The Multi-Level Dilated Nested Array for Direction of Arrival Estimation

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ABSTRACT In this paper, a more generalized dilated nested array (DNA) named multi-level dilated nested array (multi-level DNA), which further extends the original DNA to the general situation and improves the direction of arrival (DOA) estimation performance, is proposed. The original DNA, which consists of a nested array and a time-shifted array, possesses the capabilities of handling more sources and achieving improved estimation accuracy compared with the nested array. However, only one time-shifted array is employed in DNA and the performance improvement is quite limited. Here, a new multi-level DNA, which utilizes multiple time-shifted nested arrays, is proposed. The multi-level DNA can provide more degrees of freedom (DoFs), meanwhile its difference co-array is still hole-free. The closed form expression of uniform DoFs in multi-level DNA is derived. The corresponding DOA Cramér-Rao bound, which gives the low bound on the variance of estimated DOA, is deduced in detail and some properties related to it are concluded. In total, for the DOA estimation, multi-level DNA can detect more sources and achieve more accurate estimation performance compared with the original DNA. Numerical simulations are performed to verify the superiority of the proposed multi-level DNA.

INDEX TERMS Direction of arrival (DOA), co-array, nested array (NA), dilated nested array (DNA).

I. INTRODUCTION
Direction of arrival (DOA) estimation has long been viewed as an important topic for array signal processing in radar, sonar and Internet of vehicles (IoV) [1]–[7]. The traditional subspace-based DOA estimation methods, such as multiple signal classification (MUSIC) and estimation of signal parameters via rotational invariance techniques (ESPRIT), can resolve the maximum of $N - 1$ uncorrelated sources by using uniform linear array with $N$ elements [2], [8]. Later on, in order to reduce the complexity in subspace technique, the root-MUSIC, reduced-complexity MUSIC (RC-MUSIC) and RC-ESPRIT are proposed [9]–[11]. However, subspace-based methods will achieve considerably degraded DOA estimation performance when low signal-to-noise ratio (SNR) and snapshot number are met. Recently, to overcome these limitations, a number of sparse methods for DOA estimation, such as the on-grid sparse method, off-grid sparse method and gridless sparse method, have been proposed [6], [12]–[15]. Moreover, tensor-based DOA estimation methods, which utilize the multi-dimensional nature of array signal, offer another way to improve the DOA estimation performance [16], [17]. To detect large number of sources and achieve excellent performance, high degrees of freedom (DoFs) is always necessary in DOA estimation. Unfortunately, high DoFs is often unavailable due to various reasons such as the limitations of space and hardware cost. In order to solve the contradiction between the improved DoFs and the reduced number of array elements, the issue of underdetermined DOA estimation in sparse array, has been attracting the related researchers and practitioners in recent years. Kinds of sparse array structures, such as minimum redundancy array (MRA) [18], coprime array (CA) [19]–[23], nested array (NA) [24]–[29] and so on, have been put forward. MRA is a linear sparse array designed to obtain the largest possible virtual uniform linear array aperture. It is one of the earliest and most effective sparse array structures, such as minimum redundancy array (MRA) [18], coprime array (CA) [19]–[23], nested array (NA) [24]–[29] and so on, have been put forward. MRA is a linear sparse array designed to obtain the largest possible virtual uniform linear array aperture. It is one of the earliest and most effective sparse array structures, such as minimum redundancy array (MRA) [18], coprime array (CA) [19]–[23], nested array (NA) [24]–[29] and so on, have been put forward.
For overcoming the deficiency in MRA, several typical sparse arrays mainly including CA and NA have been proposed. CA, which consists of two uniform linear arrays with coprime relation, can resolve more sources than array elements and is easy to be designed. Unfortunately, its difference co-array is not hole-free and its central uniform linear set is always smaller than the difference set, which is not expected in DOA estimation.

