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A Novel DNA Sequence Vector Space over an extended Genetic Code Galois Field

*Robersy Sánchez [1,2], Ricardo Grau [2,3] and Eberto R. Morgado[3]

[1]Research Institute of Tropical Roots, Tuber Crops and Banana (INIVIT). Biotechnology group. Santo Domingo. Villa Clara. Cuba.

[2]Faculty of Mathematics Physics and Computation, Central University of Las Villas, Villa Clara, Cuba.

[3] Center of Studies on Informatics, Central University of Las Villas, Villa Clara, Cuba

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Abstract

In the vector space of DNA sequences over the Galois field of the 64 codons (*GF* (64)), recently published, deletions and insertions (indel) could not be analyzed. Now, in order to include these kinds of mutations, we have defined a new Galois field over the set of extended triplets $X_1X_2X_3$ (C_{125}), where $X_i \in$ {O, A, C, G, U}. Taking the polynomial coefficients a_0, a_1, $a_2 \in GF$ (5) and the bijective function $f: GF(5) \rightarrow$ {O, A, C, G, U}, where $f(0)$ = O, $f(1)$ = A, $f(2)$ = C, $f(3)$ = G, $f(4)$ = U, bijection Ψ is induced such that $\Psi(a_0 + a_1x + a_2x^2) = (f(a_1), f(a_2), f(a_0)) = (X_1X_2X_3)$. The field ($C_{125}$, +, •) allows the definition of a novel *N*-dimensional vector space (*S*) over the field *GF* (5^3) on the set of all 125^N sequences of extended triplets in which all possible DNA sequence alignments of length *N* are included. Here the "classical gap" produced by alignment algorithm corresponds to the neutral element "O". In the vector space *S,* all mutational events that take place in the molecular evolution process can be described by means of endomorphisms, automorphisms and translations. In particular, the homologous (generalized) recombination between two homologous DNA duplexes involving a reciprocal exchange of DNA sequences –e.g. between two chromosomes that carry the same

* Robersy Sánchez: robersy@uclv.edu.cu

Corresponding address: Apartado postal 697. Santa Clara 1. CP 50100. Villa Clara. Cuba genetic loci– algebraically corresponds to the action of two automorphism pairs over two paired DNA duplexes.

1. Introduction

A new N-dimensional vector space of DNA sequences over the Galois field of the 64 codons (GF (64)) was recently presented [SAN 05]. This vector space was derived taking into account the order of the bases proposed in the Boolean lattice of the four DNA bases [SAN 04] [SAN 04a]. The isomorphism φ: $B(X) \rightarrow (Z_2)^2$ between the Boolean lattices of the four DNA bases $B(X)$ and $((Z_2)^2, \vee, \wedge)$ ($Z_2 = \{0,1\}$), and the biological importance of base positions in the codons were used to state a partial order in the codon set. As a result every codon was represented in the field GF (64) as a binary sextuplet.

In this vector space, gene point mutations were considered linear transformations or translations of the wild type gene, however deletions and insertions (indel) could not be considered. Now, in order to include indel mutations, we have defined a new Galois field over the set of elements $X_1X_2X_3$ (C_{125}), where $X_i \in \{O, A, C, G, U\}$. This set can be called the extended triplet set and the elements $X_1X_2X_3$, the extended triplets. At present, the starting base order used here comes from the recently reported Z_{64}-algebra of the genetic code [SAN 05a]. In this Z_{64}-algebra, the base order {A, C, G, U} was obtained by considering the genetic code as a non-dimensional code scale of amino acid interaction energies in proteins.

Like in previous articles, we have kept in mind the biological importance of base position in the codon to state a codon order in the genetic code. The importance of the base position is suggested by the error frequency (accepted mutations) found in codons. Errors on the third base are more frequent than on the first base, and, in turn, these are more frequent than errors on the second base [WOE 85] [FRI 64] [PAR 89]. These positions, however, are very conservative with respect to changes in polarity of coded amino acids [ALF 69].

The principal aim of this work is to show that all mutational events that take place in the molecular evolution process can be described by means of endomorphisms, automorphisms and translations of a novel N-dimensional vector space over the Galois field GF (5^3). The new vector space defined over the set of all 125^N sequences of extended triplets includes all possible DNA sequence alignments of length N. Here the “classical gaps” produced by alignment algorithms correspond to the neutral element “O”.

2. Theoretical model

The concepts of Galois fields and vector space over a finite field are the mathematical basic ideas used in our model. A mathematical background about these structures can be found in the references [RED 67] [WAE 70] [SAN 05].

