On DNA Codes using the Ring $\mathbb{Z}_4 + w\mathbb{Z}_4$

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Abstract—In this work, we study the DNA codes from the ring $R = \mathbb{Z}_4 + w\mathbb{Z}_4$, where $w^2 = 2 + 2w$ with 16 elements. We establish a one to one correspondence between the elements of the ring $R$ and all the DNA codewords of length 2 by defining a distance preserving Gau map $\phi$. Using this map, we give several new classes of the DNA codes which satisfies reverse and reverse complement constraints. Some of the constructed DNA codes are optimal.

I. INTRODUCTION

DNA (DeoxyriboNucleic Acid) is the basic programming unit of life. DNA consists of four building blocks called nucleotides viz. Adenine (A), Thymine (T), Cytosine (C) and Guanine (G). DNA forms a double helix by the process called hybridization in which each nucleotide on a DNA strand is held by the hydrogen bonds with its complementary base, where A is complement to T, G is complement to C. The use of the DNA for computation was first demonstrated in an experiment by L. Adleman $^1$ in 1994 by solving an instance of Hamilton path problem using the DNA strands. His method used the idea of DNA hybridization which is the backbone of Hamilton path problem using the DNA strands. His method ignited the interest of coding theorist to develop the DNA codes from the ring $\mathbb{Z}_4 + w\mathbb{Z}_4$. Generally, the dissimilarity measure used for the DNA code is denoted by $\Sigma$ which are sufficiently dissimilar have been designed by using various computational and theoretical approaches in the literature $^5$. Moreover, coding theoretic approaches $^4$ have been used to construct the DNA codes from codes over fields and rings. This paper uses one such approach to develop the DNA codes from the ring $R = \mathbb{Z}_4 + w\mathbb{Z}_4$, where $w^2 = 2 + 2w$.

Let $\Sigma_{DNA} = \{A, C, G, T\}$. The DNA code is the set of $M$ distinct DNA strands each of length $n$ such that the Hamming distance between any two DNA strands is at least $d_H$, where, $d_H = \min\{d_H(x, y) : x \neq y, \forall x, y \in \Sigma_{DNA}\}$. Mathematically, the DNA code is denoted by $\mathcal{C}_{DNA}(n, M, d_H) \subseteq \Sigma_{DNA}^n$. The DNA strands are also called as DNA codewords.

Example 1: $\mathcal{C}_{DNA} = \{AGAG, AGGA, AGCT, AGTC, GAAG, GAGA, GACT, GATC, CTAG, CTGA, CTCT, CTTC, TCAG, TCGA, TCTC, TCTT\}$ is a DNA code $\mathcal{C}_{DNA}$ with parameters $n = 4$, $M = 16$ and $d_H = 2$.

Generally, the dissimilarity measure used for the DNA codewords is defined by the Hamming distance between the DNA codewords. But to avoid the mis-hybridization between the set of DNA codewords, it is important to consider the distance between the given DNA codeword, its reverse and reverse complement DNA codewords. This motivates researchers to define the combinatorial constraints on the DNA codewords.

For the given DNA codeword $x = (x_1, x_2, \ldots, x_{n-1}, x_n)$, the reverse of the DNA codeword is defined as $x' = (x_n, x_{n-1}, \ldots, x_2, x_1)$, the reverse complement of the DNA codeword is defined as $x'' = (x_1', x_2', \ldots, x_{n-1}', x_n')$, where each $x_i \in \{A, T, G, C\}$ for $i = 1, 2, \ldots, n$ and $A' = T$, $T' = A$, $G' = C$, $C' = G$. For Example, if $x = AACT$ then $x' = TCAA$, $x'' = AGTT$. These constraints ensures that the DNA hybridize with the correct match and avoids errors in the computation $^5, 6$. A DNA code with some predefined distance $d$ should satisfy one or all the combinatorial constraints which are the Hamming distance, Reverse complement and GC content constraints.

The DNA code given in the Example $^1$ satisfies all the combinatorial constraints. For any given $x, y \in \mathcal{C}_{DNA}$, note that $d_H(x', y') = d_H(x'', y') = d_H(x, y'') = d_H(x', y'')$.

The progress of DNA codes from an algebraic coding has ignited the interest of coding theorist to develop the DNA codes using rings. In 2001, reversible cyclic DNA codes using the quaternary alphabets was first developed in $^7$. But it considered only the reverse constraint for the DNA codes. King et al., in the year 2005, constructed the linear DNA codes from the ring $\mathbb{Z}_4$ $^4$ that satisfies reverse and reverse complement constraints. In order to obtain good DNA codes, researchers used different ring structures. Cyclic codes from the finite ring $\mathbb{F}_2 + u\mathbb{F}_2$ were obtained using similarity measures (a special kind of distance similarity) instead of Hamming distance $^8$. In $^9$, I. Siap et al. introduced the cyclic DNA codes from the ring $\mathbb{F}_2 + u\mathbb{F}_2$, where $u^2 = 1$ based on the deletion distance. By using the same ring $\mathbb{F}_2 + u\mathbb{F}_2$ with $u^2 = 0$, the DNA cyclic codes of an even length was constructed by Liang and Wang in $^10$. DNA cyclic irreversible odd length codes of the type simplex and Reed Muller codes from the ring $\mathbb{F}_2 + u\mathbb{F}_2$ were studied in $^11$. Odd length DNA codes was given which satisfies the Hamming distance constraints from the commutative ring $\mathbb{F}_4[u]/<u^4 - 1>$ with $u^2 = 1$ in $^12$. A new ring $\mathbb{Z}_4 + u\mathbb{Z}_4$ with 16 elements was introduced by Yildiz et al. in $^13$ and DNA codes of odd lengths from the ring were studied in $^14$.

Recently, a non-commutative ring was used for designing the reversible DNA codes from the skew cyclic codes. Generalized non-chain ring $\mathbb{F}_{16} + u\mathbb{F}_{16} + v\mathbb{F}_{16} + uv\mathbb{F}_{16}$ was
used to construct the reversible DNA codes in [15]. Very recently, Oztas et al. gave a novel approach for constructing the reversible DNA codes using the ring $F_2[u]/(u^{2k} - 1)$ [16]. For more background on this, the reader is referred to the further references in the literature [3], [17].