As a result, in this paper the NA, whose array element position can be explicitly expressed and difference co-array is hole-free, is mainly focused. Initially, NA, which consists of a dense uniform linear array and a sparse uniform linear array, is designed to possess hole-free difference co-array. It can resolve as many as \( O(N^2) \) sources by using only \( N \) array elements [24], [25]. In [26], NA is improved by adding an additional sensor to the original NA. However, both NA and improved NA suffer from mutual coupling for their close interelement intervals. In [27], [28], the super NA and its high-order extensions are designed to reduce the mutual coupling effect by rearranging the dense uniform linear array. Meanwhile, super NA and its high-order extensions also maintain many advantages in NA, such as the high uniform DoFs (UDoFs) and close-form array element location. The augmented NA (ANA), which splits the dense uniform linear array in NA into two or four parts, is proposed in [29]. ANA can be classified into four types and can achieve higher UDoFs than NA and super NA. Unfortunately, ANAs will either suffer from the mutual coupling or satisfy complicated conditions to achieve the hole-free difference co-array. Naturally, the idea of one-dimensional sparse array design can be extended to the two-dimensional (2D) sparse array for 2D DOA estimation. In [30], [31], the 2D NA and 2D CA have been designed, respectively. However, the array design methods in 1D sparse array and 2D sparse array are quite different. Here, only the 1D sparse array is considered and the 2D sparse array will be considered in the future work.

Though various ingenious designs have been cast into the static NA, the DoFs increase is limited. By adopting the moving platform, the authors in [32] created the synthetic CA, which can acquire several times higher DoFs than the original CA with the same number of array elements. Unfortunately, synthetic CA must move at least \( N_1 \lambda/4 \) to produce a hole-free difference co-array, where \( \lambda \) is the signal wavelength. \( N_1 \) and \( N_2 \) (\( N_1 > N_2 \)) are the coprime numbers used to generate CA. Therefore, when \( N_1 \) approaches large, the synthetic CA becomes impractical since it requires the stationary environment over a long period. Based on the idea of synthetic array, the authors in [33] designed a dilated nested array (DNA), which merely moves a half wavelength, to achieve two to three times higher DoFs than NA with the same number of array elements. However, the array motion is merely limited to \( \lambda/2 \) and the generalized case is not considered. Actually, longer synthetic distance than \( \lambda/2 \) can be realized when the change of signal environment is slow [34].

In this paper, for further enhancing DOA estimation performance, DNA is generalized to the multi-level dilated nested array (multi-level DNA), which consists of a NA and several time-shifted arrays. The difference co-array of the designed multi-level DNA is hole-free and can achieve much higher UDoFs than that of DNA. Furthermore, the UDoFs of multi-level DNA is derived and expressed in closed form. For DOA estimation, multi-level DNA can detect more sources and achieve more accurate estimation performance compared with the original DNA. Numerical simulations are performed to verify the superiority of the proposed multi-level DNA.

The main contributions of the paper lie in three aspects.

i) A more generalized DNA, called as multi-level DNA, which extends the original DNA to the general situation and improves the DOA estimation performance is proposed. As a result of taking more than one time-shifted arrays, the interelement interval in multi-level DNA can be designed larger than that in DNA, which reduces the mutual coupling effect between array elements.

ii) The DOA Cramér-Rao bound (CRB), which gives the low bound on the variance of estimated DOA, for multi-level DNA is deduced in detail and some properties related to its DOA CRB are concluded. The accurate expression for DOA CRB is complicated. Here, the expressions for one source case and multiple sources under certain constraints are separately approximated by the simple ones. Some useful properties with respect to CRB, such as the appropriate NA construction and the CRB decrease rate, are also concluded from the approximated expressions.

iii) The number of UDoFs for multi-level DNA is deduced and expressed in closed form. By properly setting time-shifted array position, multi-level DNA can achieve higher UDoFs than DNA, which benefits the DOA estimation.

The remainder of this paper is organized as follows. The signal model is built in Section II. Section III analyzes the difference co-array of multi-level DNA. Section IV illustrates the approximated DOA CRB expression for multi-level DNA. In Section V, the simulation experiments show the performance of multi-level DNA. Finally, we make a conclusion in Section VI.

**Notation:** Throughout this paper, matrix and vector are represented by boldface uppercase letter and boldface lowercase letter, respectively. Superscript \(^T\), * and \(^H\) separately denote transpose, conjugate and conjugate transpose of a matrix or a vector. The symbol \( \cdot \) represents the Hadamard product (i.e., the element-wise product), \( tr() \) is the trace of a matrix, \( \Re() \) is the real part of a complex number, \( C \) represents the field of complex number and \( E[\cdot] \) denotes the expectation operator. Given a vector \( \mathbf{m} \), \( diag(\mathbf{m}) \) is a diagonal matrix with \( \mathbf{m} \) on its diagonals. Given a matrix \( \mathbf{M} \), \( diag(\mathbf{M}) \) is a column vector constructed from its main diagonal. The triangular bracket notation \( [\mathbf{M}]_{i,j} \) denotes the element located at the \( i \)th row and \( j \)th column of \( \mathbf{M} \).
II. SIGNAL MODEL