Our starting point is the base order {A, C, G, U} derived from the Z_{64}-algebra of the genetic code [SAN 05a]. In order to analyze indel mutations, this alphabet may be extended including the new symbol "O" to denote base omissions (gaps) in DNA sequence alignments. As a result, a new triplet set can be built with elements $X_1X_2X_3$ where $X_i \in \{O, A, C, G, U\}$. This set can be called the extended triplet set C_{125} and the elements $X_1X_2X_3$, the extended triplets.

Now, considering the order in the set {O, A, C, G, U} and the biological importance of the base position in the codon, it is possible to establish an order in the extended triplet set, i.e. from triplet OOO to UUU. First, in the triplets $X_1X_2X_3$ keeping invariables bases X_1 and X_2, the third base X_3 is consecutively changed until all possibilities are exhausted. Next, a similar variation is applied to the first base and finally to the second one, i.e. the variations are introduced from the less biologically relevant base to the most relevant base in the codon. Then, the ordered triplet set shown in the Table 1 was obtained.

2.1. Nexus between the Galois Field Elements and the Set of Codons

As one can see in Table 1, a bijection is suggested between the orders in the extended triplet set and the $GF\,(5^3)$ elements. In particular, there is a bijective function f: $GF\,(5) \rightarrow \{O, A, C, G, U\}$, between the elements of $GF\,(5)$ and the letters $X_k \in \{O, A, C, G, U\}$. This function is explicitly given by the equalities:

$$f(0) = \mathrm{O}, f(1) = \mathrm{A}, f(2) = \mathrm{C}, f(3) = \mathrm{G}, f(4) = \mathrm{U}$$

Next, taking into account the biological importance of base positions in codons, we can state the bijective function Ψ : $GF\,(5^3) \rightarrow C_{125}$ between the extended triplet set and the polynomial representation of $GF\,(5^3)$ elements:

$$\Psi(a_0 + a_1x + a_2x^2) = (f(a_1), f(a_2), f(a_0)) = X_1X_2\,X_3$$

Table 1. Ordered set of extended triplets corresponding to the elements of *GF* (5^3).

a	O			A			C			G			U			
	I	II	III	I	II	III	I	II	III	I	II	III	I	II	III	
O	0	000	OOO	25	001	OAO	50	002	OCO	75	003	OGO	100	004	OUO	O
	1	100	OOA	26	101	OAA	51	102	OCA	76	103	OGA	101	104	OUA	A
	2	200	OOC	27	201	OAC	52	202	OCC	77	203	OGC	102	204	OUC	C
	3	300	OOG	28	301	OAG	53	302	OCG	78	303	OGG	103	304	OUG	G
	4	400	OOU	29	401	OAU	54	402	OCU	79	403	OGU	104	404	OUU	U
A	5	010	AOO	30	011	AAO	55	012	ACO	80	013	AGO	105	014	AUO	O
	6	110	AOA	31	111	AAA	56	112	ACA	81	113	AGA	106	114	AUA	A
	7	210	AOC	32	211	AAC	57	212	ACC	82	213	AGC	107	214	AUC	C
	8	310	AOG	33	311	AAG	58	312	ACG	83	313	AGG	108	314	AUG	G
	9	410	AOU	34	411	AAU	59	412	ACU	84	413	AGU	109	414	AUU	U
C	10	020	COO	35	021	CAO	60	022	CCO	85	023	CGO	110	024	CUO	O
	11	120	COA	36	121	CAA	61	122	CCA	86	123	CGA	111	124	CUA	A
	12	220	COC	37	221	CAC	62	222	CCC	87	223	CGC	112	224	CUC	C
	13	320	COG	38	321	CAG	63	322	CCG	88	323	CGG	113	324	CUG	G
	14	420	COU	39	421	CAU	64	422	CCU	89	423	CGU	114	424	CUU	U
G	15	030	GOO	40	031	GAO	65	032	GCO	90	033	GGO	115	034	GUO	O
	16	130	GOA	41	131	GAA	66	132	GCA	91	133	GGA	116	134	GUA	A
	17	230	GOC	42	231	GAC	67	232	GCC	92	233	GGC	117	234	GUC	C
	18	330	GOG	43	331	GAG	68	332	GCG	93	333	GGG	118	334	GUG	G
	19	430	GOU	44	431	GAU	69	432	GCU	94	433	GGU	119	434	GUU	U
U	20	040	UOO	45	041	UAO	70	042	UCO	95	043	UGO	120	044	UUO	O
	21	140	UOA	46	141	UAA	71	142	UCA	96	143	UGA	121	144	UUA	A
	22	240	UOC	47	241	UAC	72	242	UCC	97	243	UGC	122	244	UUC	C
	23	340	UOG	48	341	UAG	73	342	UCG	98	343	UGG	123	344	UUG	G
	24	440	UOU	49	441	UAU	74	442	UCU	99	443	UGU	124	444	UUU	U

