.

Now, before ending this article, let us say some words on the work by Shcherbak, as promised in the introduction. Shcherbak, by using the Rumer–Konopel’chenko partitioning of the 64 codons and the number of nucleons in the amino acids, separating the side chain, which is variable, from the standard blocks (with 74 nucleons), which are the same for all amino acids, established several number of amazing *exact balances* and *regularities*. Let us mention only some representative ones, but there are many other interesting ones in [1]. First, by retaining the Rumer division, one has (see Table 2):

- Total number of nucleons (whole molecule) in  $M_1$ : 925
- Total number of nucleons in the blocks, in  $M_1$ : 592
- Total number of nucleons in the side chains, in  $M_1$ : 333

- Total number of nucleons in the side chains, in  $M_2$ : 1110
- Total number of nucleons in the blocks, in  $M_2$ : 1110

For  $M_2$ , there is *exact balance*. For  $M_1$ , by invoking the Prime Quantum Divisibility by 37, one is left with the first Pythagorean triple (3, 4, 5):  $333/37 = 3^2$ ,  $592/37 = 4^2$  and  $925/37 = 5^2$ . As a second example, consider the Pyrimidine Bio–Synthetic Class (Pyr–BC), and the Purine Bio–Synthetic Class (Pur–BC), considered in the last section. They correspond in [1] to the series with the 5′–pyrimidine bases (5′ bisection) and to the series with the 5′ purine bases, respectively. In the first cases there is again an *exact balance*: the sum of nucleons in the standard blocks is 814 and the sum in the side chains is also 814, with a grand total 1628. In the other case there is no balance but the total number of nucleons is 1517. Let us note that the above numbers, 1628 and 1517, like all others are both divisible by 37. We have that  $1628/37 = 44$  and  $1517/37 = 41$ . We have already met these two numbers, 44 and 41 (see the beginning of this section). Note, importantly, that the difference between 44 and 41 (that is with or without the 3 stop–codons), is correctly “managed”: the stop–codons belong to the Pyrimidine Bio–Synthetic Class (Pyr–BC) or the 5′ bisection, see Table 2. Shcherbak has shown also that the digital representation of the balances, as consequence of the criterion of divisibility by 37, acquires the unique form  $aaa$  with  $a = 1, 2, \dots, 9$ . It is interesting to note that similar forms arise also for the codons independently of the amino acids and the numbers of their nucleons, when they are grouped *à la* Gamow (see the “**36**”, “**24**” and “**4**” Families above), into triplets (of codons). The codons in the “**36**” Family are in bold characters, in Table 2. In the fourth rows of Tables 1, 2 and 3, we have computed the sum of the numbers of the codons from the matrix (22). There is nothing magical with these particular forms: they are simply a consequence of the mathematical fact that when one sums three three–digit decimal numbers by carrying out the (three) permutations, one obtains  $abc + cab + bac = 111 \times (a + b + c)$  which is, first, of the required form and, second, divisible by 37, as 111 is. Finally, let us show briefly that the number 37, which plays a basic role in the work of Shcherbak, could be derived with the help of the above size and hydrogen bond matrices. As a matter of fact, this number is obtained in two ways and independently of the amino acid nucleon numbers. In the first, it is obtained as the ratio of two traces (invariants):

$$\frac{\text{Tr}(\Theta_c^{(ms)})}{\text{Tr}(\Theta^{(hb)})} = \frac{\text{Tr}(\Theta_c^{(ms)})}{\text{Tr}(\Theta^{(ms)})} = \frac{2220}{60} = 37 \quad (23)$$

In the second, it is obtained as the ratio of homologous norms, one from the hydrogen bond–matrix Eq. (22), and the other from the molecular size–matrix Eq. (20):

$$\frac{\|\Theta_c^{(ms)}\|_1}{\|\Theta^{(ms)}\|_1} = \frac{2664}{72} = 37, \quad \frac{\|\Theta_c^{(ms)}\|_\infty}{\|\Theta^{(ms)}\|_\infty} = \frac{3108}{84} = 37, \quad (24)$$

Note that one could also obtain 37 as the ratio of the total number of nucleons in the *amino acids* in  $M_2$  (2220, see above or compute it from Table 2) and the trace of  $\Theta^{(ms)}$  or  $\Theta^{(hb)}$  of *base-made-codons* matrices so that, while the (equational) symmetry is lost, the link between the nucleic acids and the amino acids is made. Note that fifteen amino acids are represented in  $M_2$ , which is 75% of the total of 20. The present author would be almost prone to re-name the title of this last section as “autopoietic numbers in the 16 doublets and the 64 codons”. We stop here but we shall return to these questions in a following publication [24].

**Note added.** One may wonder, as suggested by the reviewers, if there could be any applications of the above numerical relations (in section 4). This is a delicate but nevertheless an interesting question. Independently of (possible) applications, one tempting occurrence would be to look at these numbers *as* some (new) kind of *numeric genetic information* appearing “written” on the physical basic units of life (RNA–DNA, amino acids) and revealed when these are arranged into definite sets with patterns exhibiting symmetry, see reference [26], for a recent work. Now, since the submission of this paper and, perhaps, as a beginning answer in the direction of applications, we have derived, for example, *explicitly*, the number 37 which has a tantamount importance in Shcherbak’s work, by considering a *real* system (RNA–and–DNA components), in place of just deriving it from abstract matrices and norms, as we did in the present work. In fact, we did more than this: we have established a connection between Shcherbak’s work, with its ubiquitous (and omnipresent) number 37, and the recent 28–gon polyhedral theory of the genetic code by Yang, [24].

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