As shown in Fig. 1, the multi-level DNA, which is based on NA, moves at a constant velocity of $v$. $N = N_1 + N_2$ array elements in the original NA are arranged as the following positions [24]:

$$\mathcal{P}_O = \{n_1d_{NA}, n_1 = 1, \cdots, N_1\} \cup \{(N_1 + 1)n_2d_{NA}, n_2 = 1, 2, \cdots, N_2\}$$

where $d_{NA} = ad$ with $a$ being an integer and $d = \lambda/2$ being the half-wavelength interelement interval. $Q$ uncorrelated far-field narrowband sources receiving on the sparse array at time $t$ is denoted as

$$x(t) = \sum_{q=1}^{Q} s_q(t)e^{-j2\pi vt \sin(\theta_q)/\lambda}a(\theta_q) + \epsilon(t)$$

where $a(\theta_q) = [e^{-j2\pi d_1 \sin(\theta_q)/\lambda}, \cdots, e^{-j2\pi d_q \sin(\theta_q)/\lambda}]^T \in \mathbb{C}^{N \times 1}$ with $d_i \in \mathcal{P}_O, i = 1, 2, \cdots, N$ being the spatial steering vector, $\epsilon(t)$ is the complex Gaussian white noise vector, $A = [a(\theta_1), \cdots, a(\theta_Q)] \in \mathbb{C}^{N \times Q}$ represents the array manifold matrix and $s(t) = [s_1(t)e^{-j2\pi vt \sin(\theta_1)/\lambda}, \cdots, s_Q(t)e^{-j2\pi vt \sin(\theta_Q)/\lambda}]^T \in \mathbb{C}^{Q \times 1}$. $s(t)$ is the source waveform. During the whole processing period, the source directions with respect to the array elements are considered unchanged. Let $v = d/v$, for the array moving, the uncorrelated far-field narrowband sources receiving on the sparse array at time $t + kt$ is expressed as

$$x(t + kt) = \sum_{q=1}^{Q} s_q(t + kt)e^{-j2\pi v(t + kt) \sin(\theta_q)/\lambda}e^{-j2\pi kd \sin(\theta_q)/\lambda}a(\theta_q) + \epsilon(t + kt)$$

From the far-field narrowband signal fact that $s_q(t + kt) = s_q(t)e^{j2\pi f t \tau}$, (3) can be further simplified as

$$x(t + kt) = s_q(t)e^{j2\pi f t \tau}B_k(t + \epsilon(t + kt)$$

where $f$ denotes the carrier frequency of the narrowband signal, $B_k = [b_k(\theta_1), \cdots, b_k(\theta_Q)] \in \mathbb{C}^{N \times Q}$ with $b_k(\theta_q) = e^{-j2\pi kd \sin(\theta_q)/\lambda}a(\theta_q)$. The phase item $e^{j2\pi f t \tau}$ in (4) can be removed by the following phase correction operation, namely

$$\tilde{x}(t + kt) = x(t + kt)e^{-j2\pi f t \tau} = B_k(t + \epsilon(t + kt)$$

Subsequently, by stacking the signals receiving at different time into a vector yields

$$y(t) = \begin{bmatrix} x(t) \\ \tilde{x}(t + \tau) \\ \cdot \\ \cdot \\ \cdot \\ x(t + K \tau) \end{bmatrix} = \begin{bmatrix} \mathbf{A}(t) + \epsilon(t) \\ \mathbf{B}_1s(t) + \epsilon(t + \tau) \\ \cdot \\ \cdot \\ \cdot \\ \mathbf{B}_Ks(t) + \epsilon(t + K\tau) \end{bmatrix}$$

$$= \mathbf{C}s(t) + \epsilon(t) \in \mathbb{C}^{(K+1)N \times 1}$$

where $\mathbf{C} = [\mathbf{A}^T, \mathbf{B}_1^T, \cdots, \mathbf{B}_K^T]^T \in \mathbb{C}^{(K+1)N \times Q}$ and $\epsilon(t) = [\epsilon^T(t), \epsilon^T(t + \tau), \cdots, \epsilon^T(t + K\tau)]^T$. Due to the uncorrelated property between noise and source, the covariance matrix of $y(t)$ is obtained as