[a] In this table it is possible to see the bijection between the triplet set and the set of 3-tuples in $(Z_5)^3$, which are also the coefficients of the polynomials in the *GF* (5^3). The corresponding integer number of every 3-tuples is also shown. I. Triplet index number. II. Polynomial coefficients. III. Extended triplets

The polynomial coefficient a_2 of the terms with a maximal degree a_2x^2 corresponds to the base in the second codon position. The coefficient of the term with degree 1 corresponds to the first codon position, and finally, the coefficient of the term of degree 0 is assigned to the third codon position. That is, the degree of the polynomial terms decreases according to the biological meaning of the corresponding base. Notice that coefficients a_i correspond –for every triplet– to the integer digits of its 3-tuple vector representation in *GF* (5^3). The reverse of this integer digit sequence corresponds to the integer representation in base 5 of the triplet index number (see Table 1). So, as an example, the following bijections are given:

7	↔	012	↔	210	↔	$2 + x$	↔	AOC
44	↔	134	↔	431	↔	$4 + 3x + x^2$	↔	GAU
117	↔	432	↔	234	↔	$2 + 3x + 4x^2$	↔	GUC

In particular, we will use the bijective function $f\,[s]$ such that $f\!: s \rightarrow GF\ (5^3)$, between the subset of the integer number $s = \{0, 1\ldots\ 124\}$ and the elements of $GF\ (5^3)$. According to the above example $f\,[7] = 2 + x$, $f\,[44] = 4 + 3\,x + x^2$ and $f\,[117] = 2 + 3\,x + 4\,x^2$.

2.2. Vector Spaces over the Genetic Code Galois Field

Now, by means of the function Ψ, a product operation can be define in set C_{125}. Let Ψ^{-1} be the inverse function of Ψ then, for all pair of codons $X_1Y_1Z_1 \in C_{125}$ and $X_2Y_2Z_2 \in C_{125}$, their product "•" will be:

$$X_1Y_1Z_1 \bullet X_2Y_2Z_2 = \Psi[\,\Psi^{-1}(X_1Y_1Z_1)\ \Psi^{-1}(X_2Y_2Z_2)\ mod\ g(x)]$$

That is to say, the product between two triplets is obtained from the product of their corresponding polynomial module $g(x)$, where $g(x)$ is an irreducible polynomial of second degree over GF (5). Since there are 40 irreducible polynomials of second degree, 40 possible variants are available to choose the product between two extended triplets. It is not difficult to prove that the set of codons $C_{125}\backslash\{OOO\} = C_{125}^{\ *}$ with the operation product "•" is an Abelian group $(C_{125}^{\ *}, \bullet)$. Likewise, a sum operation is defined by using the sum operation in $GF\ (5^3)$. In this field, the sum is carried out by means of the polynomial sum in the usual fashion with polynomial coefficients reduced by module 5.

Then, for all pairs of codons $X_1Y_1Z_1 \in C_{125}$ and $X_2Y_2Z_2 \in C_{125}$, their sum "+" will be:

$$X_1Y_1Z_1 + X_2Y_2Z_2\ =\ \Psi[\Psi^{-1}(X_1Y_1Z_1) + \Psi^{-1}(X_2Y_2Z_2)\ mod\ 5]$$

As a result, the set of codons $(C_{125}, +)$ with operation "+" is an Abelian group and the set $(C_{125}, +, \bullet)$ is a field isomorphic to $GF(5^3)$. After that, the product of a codon $XYZ \in C_{125}$ can be defined by the element $\alpha_i \in GF\ (5^3)$. For all $\alpha_i \in GF\ (5^3)$ and for all $XYZ \in C_{125}$, this operation will be defined as:

$$\alpha_i\,(XYZ) = \Psi[\alpha_i\, \Psi^{-1}(XYZ)\ mod\ 5]$$

This operation is analogous to the multiplication rule of a vector by a scalar. So, (C_{125}, +) can be considered a one-dimensional vector space over GF (5^3). The canonical base of this space is the triplet OOA. This structure can be called the vector space of extended triplets over GF (5^3). Such structure can be extended to the N-dimensional sequence space (S) consisting of the set of all 125^N DNA alignment sequences with N extended triplets. Obviously, this set is isomorphic to the set of all N-tuples ($x_1,\ldots,x_N$) where $x_i \in C_{125}$. Then, set S can be represented by all N-tuples ($x_1,\ldots,x_N$) $\in (C_{125})^N$. As a result, the N-dimensional vector space of S over GF (5^3) will be the direct sum

$$S = (C_{125})^{\,N} = C_{125} \oplus C_{125} \oplus \ldots \oplus C_{125}\ (N \text{ times})$$

