

# The Constructions of DNA Codes from Linear Self-Dual Codes over $Z_4$

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**Abstract--It is possible to construct DNA codes from classical linear codes. However, it is difficult to determine the GC weight enumerator. In this paper, we use the  $Z_4$ -linear self-dual codes  $K_{4m}$  to construct DNA codes.  $K_{4m}$  have some good properties, so DNA codes can be easily constructed. Moreover, GC weight enumerator of the DNA codes can be easily determined.**

**Keywords--self-dual codes;  $Z_4$  codes; DNA codes**

## I INTRODUCTION

DNA is found naturally as a double stranded molecule, with a form similar to a twisted ladder. The backbone of the DNA helix is an alternating chain of sugars and phosphates, while the association between the two strands is variant combinations of the four nitrogenous bases adenine (A), thymine (T), guanine (G) and cytosine (C). The two ends of the strand are distinct and are conventionally denoted as 3' end and 5' end. Two strands of DNA can form (under suitable conditions) a double strand if the respective bases are Watson-Crick[1] complements of each other - A matches with T and C matches with G, also 3' end matches with 5' end.

The problem of designing DNA codes (sets of words of fixed length  $n$  over the alphabets  $\{A, C, G, T\}$ ) that satisfy certain combinatorial constraints has applications for reliably storing and retrieving information in synthetic DNA strands. These codes can be used in particular for DNA computing [2] or as molecular bar-codes.

In this paper, we construct DNA codes from  $K_{4m}$  which are linear self-dual codes over  $Z_4$ .  $K_{4m}$  have some particular properties, so the constructed DNA codes from them also have these properties, i.e. the GC-weight enumerator of the constructed DNA codes can be easily determined.

The paper is organized as follows. In Section 2, we recall basic notions for linear self-dual codes over  $Z_4$  and DNA codes; In Section 3, we translate the linear self-dual codes  $K_{4m}$  into DNA codes and take  $Z_4$  and  $Z_8$  for example; Also in Section 3, we detail the process of our constructions of DNA codes and finally give their advantages and tables of the constructed DNA codes.

## II PRELIMINARIES

### A. Linear Self-Dual Codes Over $Z_4$

Let [3]  $Z_4 (= \{0, 1, 2, 3\})$  denote the ring of integers modulo four. A  $Z_4$ -code  $C$  of length  $n$  is a  $Z_4$ -submodule of  $Z_4^n$ . We define an inner product on  $Z_4^n$  by  $x \cdot y = x_1 y_1 + \dots + x_n y_n \pmod{4}$  where  $x = (x_1, \dots, x_n)$  and  $y = (y_1, \dots, y_n)$ . The [4] dual code  $C^\perp$  of  $C$  is defined as  $\{x \in Z_4^n \mid x \cdot y = 0 \text{ for all } y \in C\}$  under the standard inner product  $x \cdot y$ . A code  $C$  is a self-dual code if  $C^\perp = C$ .

Theorem 2.1 Any code over  $Z_4$  is permutation-equivalent to a code  $C$  with a generator matrix of the form

$$\begin{pmatrix} I_{k_1} & A & B_1 + 2B_2 \\ 0 & 2I_{k_2} & 2D \end{pmatrix} \tag{1}$$

Where  $A, B_1, B_2$ , and  $D$  are  $(1, 0)$ -matrices. We say that a code with the generator matrix has type  $4^{k_1} 2^{k_2}$ .

Definition 2.1[5] Let  $C$  be a  $Z_4$ -code and  $n$  be its length. Let  $a$  be an element of  $Z_4$ , i.e.  $a = 0, 1, 2$  or  $3$ . For all  $x = (x_1, \dots, x_n) \in Z_4^n$ , define the weight of  $x$  at  $a$  to be  $w_a(x) = |\{i \mid x_i = a\}|$ .

Definition 2.2[6] the complete weight enumerator (or c.w.e.) of  $C$  is  $cwe_C(W, X, Y, Z) = \sum_{a \in C} W^{n_0(a)} X^{n_1(a)} Y^{n_2(a)} Z^{n_3(a)}$  where  $n_i(a)$  is the number of components of  $a$  that are congruent to  $i$  modulo 4.

Klemm[7] has studied the conditions satisfied by the complete weight enumerator of a self-dual code over  $Z_4$ . The MacWilliams transform determines a group of substitutions, each of which fixes the complete weight enumerator.