Choe and Dougherty studied the properties of the ring $R = Z_4 + wZ_4$ for the first time in [18]. Using the structure of the ring, the DNA cyclic codes of odd lengths from the ring $Z_4 + wZ_4$, where $w^2 = 2$ was proposed in [19].

Motivated by this, we investigate the structure of the ring $R = Z_4 + wZ_4$ from [18] and use it to construct the DNA codes of even lengths. In this paper, the ring $Z_4 + wZ_4$, where $w^2 = 2 + 2w$ with 16 elements is considered. A correspondence between the ring elements and the DNA codewords of length 2 is defined via a distance preserving Gau map $\phi$. We propose a new type of distance called the Gau distance on the ring $R$. Properties of the distance with respect to the DNA codes are explored. Several new families of the DNA codes are obtained which satisfies the Hamming, reverse and reverse complement constraints. In order to obtain the DNA codes with a fixed GC content, the DNA codewords that violate the GC content constraint are removed.

The paper is organized as follows. Section 2 gives a brief background of the ring $R = Z_4 + wZ_4$. Section 3 discusses the Gau distance, the Gau map and the DNA codes constructed from the ring $R$. Section 4 illustrates the results on the families of the reverse and reverse complement DNA codes with Examples. Section 5 the $r$th order Reed Muller Type code. Section 6 concludes the paper with some general Remarks.

II. PRELIMINARIES ON THE RING $Z_4 + wZ_4$

The structure of finite commutative local chain ring $R = Z_4 + wZ_4 = \{a + bw : a, b \in Z_4 \text{ and } w^2 = 2 + 2w\}$ is discussed here. The ring $R$ is a principal ideal ring with 16 elements. For the ring $R$, the set of zero divisors is $\{a + bw : a \in Z_4, b \in Z_4\} = \{0, 2, w, 2 + w, 2w, 2 + 2w, 2 + 3w, 3w, 2 + 3w\}$ and the set of units is $\{a + bw : a \in Z_4, b + 1 \in Z_4\} = \{1, 3, 1 + w, 3 + w, 1 + 2w, 3 + 2w, 1 + 3w, 3 + 3w\}$. The ring $R$ has 5 distinct ideals as $(0) \subseteq \langle w \rangle \subseteq \langle 2 \rangle \subseteq \langle 2 + w \rangle \subseteq \langle 2 + 3w \rangle \subseteq R$.

Any subset of $R^w$ is called the code over the ring $R$. Any sub-module of $R^w$ is called the linear code $\mathcal{C}$ over the ring $R$. The standard form of the generator matrix $G$ of the linear code $\mathcal{C}$ over the ring $R = Z_4 + wZ_4$ is given by:

$$
G = \begin{pmatrix}
I_{k_0} & A_{0,1} & A_{0,2} & A_{0,3} & A_{0,4} \\
0 & wI_{k_1} & wA_{1,2} & wA_{1,3} & wA_{1,4} \\
0 & 0 & 2I_{k_2} & 2A_{2,3} & 2A_{2,4} \\
0 & 0 & 0 & 2wI_{k_3} & 2wA_{3,4}
\end{pmatrix},
$$

(1)

where the matrices $A_{i,j}$ are defined over the ring $R$. Note that $A_{i,j} = B_{i,j}^1 + wB_{i,j}^2 + 2B_{i,j}^3 + 2wB_{i,j}^4$, where $B_{i,j}^k$ is binary matrix for $0 \leq i, j \leq 4$ and $k = 1, 2, 3, 4$. A code with a generator matrix in this form is of type $\{k_0, k_1, k_2, k_3\}$ and has $16^{k_0}4^{k_1}2^{k_2}2^{k_3}$ codewords [18]. We denote the row span of the matrix $G$ on the ring $R$ by $<G> R$.

In the next Section, we give a mechanism via the Gau map to construct the DNA codes from the ring $R$ that satisfies the Hamming distance, reverse and reverse complement constraints.

III. DNA CODES USING THE RING $R = Z_4 + wZ_4$

In order to construct the DNA codes using the ring $R$, a correspondence between the elements of the ring $R$ and the DNA alphabets is required. We give an isometry (distance preserving map) between the codes over the ring and the DNA codes. To define a distance on the ring $R$ (hence eventually on $R^w$), the elements of the ring and the DNA alphabets can be arranged in a manner (see the Matrix $\mathcal{M}$ in the equation [2] such that the Hamming distance $d_H$ between any two distinct pair of DNA nucleotides in the same row or same column is 1, otherwise it is 2. This motivates us to define a distance called the Gau distance on the elements of the ring $R$ such that this property is preserved.

\[ d_{\text{Gau}}(x, y) = \min\{1, i + 3i'\} + \min\{1, j + 3j'\}. \]

(3)

Example 2: For $x = 2, i = 1, j = 1$ and $y = 2 + 2w, i' = 3, j' = 3$, the Gau distance $d_{\text{Gau}}(2 + 2w) = 2$. It is easy to see that the Gau distance $d_{\text{Gau}}$ is indeed a metric on the elements of the ring $R$. Using the set of zero divisors $Z = \{0, 2, w, 2 + w, 2w, 2 + 2w, 3w, 2 + 3w\}$ and set of units $U = \{1, 3, 1 + w, 3 + w, 1 + 2w, 3 + 2w, 1 + 3w, 3 + 3w\}$ of $R$, one can simplify the formula for the Gau distance $d_{\text{Gau}}$.