$$\mathbf{R} = E[y(t)y^H(t)] = \mathbf{CPC}^H + \sigma^2 \mathbf{I} \in \mathbb{C}^{(K+1)N \times (K+1)N}$$

where $\mathbf{I} \in \mathbb{C}^{(K+1)N \times (K+1)N}$ is the identity matrix, $\sigma^2$ is the noise power and $\mathbf{P} \in \mathbb{C}^{Q \times Q}$ is the source covariance matrix. In general, since the true statistics of $\mathbf{R}$ cannot be available, it is usually replaced by the sample matrix estimator, namely

$$\hat{\mathbf{R}} = \frac{1}{L} \sum_{l=1}^{L} y(l)y^H(l),$$

where $L$ is the number of snapshots. According to the NA-based underdetermined DOA estimation method, $\mathbf{R}$ can be rearranged into a $[(K+1)N]^2 \times 1$ vector and then a new virtual steering vector with longer length can be extracted to enhance the DOA estimation performance. The core procedure lies in constructing the difference co-array. Therefore, in the following the difference co-array generated by multi-level DNA will be studied [24]–[29]. The definition of difference co-array is

**Definition 1 (Difference Co-Array):** For a sparse array specified by a sensor position set $\mathcal{P}$, its difference co-array $\mathcal{D}$ is defined as $\mathcal{D} = \{n_1 - n_2 | n_1, n_2 \in \mathcal{P}\}$.

III. THE DIFFERENCE CO-ARRAY OF MULTI-LEVEL DNA

In the following, we will show the property of difference co-array generated by multi-level DNA. The initial array element positions are expressed in (1). When NA moves a distance of $kd$, the array element positions are shifted to be

$$\mathcal{P}_k = \{n_1d_{NA} + kd, n_1 = 1, \cdots, N_1\} \cup \{(N_1 + 1)n_2d_{NA} + kd, n_2 = 1, 2, \cdots, N_2\}.$$ 

Correspondingly, the synthetically dilated nested array $\mathcal{P}$, formed by $\mathcal{P}_O$ and $\mathcal{P}_k$, is expressed as

$$\mathcal{P} = \mathcal{P}_O \cup \mathcal{P}_1 \cup \cdots \cup \mathcal{P}_K.$$ 

The difference co-array $\mathcal{D}_M$ generated by $\mathcal{P}$ is complicated. The set formed from the difference co-array can be divided into two subsets: one is the self-lags set, whereas the other is the cross-lags set. For better understanding $\mathcal{D}_M$, the self-lags
and cross-lags of different parts of $\mathcal{P}$ are examined. It is worth noting that $\mathcal{P}_O$ and $\mathcal{P}_k$ are NA and shifted NA, respectively. Therefore, the self-lags of $\mathcal{P}_O$ and $\mathcal{P}_k$ affirmatively satisfy the following uniform set

$$
\mathcal{D}_S = \{-(N_1 N_2 + N_2 - 1)d_{NA}, \ldots ,
-nd_{NA}, 0, d_{NA}, \ldots , (N_1 N_2 + N_2 - 1)d_{NA}\}. \quad (10)
$$

Accordingly, the cross-lags between $\mathcal{P}_O$ and $\mathcal{P}_k$ are expressed as

$$
\mathcal{D}_k = \{kd, d_{NA} + kd, \ldots , (N_1 N_2 + N_2 - 1)d_{NA} + kd\}
\cup \{-kd, d_{NA} - kd, \ldots , (N_1 N_2 + N_2 - 1)d_{NA} - kd\}.
\quad (11)
$$

The cross-lags between different $\mathcal{P}_k$s are expressed as

$$
\mathcal{D}_{k_1 k_2} = \{(k_1 - k_2)d, \ldots , (N_1 N_2 + N_2 - 1)d_{NA} + (k_1 - k_2)d\}
\cup \{(k_2 - k_1)d, \ldots , (N_1 N_2 + N_2 - 1)d_{NA} + (k_2 - k_1)d\}, \quad (12)
$$

where $\mathcal{D}_k$ is the set containing the cross-lags between $\mathcal{P}_O$ and $\mathcal{P}_k$, $\mathcal{D}_{k_1 k_2}$ is the set containing the cross-lags between $\mathcal{P}_O$ and $\mathcal{P}_k$, $k_1, k_2 = 1, 2, \ldots , K$ and $k_1 \neq k_2$. After obtaining the self-lags set and cross-lags set, the difference co-array of multi-level DNA is expressed as

$$
\mathcal{D}_M = \mathcal{D}_S \bigcup_{k=1}^{K} \mathcal{D}_k \bigcup_{k_1, k_2=1}^{K} \mathcal{D}_{k_1 k_2}, \quad k_1 \neq k_2. \quad (13)
$$