The sum and product in S are carried out by components (Redéi, 1967). That is, for all $\alpha \in$ GF (5^3) and for all s, s'$\in$S we have:

$$s + s' = (\,s_1, s_2,\ldots, s_N) + (s_{1'}, s_{2'},\ldots, s_{N'}) = (s_1 + s_{1'} + s_2 + s_{2'},\ldots, s_N\ + s_{N'})$$

$$\alpha\, s = \alpha\,(s_1, s_2\ldots\, s_N) = (\alpha\, s_1,\, \alpha\, s_2\ldots\, \alpha\, s_N)$$

Next, it can be proved that (S, +) is an Abelian group with the N-tuple s_e = (OOO, OOO…OOO) as its neutral element. The canonical base of this space is the set of vectors:

e_1 = (OOA, OOO, … , OOO), e_2 = (OOO, OOA,…, OOO), . . . , e_N = (OOO, OOO,..., OOA)

As a result, every sequence $s \in$ S has a unique representation:

$$s = \alpha_1\, e_1 + \alpha_2\, e_1 + \ldots + \alpha_N\, e_N\ \ (\alpha_i \in GF\,(5^3))$$

It is usually said that the N-tuple ($\alpha_1, \alpha_2,\ldots, \alpha_N$) is the coordinate representation of s in the canonical bases $\{e_i \in C_{125}\,,\, i = 1, 2,\ldots, N\}$ of S.

3. Results and Discussion

Evidently, the Galois field of codons is not unique. Actually, we have obtained forty isomorphic Galois fields, each one with the product operation defined from one of the forty irreducible polynomials. It is convenient, however, to choose a more biologically significant Galois field.

The most attractive irreducible polynomials are the primitive polynomials. If α is a root of a primitive polynomial then their powers α^n ($n = 1, \ldots 124$) are the elements of the multiplicative group of *GF* (125), i.e. α is a group generator. As it was shown in [SAN 05], a product operation in a Galois field generated by a primitive polynomial is carried out in a very simple way (see Table 2). Just twenty of the forty irreducible polynomials are primitives.

In [SAN 05a] the sum operation is a manner to consecutively obtain all codons from the codon AAC in such a way that the genetic code will represent a non-dimensional code scale of amino acid interaction energy in proteins. Here, in order to consecutively obtain all codons from the codon AAC, primitive polynomials are chosen with root $\alpha = 2 + x + x^2$ –corresponding to codon AAC. Only primitive polynomial $g(x) = 2 + 3\,x^{2} + x^{3}$ has the root α, in this way the product operation is unique.

Notice that, in the vector space *S,* all 125^N possible DNA alignment sequences of length N are represented. Here the "classical gap", produced by alignment algorithms corresponds to the neutral element "O". The neutral element appears from algebraic operations with codons. For instance, in the additive group (C_{125}, +), the inverse of codons X_1AX_3 coding to hydrophilic amino acids are the codons (-X_1)U(-X_3) that in turn code to hydrophobic amino acids. The sum of a X_1AX_3 codon to a X_1UX_3 codon produces an extended triplet X_1OX_3. Then, this sum introduces, at least, one base deletion in the obtained extended triplet. In general, indel mutations found in the molecular evolution process can be described by means of algebraic operations in (C_{125}, +, •), i.e. any deletion or insertion presented in any mutant DNA sequence is described by means of algebraic transformations of the corresponding wild type gene.

Table 2. Logarithm table of the elements of the $GF(5^3)$ generated by the primitive polynomial $g(x) = 2 + 3\,x^2 + x^3$.