For both $x$ and $y$ in $Z$ or both $x$ and $y$ in $U$ we have,

\[ d_{\text{Gau}}(x, y) = \begin{cases} 0 & \text{if } x = y, \
1 & \text{if } x \neq y \text{ and } x + 3y \in \{2 + w, 2 + 3w\}, \\
2 & \text{otherwise}. \end{cases} \]

For any $x \in \{0, 2, 2w, 2 + 2w\}$ and $y \in U$,

\[ d_{\text{Gau}}(x, y) = \begin{cases} 0 & \text{if } x = y, \
1 & \text{if } x \neq y \text{ and } x + 3y \in \{1, 3, 1 + w, 3 + 3w\}, \\
2 & \text{otherwise}. \end{cases} \]

For any $x \in \{w, 3w, 2 + w, 2 + 3w\}$ and $y \in U$,

\[ d_{\text{Gau}}(x, y) = \begin{cases} 0 & \text{if } x = y, \
1 & \text{if } x \neq y \text{ and } x + 3y \in \{1, 3, 3 + w, 1 + 3w\}, \\
2 & \text{otherwise}. \end{cases} \]
For any two arbitrary vectors $x = (x_1, x_2, x_3, \ldots, x_n) \in R^n$ and $y = (y_1, y_2, y_3, \ldots, y_n) \in R^n$, the Gau distance $d_Gau(x, y) = \sum_{i=1}^{n} d_Gau(x_i, y_i)$ is a metric on $R^n$ induced by the metric on the elements of the ring $R$. We use the same notation $d_Gau$ for both the metrics on $R$ and $R^n$. For a linear code $\mathcal{C}$ on $R$, one can define a minimum Gau distance $d_{\text{Gau}} = \min\{d_{Gau}(x, y) : x, y \in \mathcal{C} \text{ and } x \neq y\}$.

Example 3: For $x = (2 2 + 2w 0 2w)$ and $y = (0 2 2w 2 + 2w)$, $d_{Gau}(x, y) = 8$.

Now, we define a Gau map $\phi$ (as shown in the Table I) from the elements of $R$ to all DNA vectors of length $2n$ as:

$$\phi : R \rightarrow \Sigma_{DN,A}^{2n}$$

One can observe the following properties of the Gau map $\phi$.

1) The additive inverse of each element $x \in R$ is unique, similarly the reverse $\phi(x)^r$ of each $\phi(x) \in \Sigma_{DN,A}^{2n}$ is unique.

2) Four elements $0, 2, 2w, 2 + 2w \in R$ are self invertible under the addition operation. One can observe that the DNA nucleotides, $\phi(0) = AA, \phi(2) = GG, \phi(2w) = CC, \phi(2 + 2w) = TT$ are all self reversible.

3) For each $\phi(x) \in \Sigma_{DN,A}^{2n}, \exists \phi(y) \neq \phi(x)$ such that $\phi(x)^c = \phi(y)$ and $\phi(y)^c = \phi(x)$. Similarly, for any $x \in R$ there exists $y \notin R$ ($y \neq x$) such that $y = x + a = a + x$ and $x = a + y = a + y$, for some $a \in R$. In this work, we have consider $a = 2 + 2w$.

4) The Gau map $\phi$ has a property $\phi^{-1}(\phi(x)^r) = x + (2 + 2w)$ and $x + \phi^{-1}(\phi(x)^r) = 0 \forall x \in R$.

5) For the ring $R$, \exists four distinct elements $3 + 3w, 1 + w, 3 + w, 1 + 3w \in R$ such that $x + a$ is additive inverse of $x$, where $a = 2 + 2w$. From the Table I one can observe that $\phi(x)^r = \phi(x)^c$ for $x \in \{3 + 3w, 1 + w, 3 + w, 1 + 3w\}$.

For any vector $x = (x_1, x_2, \ldots, x_{2n}) \in R^{2n}$, we define $\phi(x) = (\phi(x_1), \phi(x_2), \ldots, \phi(x_{2n})) \in \Sigma_{DN,A}^{2n}$.

**Theorem 1:** $\phi : (R^n, d_Gau)$ to $(\Sigma_{DN,A}^{2n}, d_H)$ is a distance preserving map.

**Example 4:** For $x = (2 0 2 + 2w, 0 2 + 2w)$, $y = (2 + 2w 0 2w, 2 + 2w 0 2w)$, $\phi(x) = (GG AA TT GG), \phi(y) = (TT AA CC GG)$, $d_{Gau}(x, y) = 4$, one can observe that $d_H(\phi(x), \phi(y)) = 4$.

**Remark 1:** For any $x \in \mathcal{C}$, $\phi^{-1}(\phi(x)^r)^c \notin \mathcal{C}$ if and only if the DNA code $\phi(\mathcal{C})$ is closed under reverse.

**Remark 2:** For any $x \in \mathcal{C}$, $\phi^{-1}(\phi(x)^r)^c \notin \mathcal{C}$ if and only if the DNA code $\phi(\mathcal{C})$ is closed under complement constraint.

**Remark 3:** For any $x \in \phi(\mathcal{C})$, if $x^r \in \phi(\mathcal{C})$ and $x^c \in \phi(\mathcal{C})$, then $x^c \notin \phi(\mathcal{C})$.

**Lemma 1:** For any $x, y \in R^n, \phi^{-1}(\phi(ax + by)^r) = a\phi^{-1}(\phi(x)^r) + b\phi^{-1}(\phi(y)^r)$, where $a, b \in R$.

**Proof:** The proof is given in the subsection VII-A of the Appendix.

Using similar approach, for the higher order, one can observe the following Remark on the linearity of the reverse constraint.

**Remark 4:** For any positive integer $k$ and $1 \leq i \leq k$, if $x_i \in R^n$, then $\phi^{-1}(\phi(\sum_{i=1}^{k} a_i x_i)^r) = \sum_{i=1}^{k} a_i \phi^{-1}(\phi(x_i)^r)$, where $a_i \in R$.

**Corollary 1:** For any $x, y \in R^n, \phi^{-1}(\phi(ax + by)^r) = a\phi^{-1}(\phi(x)^r) + b\phi^{-1}(\phi(y)^r)$ if $a + b \in \{1, 1 + 2w, 3 + 2w\}$, where $a, b \in R$.

**Proof:** The proof is given in the subsection VII-A of the Appendix.

Using similar approach, for the higher order, one can observe the following Remark on the linearity for the complement constraint.

**Remark 5:** For any positive integer $k$ and $1 \leq i \leq k$, if $x_i \in R^n$, then $\phi^{-1}(\phi(\sum_{i=1}^{k} a_i x_i)^c) = \sum_{i=1}^{k} a_i \phi^{-1}(\phi(x_i)^c)$, where $a_i \in R$.

**Lemma 2:** For any row $x \in G$ over the ring $R$, the DNA code $\phi < G > R$ is closed under reverse if and only if $\phi^{-1}(\phi(x)^r) \notin < G > R$, the row span of $G$ over $R$.