In fact, $\mathcal{D}_S$, $\mathcal{D}_k$ and $\mathcal{D}_{k_1 k_2}$ in (10), (11) and (12) can be rewritten as the form in (14) that

$$
\mathcal{D}_S = \{\beta d_{NA}\}, \mathcal{D}_k = \{\beta d_{NA} + kd\} \cup \{-\beta d_{NA} - kd\}
\mathcal{D}_{k_1 k_2} = \{\beta d_{NA} + (k_1 - k_2)d\} \cup \{\beta d_{NA} + (k_2 - k_1)d\}
\beta = -(N_1 N_2 + N_2 - 1), \ldots , -1, 0, 1, \ldots , (N_1 N_2 + N_2 - 1). \quad (14)
$$

By using the relation $d_{NA} = \eta d$ and the symmetry property of $\mathcal{D}_M$, the non-negative part of $\mathcal{D}_M$, called $\mathcal{D}_M^+$, is expressed as

$$
\mathcal{D}_M^+ = \mathcal{D}_M^+ \mathcal{e}(\mathcal{D}_M^+) \quad (15)
$$

where $\mathcal{D}_M^+$ is expressed as

$$
\mathcal{D}_M^+ = d(0, 1, \ldots , a\beta' - 1) + K, (a\beta' - K), \ldots , a\beta', \ldots , a\beta' + K, \ldots , a(N_1 N_2 + N_2 - 1) + K)
\beta' = 0, 1, 2, \ldots , (N_1 N_2 + N_2 - 1) \quad (16)
$$

and the function

$$
\mathcal{e}(t) = \begin{cases} 1, & t > 0 \\ 0, & \text{otherwise}. \end{cases}
$$

As a result, three properties can be pointed out from $\mathcal{D}_M^+$.

**Property 1:** The maximum value $M_{\text{max}}$ in $\mathcal{D}_M^+$ is $[a(N_1 N_2 + N_2 - 1) + K]d$, which infers the maximum consecutive length the difference co-array can achieve.

**Property 2:** $\mathcal{D}_M^+$ is fully filled when $1 \leq a \leq 2K + 1$ while it is not fully filled when $a > 2K + 1$.

**Property 3:** $\mathcal{D}_M^+$ is the least redundant when $a = 2K + 1$.

**Proof:** Property 1 is obvious and straightforward.

We will put the emphasis on Property 2 and Property 3. As shown in (15) and (16), $2K$ consecutive elements are filled between $a\beta'$ and $a(\beta' + 1)$. For achieving consecutive and hole-free $\mathcal{D}_M^+$, the gap between $a\beta'$ and $a(\beta' + 1)$ must be smaller than $2K$, i.e. $a(\beta' + 1) - a\beta' - 1 = a - 1 \leq 2K$. On the other hand, $a \geq 1$ for it being a positive integer. Then Property 2 is proved.

Through Property 2, $a$ is restricted between $1$ and $2K + 1$ for achieving the hole-free difference co-array. However, it is still a large range when $K$ is not small. Moreover, various choice of $a$ will influence the performance of the difference co-array for DOA estimation. Through Property 1, large value of $a$ will increase the value of $M_{\text{max}}$, which benefits DOA estimation. Unfortunately, through Property 2, $a$ cannot be larger than $2K + 1$ since the difference co-array will become hole-filled under this condition, which is not expected. Especially, when $a = 2K + 1$, $a\beta' + K$ will not overlap with $a(\beta' + 1) - K$, which means that the subset $[a(\beta' - 1) + K, a\beta' - K, \ldots , a\beta', \ldots , a\beta' + K, a(\beta' + 1) - K]$ becomes fully filled and has no redundant element. As a consequence, when $a = 2K + 1$, the difference co-array with the largest consecutive length and the least redundant element can be achieved. The proof of Property 3 is completed.