Element	f[1]	f[2]	f[3]	f[4]	f[5]	f[6]	f[7]	f[8]	f[9]	f[10]	f[11]	f[12]
n (1)	0	93	31	62	25	4	42	105	102	118	74	97
Element	f[13]	f[14]	f[15]	f[16]	f[17]	f[18]	f[19]	f[20]	f[21]	f[22]	f[23]	f[24]
n	71	11	56	73	9	35	12	87	40	43	104	66
Element	f[25]	f[26]	f[27]	f[28]	f[29]	f[30]	f[31]	f[32]	f[33]	f[34]	f[35]	f[36]
n	50	23	30	28	106	29	14	1	20	86	67	8
Element	f[37]	f[38]	f[39]	f[40]	f[41]	f[42]	f[43]	f[44]	f[45]	f[46]	f[47]	f[48]
n	83	120	38	6	80	46	10	79	3	119	95	109
Element	f[49]	f[50]	f[51]	f[52]	f[53]	f[54]	f[55]	f[56]	f[57]	f[58]	f[59]	f[60]
n	84	19	121	116	75	123	99	103	49	48	15	122
Element	f[61]	f[62]	f[63]	f[64]	f[65]	f[66]	f[67]	f[68]	f[69]	f[70]	f[71]	f[72]
n	113	107	55	94	96	78	88	53	64	36	89	101
Element	f[73]	f[74]	f[75]	f[76]	f[77]	f[78]	f[79]	f[80]	f[81]	f[82]	f[83]	f[84]
n	7	52	81	61	13	54	59	98	114	69	39	27
Element	f[85]	f[86]	f[87]	f[88]	f[89]	f[90]	f[91]	f[92]	f[93]	f[94]	f[95]	f[96]
n	34	2	115	26	16	60	32	117	45	51	37	77
Element	f[97]	f[98]	f[99]	F[100]	f[101]	f[102]	f[103]	F[104]	f[105]	f[106]	f[107]	f[108]
n	110	111	41	112	44	90	92	85	65	22	47	33
Element	f[109]	f[110]	f[111]	F[112]	f[113]	f[114]	f[115]	F[116]	f[117]	f[118]	f[119]	f[120]
n	57	68	17	72	108	18	5	100	58	21	70	91
Element	f[121]	f[122]	f[123]	F[124]								
n	24	82	63	76								

[1] Here, codon AAC corresponds to the primitive root $\alpha = 2 + x + x^2$, i.e. $f[s] = (2 + x + x^2)^{\boldsymbol{n}}$ *mod* $g(x)$ and $\boldsymbol{n}$ = logarithm base $\boldsymbol{\alpha}$ of $f[s] = \log_\alpha f[s]$. The properties of this logarithm function are alike to the classical definition in arithmetic:

i. $\log_\alpha (f[x]*f[y]) = (\log_\alpha f[x] + \log_\alpha f[y])\ mod\ 124 = (n_x + n_y)\ mod\ 124$
ii. $\log_\alpha (f[x]/f[y]) = (\log_\alpha f[x] - \log_\alpha f[y])\ mod\ 124 = (n_x - n_y)\ mod\ 124$
iii. $\log_\alpha f[x]^m = m \log_\alpha f[x]\ mod\ 124$

3.1. Transformations of the DNA Extended Sequences

Gene mutations can be considered as linear transformations of the wild type gene in the N-dimensional vector space of DNA sequences. These linear transformations are endomorphisms and automorphisms. In particular, there are some remarkable automorphisms. Automorphisms are one-one transformations on the group $(C_{125})^N$, such that, for all extended DNA sequences α and β in $(C_{125})^N$ and $a \in GF\,(124)$, we have:

$$f\,(a\cdot(\alpha+\beta))= a\cdot f\,(\alpha) + a\cdot f\,(\beta)$$

That is, automorphisms forecast mutation reversions, and if the molecular evolution process went by through automorphisms then, the observed current DNA sequences would not depend on the mutational pathway followed by the ancestral DNA sequences. In addition, the set of all automorphisms is a group.

For every endomorphism (or automorphism) f: $(C_{125})^N \rightarrow (C_{125})^N$, there is a $N\times N$ matrix:

$$A = \begin{pmatrix} a_{11} & \ldots & a_{1N} \\ . & . & . \\ a_{N1} & \ldots & a_{NN} \end{pmatrix}$$

where the rows are the image vectors $f(e_i)$ and i = 1, 2,…N. This matrix will be called the representing matrix of the endomorphism f with respect to the canonical base e_i $\{i = 1,2\ldots,N\}$.