**Proof:** Let $\phi(y) \in < G > R = \phi(\mathcal{C})$ for any $y \notin \mathcal{C}$. Thus $y = \sum_{i=1}^{k} a_i x_i$, for rows $x_i \in G$. Consider $\phi^{-1}(\phi(y)^r) = \phi^{-1}(\phi(\sum_{i=1}^{k} a_i x_i)^r) = \sum_{i=1}^{k} a_i \phi^{-1}(\phi(x_i)^c) \in \mathcal{C}$ (by using the Remark 2). Thus $\phi^{-1}(\phi(y)^c) \in \mathcal{C}$ which directs $\phi(y)^c \notin \phi(\mathcal{C})$. Hence the DNA code is closed under reverse (by the Remark 2). The invert statement is obvious.

**Lemma 3:** For a matrix $G$ over the ring $R$, the DNA code $\phi < G > R$ is closed under complement if and only if $2 + 2w \in < G > R$, where $2 + 2w$ is a string with each element $2 + 2w$.

**Proof:** Let $\phi(x) \in < G > R = \phi(\mathcal{C})$ for any $x \in \mathcal{C}$ and $2 + 2w = (2 + 2w, 2 + 2w, 2 + 2w) \ldots$ \in $\mathcal{C}$. Thus $x + 2 + 2w \in \mathcal{C}$ but $\phi^{-1}(\phi(x)^c) = x + 2 + 2w$ (by using the Table I). Thus $\phi^{-1}(\phi(x)^c) \in \mathcal{C}$ and $\phi(x) \in \phi(\mathcal{C})$. Hence the DNA code is closed under complement using the Remark 2.

For inverse statement, if $\phi(\mathcal{C})$ is closed under complement, then $\phi^{-1}(\phi(0)^c) \in \mathcal{C}$ (Since 0 \in \mathcal{C}). But $\phi^{-1}(\phi(0)^c) = 0 + 2 + 2w = 2 + 2w$. Hence $2 + 2w \in \mathcal{C}$.

The following Theorem is obvious using the Lemma 1, 2 and 3.
Theorem 2: Let \( C(n, M, d_{Gau}) \) be a code over the ring \( R = \mathbb{Z}_4 + w\mathbb{Z}_4 \) with the length \( n \), the number of the codewords \( M \) and the minimum Gau distance \( d_{Gau} \), such that the rows of the generator matrix of \( C \) satisfies the conditions given in the Lemma \([2,3]\) then \( \phi(C) \) is a \( C_{DNA}(2n, M, d_H) \) DNA code with the length \( 2n \), the number of the codewords \( M \) and the minimum Hamming distance \( d_H \). The DNA code \( C_{DNA} \) satisfies the reverse and reverse complement constraints.

In the next Section, we construct some new families of the DNA codes.

IV. FAMILIES OF DNA CODES FROM THE RING \( R = \mathbb{Z}_4 + w\mathbb{Z}_4 \)

By using the results discussed in the Section III we give new classes of the DNA codes that satisfies the Hamming, reverse and reverse complement constraints.

A. DNA Codes from the Octacodes Type Codes

There has been an interesting history of connecting two non-linear binary codes (Kerdock and Preparata) with linear codes over \( \mathbb{Z}_4 \) \([20]\). Octacode (a linear self dual code of length \( n = 8 \), code size \( M = 256 \) and minimum Lee weight 8 over \( \mathbb{Z}_4 \)) turns out to be a special case connecting the binary non-linear codes (the Nordstrom-Robinson code) \([20]\). In this section, we construct a code similar to the original Octacode from the ring \( \mathbb{Z}_4 + w\mathbb{Z}_4 \). The self dual code is generated by a generator matrix consisting of the cyclic shifts of the vector \( (0 2 2w 2 + 2w 0 2 2w 2 + 2w) \) over \( R \). The DNA code is generated from the generator matrix \( \theta \) of Octacode in the Example 5 It satisfies the reverse and reverse complement constraints.

Example 5: DNA code \( C_{DNA}(n = 16, M = 64, d_H = 8) \) can be obtained from cyclic shifts of the vector \( (0 2w 2 2 + 2w 0 2w 2 2 + 2w) \).

Remark 6: On similar lines, one can obtain Octacodes type DNA codes with parameters listed in the Table I using the different first row vector.

| First Row Vector | DNA Code \( C_{DNA}(n, M, d_H) \) |
|------------------|----------------------------------|
| \( (0 2w 2 2 + 2w) \) | \( (8, 16, 4) \) |
| \( (0 2w 2 2 + 2w) \) | \( (16, 4, 8) \) |
| \( (0 2w 2 2 + 2w 0 2w 2 2 + 2w) \) | \( (16, 4, 8) \) |

Table I

DNA codewords generated from the Octacodes have an interesting properties from the application point of view. By removing the trivial codewords (codewords with no GCs or all GCs), one can obtain the DNA codewords with 50% GC content which are important for the DNA computation.

B. DNA Codes from Simplex Type Codes

Binary simplex codes have a unique geometrical significance (being the dual of the Hamming codes and each having a fixed weight) and were known in 1945 \([21]\) in statistical connections before the actual discovery of the Hamming codes by R.Hamming in 1948. Simplex codes over rings have been considered by many researchers \([22]\). The simplex codes of type \( \alpha \) and \( \beta \) over the ring \( \mathbb{Z}_4 \) have been studied in \([23]\). The simplex codes over the ring \( \mathbb{Z}_4 + w\mathbb{Z}_4 \) was given in \([24]\). It is natural to study the DNA codes using the simplex codes. DNA codes that avoids the secondary structure formation were designed in \([2]\) by using the cyclic simplex codes. In this section, we have designed the DNA codes using the simplex type codes over the ring \( \mathbb{Z}_4 + w\mathbb{Z}_4 \).