Example 2.1 Let  $K_4$  denote the  $Z_4$ -linear code with generator matrix

$$\begin{pmatrix} 1 & 1 & 1 & 1 \\ 0 & 2 & 0 & 2 \\ 0 & 0 & 2 & 2 \end{pmatrix} \tag{2}$$

$K_4$  is of type  $4^1 2^2$ . Therefore  $|K_4| = 16$ .  $K_4^\perp$  is also of type  $4^1 2^2$  with respect to theorem 2.1. Therefore  $|K_4^\perp| = 16$ . It is obvious that any two rows of (2), distinct or not, are orthogonal. Therefore  $K_4 \subseteq K_4^\perp$ . Hence  $K_4 = K_4^\perp$  and  $K_4$  is a self-dual code.

Let  $K_4$  be the  $Z_4$ -linear codes. Its 16 codewords and the numbers  $w_a(c)$  of them, where  $a \in Z_4$  and  $c \in K_4$ , are shown in the following table.

TABLE I

$K_4$	$w_0$	$w_1$	$w_2$	$w_3$
(0000)	4	0	0	0
(1111)	0	4	0	0
(2222)	0	0	4	0
(3333)	0	0	0	4
(0202)	2	0	2	0
(1313)	0	2	0	2
(2020)	2	0	2	0
(3131)	0	2	0	2
(0022)	2	0	2	0
(1133)	0	2	0	2
(2200)	2	0	2	0
(3311)	0	2	0	2
(0220)	2	0	2	0
(1331)	0	2	0	2
(2002)	2	0	2	0
(3113)	0	2	0	2

Then the complete weight enumerator of  $C$  is defined to be the homogeneous polynomial of degree  $n$  in four indeterminates  $X_0, X_1, X_2$  and  $X_3$

$$cwe_{K_4}(X_0, X_1, X_2, X_3) = \frac{1}{2}((X_0 + X_2)^4 + (X_1 + X_3)^4 + (X_0 - X_1)^4 + (X_1 - X_3)^4) \quad (3)$$

### B. DNA Codes

DNA is found naturally as a double stranded molecule, with a form similar to a twisted ladder. The backbone of the DNA helix is an alternating chain of sugars and phosphates. Every DNA molecule consists of two complementary strands which are sequences of four different nucleotide bases. These are called adenine (A), cytosine (C), guanine (G) and thymine (T). The two ends of the strand are distinct and are conventionally denoted as 3' end and 5' end. A matches with T and C matches with G, also 3' end matches with 5' end.

Coding theory has several applications in Genetics and Bioengineering. The problem of designing DNA codes (sets of words of fixed length  $n$  over the alphabet  $\{A, C, G, T\}$  that satisfy certain combinatorial constraints) has applications for reliably storing and retrieving information in synthetic DNA strands.

A DNA code of length  $n$  is a set of codewords  $(x_1, \dots, x_n)$  with  $x_i \in \{A, C, G, T\}$  (representing the four nucleotides in DNA). We use a hat to denote the Watson-Crick complement of a nucleotide, so A matches with T and C matches with G.

### III CONSTRUCTIONS FOR DNA CODES

Because the DNA codes are sets of words of fixed length  $n$  over the alphabet  $\{A, C, G, T\}$ , we can follow the map  $A \rightarrow 0, C \rightarrow 1, T \rightarrow 2$ , and  $G \rightarrow 3$ . Therefore the problem of the DNA codes is corresponding to the problem of the  $Z_4$ -linear codes. These transpositions do not affect the GC-weight of the codeword (the number of entries that are C or G). In our work, by using the above map, we construct DNA codes from the self-dual  $Z_4$ -codes  $K_{4m}$ .

Definition 3.1[8] Let  $K_{4m} (m \geq 1)$  denote the  $Z_4$ -linear code with generator matrix

$$\begin{pmatrix} 1 & 1 & 1 & \dots & 1 & 1 \\ 0 & 2 & 0 & \dots & 0 & 2 \\ 0 & 0 & 2 & \dots & 0 & 2 \\ \cdot & \cdot & \cdot & \dots & \cdot & \cdot \\ 0 & 0 & 0 & \dots & 2 & 2 \end{pmatrix} \quad (4)$$

Which is a  $(4m - 1) \times 4m$  matrix.  $K_{4m} (m \geq 1)$  was introduced by Klemm(1989).

Definition 3.2 Let  $d = (d_1, \dots, d_n) \in \{A, C, T, G\}^n$  and  $n$  be its length. Let  $b$  be an element of  $\{A, G, T, C\}$ . For all  $d = (d_1, \dots, d_n) \in \{A, C, T, G\}^n$ , define the weight of  $d$  at  $b$  to be  $w_b(d) = |\{i | x_i = b\}|$ .