As in [SAN 05], single point mutations can be considered local endomorphisms. An endomorphism f: $S \rightarrow S$ will be called local endomorphism if there exists $k \in \{1, 2,\ldots, N\}$ and $a_{ik} \in GF\ (125)$ (i = 1, 2,…,N) such that:

$$f(e_i) \ = a_{ik}e_k + e_i, \text{ for } i{\neq}k,$$

and

$$f(e_k) \ = \ a_{kk}e_k$$

This means that:

$$f(x_1, x_2, \ldots x_n) = (x_1, x_2, \ldots \sum_{i=1}^{n} x_i a_{ik}, \ldots x_n)$$

It is evident that a local endomorphism will be a local automorphism if, and only if, the element a_{kk} is different from cero. The local endomorphism f will be considered diagonal if $f(e_k) = (0,\ldots,a_{kk},\ldots,0) = a_{kk}e_k$ and $f(e_i) \ = e_i$, for $i \neq k$. This means that:

$$f(x_1,\ x_2,\ldots x_N) = (x_1,\ x_2,\ldots a_{kk}\,x_k,\ldots x_N)$$

The previous concepts allow us to present the following theorem:

Theorem 1. For every single point mutation changing the codon α_i of the wild type gene $\alpha = (\alpha_1, \alpha_2,\ldots, \alpha_i,\ldots, \alpha_N)$ (α different from the null vector) by the codon β_i of the mutant gene $\beta = (\alpha_1, \alpha_2,\ldots,\beta_I,\ldots, \alpha_N)$, there is:

i. At least a local endomorphism f such that $f(\alpha) = \beta$.
ii. At least a local automorphism f such that $f(\alpha) = \beta$.
iii. A unique diagonal automorphism f such that $f(\alpha) = \beta$ if, and only if, the codons α_i and β_i of the wild type and mutant genes, respectively, are different of OOO.

Proof: Since genes are included in the vector space over a Galois Field, this proves is similar to those reported in [SAN 05]. □

According to the last theorem, any point mutation presented in the vector space $(C_{125})^N$ of all DNA alignment sequences of length N sequences are described by means of automorphisms of the corresponding wild type gene. Specifically, the most frequent mutations can be described by means of diagonal automorphisms [see SAN 05]. For example, the sequence α=UAUAUGAGUGAC can be considered. Let us suppose that, with successive mutations, this sequence becomes the sequence β = UGUAUAAGUOAG. According to Table 1 these sequences correspond in the vector space $(C_{125})^4$ to vectors α = (f [24], f [108], f [84], f [42]) and β = (f [99], f [106], f [84], f [28]). Hence, according to the Theorem, there exists a diagonal endomorphism f, so that $\beta = f(\alpha)$. Our Galois field is generated by the primitive polynomial $g(x) = 2 + 3x^2 + x^3$. In this field, the root $\alpha = 2 + x + x^2$ –corresponding to codon AAC– is a generator of the multiplicative group. Next, by means of Table 2 we can compute:

$$(f[99], f[106], f[84], f[28]) = (f[24], f[108], f[84], f[42])\begin{pmatrix} f[55] & 0 & 0 & 0 \\ 0 & f[61] & 0 & 0 \\ 0 & 0 & f[1] & 0 \\ 0 & 0 & 0 & f[29] \end{pmatrix}$$

On the other hand, mutations can be considered translations of the wild type gene in the N-dimensional vector space of the DNA extended sequences. In the Abelian group $(C_{125}, +)$, for two extended triplets $a, b \in (C_{125}, +)$, equation $a + x = b$ always has a solution. Then, for all pair of aligned sequences α, $\beta \in (C_{125}, +)^N$ there is always a sequence $\kappa \in (C_{125}, +)^N$ so that $\alpha + \kappa = \beta$. That is, there exists translation T: $\alpha \rightarrow \beta$. Translation T_k with constant k acting on triplet x will be represented as:

$$T_k\,(x) = x + k$$

Next, given applications: $W \xrightarrow{f} X \xrightarrow{g} Y$, the composition $g \circ f : W \rightarrow Y$ of translations g and f is defined by $(g \circ f)(x) = g(f(x))$. It is well known that the set of all translations with composition operations is a group G.