The DNA codes which satisfies the reverse and reverse complement constraints is given in the Example 6

Let \( G_k^\beta \) be a matrix over \( \mathbb{Z}_4 + w\mathbb{Z}_4 \) defined inductively by

\[
G_k^\beta = \left( \begin{array}{cccc}
0 & \cdots & 0 & 1 \\
2 & \cdots & 2 & 2w & \cdots & 2w & \cdots & 2 + 2w & \cdots & 2 + 2w \\
G_{k-1}^\alpha & G_{k-1}^\alpha & G_{k-1}^\alpha & G_{k-1}^\alpha & G_{k-1}^\alpha & G_{k-1}^\alpha & \cdots & G_{k-1}^\alpha
\end{array} \right), \quad k \geq 3
\]

with

\[
G_0^\beta = \left( \begin{array}{cccc}
1 & 1 & 2w & 2 + 2w \\
0 & 2 & 2 + 2w & 1 & 0 & 2w & \cdots & \cdots & 2w \\
0 & 2 & 2 + 2w & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots
\end{array} \right).
\]

Example 6: DNA code \( G_3^\beta \) the DNA codes with parameters \( (16, 256, 8) \) satisfying the reverse and reverse complement constraints can be obtained Inductively from \( G_3^\beta \), DNA codes with length \( n = 64 \), \( M = 1024 \), \( d_H = 32 \) is constructed.

The DNA codes obtained from the simplex class has purine rich DNA codewords (composition of AGs in the DNA codeword). These DNA codewords are important for the DNA motifs (small length of functional DNA codewords). They also play significant role in the transcription of genes.

C. DNA codes from Reed Muller Type Codes

The Reed Muller codes (RM) are one of the best known oldest error correcting codes discovered by Reed and Muller in 1954 \([25]\). First, the binary Reed Muller codes were introduced and then it was generalized to any \( q \)-ary alphabets \([26]\).

The Reed Muller code is denoted as \( R(r, m) \), where \( r \) is the order of the code, and \( m \) determines the length of code, \( n = 2^m \). In this work, we defined the Reed Muller Type codes over the ring \( \mathbb{Z}_4 + w\mathbb{Z}_4 \). Using a special type of Reed Muller codes, we give the DNA codes satisfying the reverse and reverse complement constraints.

For each positive integers \( r \) and \( m \) \((1 \leq r \leq m) \), the first order Reed Muller Type code \( R(1, m) \) over \( \mathbb{Z}_4 + w\mathbb{Z}_4 \) where, \( w^2 = 2 + 2w \forall m \geq 1 \), is defined by the generator matrix:

\[
G_{1,m+1} = \left( \begin{array}{cccc}
G_{1,m} & 0 & \cdots & 0 \\
G_{1,m} & \cdots & \cdots & \cdots \\
0 & \cdots & \cdots & \cdots \\
\vdots & \ddots & \ddots & \ddots \\
0 & \cdots & \cdots & \cdots \\
0 & \cdots & \cdots & \cdots
\end{array} \right), \quad m \geq 1
\]
\[ \phi = \begin{pmatrix} 0 & 2w & 2 & 2 + 2w & 0 & 2w & 2 & 2 + 2w \\ 2 + 2w & 0 & 2w & 2 & 2 + 2w & 0 & 2w & 2 \\ 2 & 2 + 2w & 0 & 2w & 2 & 2 + 2w & 0 & 2w \\ 2w & 2 & 2 + 2w & 0 & 2w & 2 & 2 + 2w & 0 \end{pmatrix} \]

with

\[ G_{1,1} = \begin{pmatrix} 1 & 1 \\ 0 & z \end{pmatrix} \]

where \( z \in \{2, w, 2 + w, 2w, 2 + 2w, 3w, 2 + 3w\} \).

**Theorem 4:** For the first order Reed Muller Type code \( \mathcal{R}(1, m) \) over \( \mathbb{Z}_4 + w\mathbb{Z}_4 \), \( \exists a DNA code \( \mathcal{C}_{DNA}(n, M, d_H) \) that satisfies reverse and reverse complement constraints with \( n = 2^{m+1} \).

\[ M = \begin{cases} 2^{m+4} & \text{if } z \in \{2w\}, \\ 2^{2m+4} & \text{if } z \in \{2, 2 + 2w\}, \\ 2^{3m+4} & \text{if } z \in \{w, 2 + w, 3w, 2 + 3w\}, \end{cases} \]

and

\[ d_H = \begin{cases} 2^m & \text{if } z \in \{2w, 2 + 2w\}, \\ 2^{m-1} & \text{if } z \in \{w, 2 + w, 3w, 2 + 3w\}. \]

**Example 7:** DNA code \( \mathcal{C}_{DNA}(n = 16, M = 8192, d_H = 4) \) obtained by the generator matrix

\[ G_{1,3} = \begin{pmatrix} 1 & 1 & 1 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & w & w \\ 0 & 0 & w & w & 0 & 0 \\ 0 & w & 0 & 0 & w & 0 \end{pmatrix} \]

of Reed Muller Type code \( \mathcal{R}(1, 3) \) satisfies the reverse and reverse complement constraints.

One can obtain various DNA code of type Reed Muller using different \( m \) and \( z \) as shown in the Table III

| \( m \) | Zero divisor \( z \) | DNA Code \( \mathcal{C}_{DNA}(n, M, d_H) \) |
|-------|----------------|----------------------------------|
| 1     | 2              | \( (4, 64, 2) \)                  |
| 2     | 2              | \( (8, 256, 4) \)                 |
| 3     | 2              | \( (16, 1024, 8) \)               |
| 2     | \( w \)        | \( (8, 1024, 2) \)                |
| 3     | \( w \)        | \( (16, 8192, 4) \)               |

**D. Results**

The DNA codes designed in this work, have improved the lower bound on \( A_{RC,GCC} \) and obtained the better code size for some instances compare to DNA codes constructed using the similar rings in the literature. For \( n = 8, d = 16, M = 2^{15} \), the lower bound obtained for \( A_{RC,GCC}(8, 4) \) is 224 which is greater than the lower bound observed in \( \text{[27, 28]} \) as 128. Hence it is the best known lower bound on \( A_{RC,GCC} \) obtained for \( n = 8, d_H = 4, M = 4 \) known in the literature. Results obtained, for the DNA codes, in this work are better than the examples described in \( \text{[10, 28, 29]} \). For an instance the DNA code \( \mathcal{C}_{DNA}(n = 16, M = 8192, d_H = 4) \) is better than \( \mathcal{C}_{DNA}(n = 16, M = 28, d_H = 4) \) \( \text{[30]} \). Also the DNA code \( \mathcal{C}_{DNA}(n = 8, M = 256, d_H = 4) \) is better than \( \mathcal{C}_{DNA}(n = 8, M = 16, d_H = 4) \) \( \text{[10, 28]} \). One can observe that the Reed Muller Type codes attains the lower bound on size \( M \) for \( A_{1}^{GC}(n, d_H, u) \) and \( A_{1}^{RC,GCC}(n, d_H, u) \) \( \text{[5]} \) on the DNA code for some values of \( n, d_H \) and \( u = n/2 \). For \( n = 2^m \) and \( z = 2w \), the first order Reed Muller Type code for \( (n, d_H, u) = (4, 2, 2) \) is an optimal code with respect to \( A_{1}^{GC}(n, d_H, u) \) and \( A_{1}^{RC,GCC}(n, d_H, u) \) respectively.