Theorem 3.1 Let  $C$  be the  $K_{4m} (m \geq 1)$  codes. Then there exists DNA codes of length  $4m$ , with  $2^{4m}$  codewords, and GC weight enumerator is

$$W_{GC} = X_C^{4m} + X_G^{4m} + C_{4m}^{2m} X_C^{2m} X_G^{2m} \quad (5)$$

Next we present illustrative examples to show how the proposed construction works.

Example 3.1 Let  $C$  be the self-dual  $Z_4$ -codes  $K_4$ . From Theorem 3.1, we obtain DNA codes of length 4, with 16 codewords, and GC weight enumerator is

$$W_{GC} = X_C^4 + X_G^4 + 6X_C^2 X_G^2. \quad (6)$$

Obviously  $K_4$  are just corresponding to 16 DNA codes. So we have the following table:

TABLE II

$K_4$	$D_4$	$w_a(d)$	$w_c(d)$	$w_t(d)$	$w_g(d)$
(0000)	(AAAA)	4	0	0	0
(1111)	(CCCC)	0	4	0	0
(2222)	(TTTT)	0	0	4	0
(3333)	(GGGG)	0	0	0	4
(0202)	(ATAT)	2	0	2	0
(1313)	(CGCG)	0	2	0	2
(2020)	(TATA)	2	0	2	0
(3131)	(GCGC)	0	2	0	2
(0022)	(AATT)	2	0	2	0
(1133)	(CCGG)	0	2	0	2
(2200)	(TTAA)	2	0	2	0
(3311)	(GGCC)	0	2	0	2
(0220)	(ATTA)	2	0	2	0
(1331)	(CGGC)	0	2	0	2
(2002)	(TAAT)	2	0	2	0
(3113)	(GCCG)	0	2	0	2

Then the complete weight enumerator of  $D_4$  is defined to be the homogeneous polynomial of degree  $n$  in four indeterminates  $X_A, X_C, X_T$  and  $X_G$ :

$$cwe_{D_4}(X_A, X_C, X_T, X_G) = \frac{1}{2}((X_A + X_T)^4 + (X_C + X_G)^4 + (X_A - X_C)^4 + (X_C - X_G)^4) \quad (7)$$

The GC-weight enumerator of  $D_4$ :

$$W_{GC} = X_C^4 + X_G^4 + 6X_C^2X_G^2 \quad (8)$$

Example 3.2 Let  $K_8$  be the  $Z_4$ -linear codes with generator matrix

$$\begin{pmatrix} 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\ 0 & 2 & 0 & 0 & 0 & 0 & 0 & 2 \\ 0 & 0 & 2 & 0 & 0 & 0 & 0 & 2 \\ 0 & 0 & 0 & 2 & 0 & 0 & 0 & 2 \\ 0 & 0 & 0 & 0 & 2 & 0 & 0 & 2 \\ 0 & 0 & 0 & 0 & 0 & 2 & 0 & 2 \\ 0 & 0 & 0 & 0 & 0 & 0 & 2 & 2 \end{pmatrix} \quad (9)$$

Clearly, any two rows of the generator matrix, distinct or not, are orthogonal. Therefore  $K_8 = K_8^\perp$  and  $K_8$  is self-dual. From Theorem 2.1.1 and Theorem 2.1,  $K_8$  is of type  $4^1 2^6$  and then  $K_8^\perp$  is also of type  $4^1 2^6$ . Let  $C$  be the self-dual  $Z_4$ -codes  $K_8$ . From Theorem 3.1, we obtain DNA codes of length 8, with 256 codewords. Therefore

$$cwe_{D_8}(X_A, X_C, X_T, X_G) = \frac{1}{2}((X_A + X_T)^8 + (X_C + X_G)^8 + (X_A - X_C)^8 + (X_C - X_G)^8) \quad (10)$$

The GC-weight enumerator of  $D_8$ :

$$W_{GC} = X_C^8 + X_G^8 + 70X_C^4X_G^4 \quad (11)$$

Obviously, one of the advantages of DNA codes construction is that it is less of complexity than pre-existing DNA codes construction. Moreover, GC weight enumerator can be easily determined.

#### IV CONCLUSIONS

In this paper, we have introduced a new way of constructing good DNA codes. Due to  $K_{4m}$  be the self-dual  $Z_4$ -codes, the constructed DNA codes have some particular properties. It is less of complexity than pre-existing DNA codes construction. Moreover, GC weight enumerator can be easily determined. But the constructed DNA codes have not applied to Genetics and Bioengineering. We must stick at the study of DNA codes.

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