3.2. Stabilizer subgroup of the wild type conserved regions

It is well known that in a wild type ORF, normally, not all codon sequences are susceptible to experimental mutations. Usually, conserved variables and hypervariables regions are found in genes. A typical case is the antibody where heavy chain variable domain (V_H) and a light chain variable domain (V_L) are found. Within V_L and $V_{H,}$ there are "hot spots" of variability. These hot spots of variability were termed hypervariable regions. The hypervariable regions of the heavy and light chains together form the antigen binding site of the immunoglobulin molecule. Next, let P be the subset of mutant DNA sequences conserving the same regions from a wild type DNA coding sequence $\alpha_0 \in (C_{125})^N$. Then, according to the group theory [RED 67], the set St (α_0) of automorphisms $f \in G$ that preserves these regions is a subgroup of G, that is:

$$St\,(\alpha_0) = \{f \in G, \text{ such that: } f\,(\alpha_0) = \beta \in P\} \subset G$$

This subgroup could be called the stabilizer subgroup in G of the conserved regions of wild type α_0. Notice that the stabilizer subgroup St (α_0) is connected with the homologous recombination that involves a reciprocal exchange of DNA sequences –e.g. between two chromosomes that carry the same genetic loci. The homologous recombination algebraically corresponds to the action of two automorphism pairs that could be included in the St (α_0) (see Fig. 1).

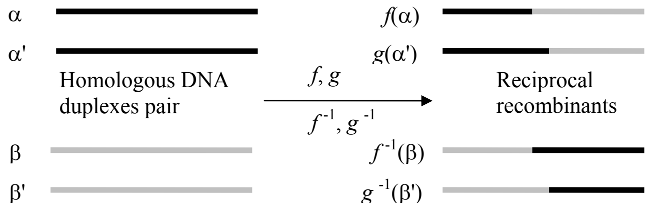
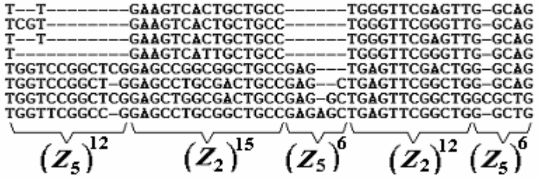


Figure 1. The homologous (generalized) recombination between two homologous DNA duplexes algebraically corresponds to the action of two automorphism pairs over two paired DNA duplexes. The two automorphism pairs express a reciprocal exchange of DNA sequences and could be included in the subgroup of automorphism *St* (α_0).

For instance, the pair *f* and f^{-1} acts over the homologous strands α and β to produce the homologous reciprocal recombinants *f*(α) and f^{-1}(β). Likewise, the pair *g* and g^{-1} acts over the homologous strands α' and β' to produce the homologous reciprocal recombinants *g*(α') and g^{-1}(β'). As a result, two reciprocal recombinant DNA sequences are generated. In particular, if homologous recombination results in an exact exchange of genetic information, then the automorphism pairs are diagonal automorphisms. Since evolution could not happen without genetic recombination, this algebraic description is biologically relevant. If it were not possible to exchange material between (homologous) chromosomes, the content of each individual chromosome would be irretrievably fixed in its particular alleles. When mutations occurred, it would not be possible to separate favourable and unfavourable changes [LEW 04]. Hence, the study of the automorphism subgroup involved in this transformation –the homologous recombination– could reveal new rules of molecular evolution process so far unknown.

3.3. Finite Abelian group of DNA sequences

The multiple sequence alignment is the corner stone of Bioinformatic. Now, some subset of DNA alignment sequences with length *N* will be analysed. By means of multiple sequence alignments, it is possible to find in the DNA genomic sequences small subregions in which there are not introduced gaps.



```
T--T--------GAAGTCACTGCTGCC------TGGGTTCGAGTTG-GCAG
TCGT--------GAAGTCACTGCTGCC------TGGGTTCGGGTTG-GCAG
T--T--------GAAGTCACTGCTGCC------TGGGTTCGAGTTG-GCAG
T-----------GAAGTCATTGCTGCC------TGGGTTCGGGTTG-GCAG
TGGTCCGGCTCGGAGCCGGCGGCTGCCGAG---TGAGTTCGACTGG-GCAG
TGGTCCGGCT-GGAGCCTGCGACTGCCGAG--CTGAGTTCGGCTGG-GCAG
TGGTCCGGCTCGGAGCTGGCGACTGCCGAG-GCTGAGTTCGGCTGGCGCTG
TGGTTCGGCC-GGAGCCTGCGGCTGCCGAGAGCTGAGTTCGGCTGG-GCTG
```

Figure 2. An example of alignment group: $S = (Z_5)^{12} \oplus (Z_2)^{15} \oplus (Z_5)^{6} \oplus (Z_2)^{12} \oplus (Z_5)^{6}$. Building blocks correspond to ungapped sub-sequences (power of Z_2).