**V. THE \( r^{TH} \) ORDER REED MULLER TYPE CODE**

In order to study the \( r^{TH} \) order Reed Muller type code, we need the following result.

**Lemma 4:** Let \( G \) and \( H \) be two matrices over the ring \( R \) such that both the DNA codes \( \phi(< G > R) \) and \( \phi(< H > R) \) are closed under reverse constraint. If each row of \( H \) is a row of \( G \) then the DNA code \( \phi(< T > R) \) will be closed under reverse, where

\[ T = \begin{pmatrix} G & G \\ 0 & H \end{pmatrix} \]

One can also define \( r^{th} \) order Reed Muller code as follows. For the given zero divisor \( z \in R \) and each integers \( r, m (0 \leq r \leq m) \), the \( r^{th} \) order Reed Muller code \( \mathcal{R}(r, m) \) over the ring \( R \) is defined by the generator matrix

\[ G_{r,m} = \begin{pmatrix} G_{r,m-1} & G_{r,m-1} \\ 0 & G_{r-1,m-1} \end{pmatrix}, 1 \leq r \leq m - 1 \]

with

\[ G_{m,m} = \begin{pmatrix} G_{m-1,m} \\ 0 \ldots 0 \end{pmatrix} \]

and \( G_{0,m} = (1 \ldots 1) \) is the all one matrix with length \( 2^m \).

**Theorem 5:** For the \( r^{TH} \) order Reed Muller code \( \mathcal{R}(r, m) \) over the ring \( R \), the DNA code \( \mathcal{C}_{DNA} = \phi(\mathcal{R}(r, m)) \) satisfies the reverse and reverse complement constraints. The \( (n, M, d_H) \) parameters of the DNA code \( \mathcal{C}_{DNA} \) are \( n = 2^{m+1} \).

\[ M = \begin{cases} 2^{4b-3a} & \text{if } z \in \{2w\}, \\ 2^{4b-2a} & \text{if } z \in \{2, 2 + 2w\}, \\ 2^{4b-a} & \text{if } z \in \{w, 2 + w, 3w, 2 + 3w\}, \end{cases} \]

and

\[ d_H = \begin{cases} 2^{m-r+1} & \text{if } z \in \{2w, 2, 2 + 2w\}, \\ 2^{m-r} & \text{if } z \in \{w, 2 + w, 3w, 2 + 3w\}, \end{cases} \]

where \( a = \sum_{i=0}^{r-1} (m-1) \) and \( b = \sum_{i=0}^{r} (m_i) \).

The results obtained on the reverse and reverse complement constraints for the family of Octa type and Simplex type DNA codes suggest the following general Theorems and Remarks.

For a positive integer \( k \), let \( P \) be a matrix over the ring \( R \) with \( 4k \) length vector \((2 \ldots 2) \in \mathcal{P} > R \). For \( i = 1, 2, 3, 4, \ldots \),
all the four elements \( z_i \in \{0, 2, 2w, 2 + 2w\} \) are distinct and all the four vectors \( z_i = (z_i, z_2, z_3, z_4) \) have same length \( k \). Now, consider the matrix
\[
G = \begin{pmatrix}
  z_1 & z_2 & z_3 & z_4 \\
  P & P & P & P
\end{pmatrix}.
\]

For the matrix \( G \), parameters and constraints are discussed in the following Theorems 6 and 7.

**Theorem 6:** If the parameters of the DNA code \( \phi(\langle P >_R) \) are \((8k, M^P, d_{HI}^P)\) then the parameters of the DNA code \( \phi(\langle G >_R) \) are \((8k, M^G, d_{HI}^G)\), where \( d_{HI}^G \leq \min\{4k, d^P\} \) and
\[
M^G = \begin{cases} M^P & \text{if } (z_1, z_2, z_3, z_4) \leq \langle P >_R, \\
4M^P & \text{if } (z_1, z_2, z_3, z_4) \notin \langle P >_R.
\end{cases}
\]

**Theorem 7:** If the DNA code \( \phi(\langle P >_R) \) is closed under the reverse constraint then the DNA code \( \phi(\langle G >_R) \) will be closed under the reverse and reverse complement constraints.

**Remark 7:** In the Theorem 6, one can obtain the DNA code with the higher parameters using induction on the matrix \( G \) with the base case \( P \) such that the DNA code satisfies reverse and reverse complement constraints.

**Lemma 5:** For a matrix \( G_1 \) over the ring \( R \), if the DNA code \( \phi(\langle G_1 >_R) \) is closed under reverse constraint then the DNA code \( \phi(\langle G_k >_R) \) will be closed under reverse constraint, where \( G_k = (G_{k-1}G_1) \) for \( k > 1 \).

**Remark 8:** If a matrix \( G_1 \) over the ring \( R \), if \( 2+2w = (2 + 2w, 2 + 2w, 2 + 2w) \) and \( (G_1 >_R) \) then \( (2+2w, 2+2w, 2+2w, 2+2w) \) and \( G_k = (G_{k-1}G_1) \) for \( k > 1 \). Hence, if the DNA code \( \phi(\langle G_1 >_R) \) is closed under complement constraint then the DNA code \( \phi(\langle G_k >_R) \) will be closed under complement constraint.

VI. CONCLUSION

This paper scratches an interesting area of the DNA codes using the ring \( R = \mathbb{Z}_4 + u\mathbb{Z}_4 \), where \( u^2 = 2 + 2w \). A new distance called the Gau distance on the ring \( R \phi \) is introduced. We have also proposed a new distance preserving Gau map \( \phi \) from the elements of the ring \( R \) to all the DNA codewords of length \( 2 \). Several new families of the DNA codes are obtained. Some of them are optimal with respect to the bounds and are better than the DNA codes obtained in the literature. For the future study, it would be an interesting task to investigate the algebraic structure of the cyclic codes over the ring \( R \) and their correspondence to the DNA codes using the map \( \phi \). Using algebraic coding, constructing the optimal DNA codes meeting the bounds on reverse, reverse complement, \( GC \) content constraints is also an interesting future work.

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A. Proofs

1) The proof of the Theorem. We prove it for $n = 1$. Higher case is obvious. For $x, y \in R$, let $x = m_{ij} y \in M$ for some $0 \leq i, j \leq 3$ and $0 \leq i, j \leq 3$. Let us discuss the different cases of $x, y \in R$.

1. If $i = i'$ and $j = j'$, then $x = y$ and $\phi(x) = \phi(y) \implies d_H(\phi(x), \phi(y)) = 0$ and $d_{Gau}(x, y) = 0$.
2. If $i \neq i'$ and $j = j'$, then $d_H(\phi(x), \phi(y)) = 1$ and $d_{Gau}(x, y) = 1$.
3. If $i = i'$ and $j \neq j'$, then $d_H(\phi(x), \phi(y)) = 1$ and $d_{Gau}(x, y) = 1$.
4. If $i \neq i'$ and $j \neq j'$, then $d_H(\phi(x), \phi(y)) = 2$ and $d_{Gau}(x, y) = 2$.

Considering all the above cases, it is obvious that $\phi : (R^n, d_{Gau}) \to (\Sigma^n_{DNA}, d_I)$ is an isometry. 

2) The proof of the Theorem. The proof has two parts. The first part contains the proof for the parameters of the DNA code $\mathcal{C}_{DNA} = \phi(S^0_k)$. The second part proves that the DNA code satisfies reverse and reverse complement constraints.

1) By using the induction on $k$, one can observe that the length $n = 2^{k+1}$ of $\mathcal{C}_{DNA}$ with the base case $G_{1,1}$. For $z \in \{w, 2^w, w+2w, 2+3w\}$, the matrix $G_{1,m}$ is of type $\{1, m, 0, 0\}$, for $z \in \{2, 2^w\}$, the matrix $G_{1,m}$ is of type $\{0, m, 0, 0\}$ and for $z \in \{2^w\}$, the matrix $G_{1,m}$ is of type $\{1, 0, 0, 0\}$, hence the result holds for number of codewords $M$ (using the Theorem). Due to the symmetry of the matrix $G_{1,m}$, note that any two codewords differ at least at $2^{m-1}$ positions. Hence, the minimum Gau distance $d_{Gau}$ is $2^{m-1}$, where $d = \min(\{d_{Gau}(x,y) : x \neq y, x, y \leq 0\})$. Therefore for all the different cases of zero divisors $z$, the results hold.

2) For each integer $m \geq 1$, the codeword $2^m 2w$ is obtained by multiplying $2 + 2w$ to the row $I$ of the matrix $G_{1,m}$ over the ring $R$, where $I = (1 \ldots 1)$. From the Lemma the DNA code $\mathcal{C}_{DNA}$ is closed under complement. The closure of $\mathcal{C}_{DNA}$ with respect to reverse can be proved by using the Lemma. Let $x_i$ be the $i$th row of the matrix $G_{1,m}$, then for each $x_i \in G_{1,m}$, observe that

$$\phi^{-1}(\phi(x_i)') = \begin{cases} 3 & \text{if } i = 1, \\ 3z + x_i & \text{if } i = 2, 3, \ldots, m + 1. \end{cases}$$

Therefore $\phi^{-1}(\phi(x_i)') \in R(1, m)$ because $x_i, z \in R(1, m)$ for each $i = 1, 2, \ldots, m + 1$. Thus from the Lemma the DNA code $\mathcal{C}_{DNA}$ is closed under reverse. Hence, by using the Remark the DNA code satisfies reverse and reverse complement constraints.

4) The proof of the Lemma. Any row of $T$ is the row of either matrix $(G G)$ or the matrix $(0 H)$. Now consider two cases for this:

Case: 1 If $(x x)$ is the row of the matrix $(G G)$ then $x$ will be the row of the matrix $G$. Using the Lemma $\phi^{-1}(\phi(x))' \in G$ and therefore $\phi^{-1}(\phi(x))' \in G \implies \phi^{-1}(\phi(x))' \in G$. By using the Lemma for each row of the matrix $G$.

Case: 2 If $(0 y)$ is the row of the matrix $(0 H)$ then $y$ will be the row of $H$. By using the Lemma $\phi^{-1}(\phi(y))' \in H$. Hence $(\phi^{-1}(\phi(y))' \in H$. But $y$ is also the row of $G$ so from the case 1, $(\phi^{-1}(\phi(y))' \in G \implies \phi^{-1}(\phi(y))' \in H$. Thus $\phi^{-1}(\phi(y))' \in H$. Now by case 1 and case 2, it is concluded that $\phi^{-1}(\phi(y))' \in H$ for each row $t$ of the matrix $T$. Hence by using the Lemma the DNA code $\phi^{-1}(\phi(y))' \in H$ is closed under reverse.

5) The proof of the Theorem. The proof of the Theorem follows in two parts. The first part prove the parameters of the DNA code $\mathcal{C}_{DNA}$ and the second part proves the reverse and reverse complement constraints.

1) Using induction on $m$, one can observe that the length $n = 2^{m+1}$ of $\mathcal{C}_{DNA}$ with the base case $G_{1,1}$. Note that in the matrix $G_{1,m}$, the total number of rows which contain the zero divisor $z$ are $b = \sum_{i=0}^{m} (m-i)$ and the total number of rows are $a = \sum_{i=0}^{m-1} (m-i)$.