For instance, if multiple sequence alignments of open reading frames (ORF) from gene super families are observed, small blocks of ungaped aligned sequences from different genes can be detected. These small blocks of codon sequences may be called “building blocks” (see Fig 2). Theoretically, a building block will be a set of aligned sequences $X_1 X_2 \ldots X_N$ where $X_i \in \{A, C, G, U\}$ $(i = 1 \ldots N)$ with some evolutionary relationship between them. The building blocks with length N can be described by vector spaces over GF (64); in particular, these can be described by the Abelian group $((C_{64})^N, +)$ of the N-dimensional vector space of DNA sequences. Whereas regions with gaps can be described by means of the group $((C_{125})^N, +)$.

Notice that groups $(C_{64}, +)$ and $(C_{125}, +)$ are isomorphic to the p-groups (p a prime number) $(Z_2)^3$ (a 2-group) and $(Z_5)^3$ (a 5-group) respectively. It is well known that every Abelian group can be written as a direct sum of p-groups [DUB 63]. Actually, in the set of all alignment sequences with length N, several finite Abelian groups over the subsets of all $2^{m_1+m_2+\ldots+m_p}5^{n_1+n_2+\ldots+n_q}$ possible alignment sequences ($N = n_1+\ldots+n_p+m_1+\ldots+m_q$) can be defined. An example of these is shown in Fig 1. These groups may be called “alignment groups”.

If a finite group G is written as a direct sum $G = G_1 \oplus G_2 \oplus \ldots \oplus G_s$, then endomorphism ring End(G) is isomorphic to the ring of matrices (A_{ij}), where $A_{ij} \in \mathrm{Hom}(G_i, G_j)$, with the usual matrix operations. In our case the endomorphism that transform the DNA alignment sequence α into β ($\alpha, \beta \in G$) is represented by a matrix with only non-cero elements in the principal diagonal. These diagonal elements are sub-matrices $A_{i\,i} \in \mathrm{End}(G_i)$ (o $A_{ii} \in \mathrm{Aut}(G_i)$).

Finally, since the canonical decomposition of an Abelian group G into p-groups is unique up to isomorphism [DUB 63], it is possible to characterize alignment groups for a fixed sequence length N. That is to say, two alignment groups can have different p-group decompositions and simultaneously be isomorphic by holding the same canonical decomposition into p-groups. This algebraic description biologically suggests that the same biological architectural principium underlies the alignment groups with the same canonical decomposition into p-groups. Here the basic construction materials come from building blocks. It could also corresponds to the fact that in the molecular evolution process, the new genetic information frequently comes into being from the rearrangements of existing genetic material in the chromosomes.

4. Conclusions

In this paper, the starting point to analyze deletions and mutations in DNA sequences is the extended triplet set with elements $X_1X_2X_3$, where $X_i \in \{O, A, C, G, U\}$. Taking into account the order in the set {O, A, C, G, U} and the biological importance of base positions in the codon, it is possible to establish a bijection between the extended triplet set and the Galois field $GF(5^3)$. This bijection allows us to define the Galois field of the extended triplet set. Over this new field, a new N-dimensional vector space is defined in the set of all possible DNA alignment sequences where gene mutations can be considered linear transformations or translations of the wild type gene.

For every single point mutation in the wild type gene, there is at least an automorphism that transforms the wild type in the mutant gene. So, automorphism- group could be a useful tool to study the mutational pathway followed by genes in the N-dimensional vector space of all possible DNA alignment sequences.

Besides this, the set St (α_0) of automorphisms that conserve the same regions from a wild type DNA coding sequence $\alpha_0 \in (C_{125})^N$ is a subgroup connected with the homologous recombination that involves a reciprocal exchange of DNA sequences –e.g. between two chromosomes that carry the same genetic loci. The homologous recombination algebraically corresponds to the action of two automorphism pairs that could be included in the St (α_0)

By means of multiple sequence alignments, it is possible to define several finite Abelian groups –alignment groups– over the subsets of all $2^{m_1+m_2+...+m_p}5^{n_1+n_2+...+n_q}$ possible alignment sequences ($N = n_1+...+n_p+m_1+...+m_q$). Two alignment groups can have different *p*-group decompositions and simultaneously be isomorphic holding the same canonical decomposition into *p*-groups. For alignment groups with the same canonical *p*-group, decompositions could underlie the same biological architectural principium.

This algebraic structure of DNA sequences over the extended Galois field of the genetic code is an attempt to formalize the biological interpretation of the multiple sequence alignment results, the corner stone of Bioinformatic. Our first approach leads us to the concept of building blocks in DNA sequences that could be a key to help us understand how DNA genomic sequences are assembled.

Acknowledgments

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