For $z \in \{w, 2^w, 3w, 2+3w\}$, the matrix $G_{1,m}$ is of type $\{b-a, a, 0, 0\}$, for $z \in \{2, 2^w\}$, the matrix $G_{1,m}$ is of
type \( \{ b - a, 0, a, 0 \} \) and for \( z \in \{ 2w \} \), the matrix \( G_{r,m} \) is of type \( \{ b - a, 0, a, 0 \} \), hence the result holds for number of codewords \( M \). Due to the symmetry of the matrix \( G_{r,m} \), note that any two codewords are differ at least at 2\(^{m-1} \) positions. Hence, the minimum Gau distance \( d_{Gau} \) is 2\(^{m-1} \), where \( d = \min \{ d_{Gau}(x, y) : x \neq y \text{ and } x, y \in \{ 2^m \} \} \). Therefore for all the different cases of zero divisor \( z \), the result holds for the distance by using the Theorem 2.

2) For each integers \( r, m (0 \leq r \leq m) \), the codeword \( 2^r 2^w \) is obtained by multiplying \( 2^r + 2^w \) to the row 1 of the matrix \( G_{1,m} \) over the ring \( R \), where \( 1 = \{ 1, 2, \ldots, 1 \} \).

For the DNA code \( \mathcal{C}_{DNA} \), the reverse constraint can be proved using induction on \( r \). For any integer \( m \geq 0 \), the matrix \( G_{0,m} = \{ 1, 2, \ldots, 1 \} \) with \( 2^m \) columns and therefore \( \{ 3, 3 \ldots, 3 \} \in R(0, m) \). Using the Lemma 2, the DNA code \( \phi(R(0, m)) \) is closed under the reverse constraint. Now, assume that the DNA code \( \phi(R(r - 1, m)) \) is closed under reverse for each integer \( m \geq r - 1 \). For the given integer \( r \), the reverse constraint of \( \phi(R(r, m)) \) can be proved using induction on \( m (\geq r) \). For the base case \( m = r \), we will prove that \( \phi(R(r, r)) \) is closed under reverse. Note that

\[
G_{r,r} = \begin{pmatrix}
G_{r-1,r} & 0 \\
0 & \ldots & 0
\end{pmatrix} = \begin{pmatrix}
G_{r-1,r-1} & 0 \\
0 & G_{r-1,r-1}
\end{pmatrix}
\]

Using the Lemma 4 \( \phi(R(r, r)) \) is closed under reverse. By recurrence construction of the matrix, each row of the matrix \( G_{r-1,m-1} \) is the row of the matrix \( G_{r,m-1} \). Using the Lemma 4, the DNA code \( \mathcal{C}_{DNA} \) is closed under reverse.

6) The proof of the Theorem 6: Both the matrices \( G \) and \( P \) have 4\( k \) number of columns so, by using the Theorem 2, the length of a codeword of the DNA code \( \phi(\mathcal{C}_{DNA}) \) is \( 8k \). Let the matrix \( P \) be of type \( \{ k_0, k_1, k_2, k_3 \} \). If \( (z_1, z_2, z_3, z_4) \in \langle P \rangle \) then the matrix \( G \) is of type \( \{ k_0, k_1, k_2, k_3, k_4 \} \) and if \( (z_1, z_2, z_3, z_4) \notin \langle P \rangle \) then the matrix \( G \) is of type \( \{ k_0, k_1, k_2, k_3 \} \). Hence, the result holds for the code size \( M \). The minimum Gau distance for \( < z_1, z_2, z_3, z_4 > \), is 4\( k \) and the minimum Gau distance for \( < z > \), is \( d_{Gau} \). Hence, the minimum Gau distance for \( < z > \) is bounded by \( \min \{ 4k, d_{Gau} \} \). Using the Theorem 2, the result holds.

7) The proof of the Theorem 7: For the complement constraint, note that \( (2^r + 2^w) \in \langle P \rangle \) because \( (2^r + 2^w) \notin \langle P \rangle \). Using the Lemma 3, the DNA code \( \phi(\mathcal{C}_{DNA}) \) is closed under complement constraint. For the reverse constraint, consider \( \phi^{-1}(\phi(z_1, z_2, z_3, z_4)^r) = (z_4, z_3, z_2, z_1) \) because \( \phi^{-1}(\phi(z)^r) = z \), for any \( z \in \{ 0, 2, 2^w, 2 + 2^w \} \). For the elements 0, 2, 2\( w \), 2 + 2\( w \) of the ring \( R \), note that the sum of any two elements is equal to the sum of the another two elements. If the length of the vectors \( z_1, z_2, z_3, z_4 \) is same then \( z_1 + z_2 = z_2 + z_1 \). If \( z_1 + z_4 = z_2 + z_3 = z \) then \( (z_1, z_2, z_3, z_4) + (z_1, z_2, z_3, z_4) = (z z z z) \) for some \( z \), where \( z = (z_1, z_2, z_3, z_4) \) is \( k \) length codeword. But, \( (2^r + 2^w) \in \langle P \rangle \) so \( (z z z z) \in \langle P \rangle \) and therefore \( (z_1, z_2, z_3, z_4) = (z z z z) - (z_1, z_2, z_3, z_4) \in \langle G \rangle \).
9) The proof of the Lemma: For any \( x, y \in \mathbb{R}^n \), \( x = (x_1, x_2, \ldots, x_n) \) and \( y = (y_1, y_2, \ldots, y_n) \).

Consider \( \phi(a x + b y)^r = (a x_n + b y_n)^r \phi(a x_{n-1} + b y_{n-1})^r \ldots \phi(a x_1 + b y_1)^r \).

Thus \( \phi^{-1}(\phi(a x + b y)^r) = \phi^{-1}(a x_n + b y_n)^r \phi^{-1}(a x_{n-1} + b y_{n-1})^r \ldots \phi^{-1}(a x_1 + b y_1)^r \) for any \( \phi \).

10) The proof of the Corollary: For any \( x, y \in \mathbb{R}^n \), \( x = (x_1, x_2, \ldots, x_n) \) and \( y = (y_1, y_2, \ldots, y_n) \).

Consider \( \phi(a x + b y)^c = (a x_1 + b y_1)^c \phi(a x_2 + b y_2)^c \ldots \phi(a x_n + b y_n)^c \).

Thus \( \phi^{-1}(\phi(a x + b y)^c) = (a x_n + b y_n)^c \phi^{-1}(a x_{n-1} + b y_{n-1})^c \ldots \phi^{-1}(a x_1 + b y_1)^c \) for any \( \phi \).