**Definition 2 (UDoS $[27]$):** Given a sparse array, let $U$ denote the maximum consecutive segment of its difference co-array. The cardinality of $U$ is referred to as the number of “uniform DoFs (UDoSs)”.

**Remark:** When $1 \leq a \leq 2K + 1$, the number of UDoFs in multi-level DNA is $2a(N_1 N_2 + N_2 - 1) + 2K + 1$.

**Proof:** By combining the symmetry property of $\mathcal{D}_M$, Property 1 and Property 2, we can immediately deduce that when $1 \leq a \leq 2K + 1$, the UDoFs of multi-level DNA is

$$
m = 2m_{\text{max}} + 1 = 2a(N_1 N_2 + N_2 - 1) + 2K + 1. \quad (17)
$$

Suppose the total of $N$ array elements be exploited to construct the NA. Then the maximum UDoFs the multi-level DNA can obtain is

$$
\eta_{\text{max}} = a\eta + 2K + 1 - a, \quad 1 \leq a \leq 2K + 1 \quad (18)
$$

where

$$
\eta_N = \begin{cases} N^2/2 + N - 1, & \text{if } N \text{ is even} \\ (N + 1)^2/2 - 1, & \text{if } N \text{ is odd} \end{cases}
$$

is the maximum UDoFs of NA. From (18), it can be seen that the UDoFs of multi-level DNA is in proportion to $a$ and related to $K$. As a consequence, multi-level DNA can achieve improved DOA estimation performance with the increases of $a$ and $K$ as long as the aforementioned properties are satisfied. When $a = 2K + 1$, multi-level DNA can achieve the maximum UDoFs. Specially, when $K = 1$, multi-level DNA degrades to DNA and the UDoFs is in accordance with [33].

For better understanding the UDoFs improvement, the maximum DoFs of NA, DNA and two-level DNA ($K = 2$)
TABLE 1. Maximum UDoFs comparison for fixed number of array elements.

| N   | 4   | 6   | 8   | 10  | 12  |
|-----|-----|-----|-----|-----|-----|
| NA  | 11  | 23  | 39  | 59  | 83  |
| DNA | 33  | 69  | 117 | 177 | 249 |
| Multi-level DNA | 55 | 115 | 195 | 295 | 415 |

FIGURE 2. Non-negative part of difference co-array generated by two-level DNA.

are listed in Table 1 when the number of array elements is fixed. In addition, the non-negative part of difference co-array generated by two-level DNA with \( a \) varying between 1 and 5 is demonstrated in Fig. 2, where \( N_1 \) and \( N_2 \) are both set to be 4. It is worth noting that even with the same \( a \), the UDoFs of two-level DNA is still higher than that of DNA for \( 2K + 1 > 3 \) when \( K = 2 \).

IV. DOA CRB ANALYSIS

In this section, the DOA CRB (denoted as CRB(\( \hat{\theta} \))), which gives the low bound on the variance of estimated DOA, on multi-level DNA is focused. In [35]–[37], the authors have investigated some closed-form CRB(\( \hat{\theta} \)) expressions for several classical sparse arrays and found their validity even when the number of sources exceeds the number of array elements. Here, CRB(\( \hat{\theta} \)) for sparse array is reviewed and some new results will be obtained when CRB(\( \hat{\theta} \)) is applied into multi-level DNA. Let the estimated parameters denote as \( \hat{\theta} = d \sin(\hat{\phi})/\lambda, \hat{p} = \hat{\sigma}_x, \) and \( \hat{\sigma} \), the Fisher information matrix (FIM) with respect to the receiving signal under the uncorrelated source assumption is expressed as

\[
J = N \begin{bmatrix} J_{\theta\theta} & J_{\theta p} & J_{\theta \sigma} \\ J_{p\theta} & J_{pp} & J_{p\sigma} \\ J_{\sigma\theta} & J_{\sigma p} & J_{\sigma\sigma} \end{bmatrix} \in \mathbb{C}^{(2Q+1) \times (2Q+1)}
\]

(19)

where

\[
J_{\theta\theta} = (\hat{C}^H R^{-1} C)^* \cdot (\hat{C}^H R^{-1} C) \in \mathbb{C}^{Q \times Q},
\]

\[
J_{\theta p} = 2 \text{Re}[\hat{C}^H R^{-1} \hat{C}]^* \cdot (\hat{C}^H P^{-1} C) + (\hat{C}^H R^{-1} C)^* \cdot (\hat{C}^H P^{-1} \hat{C} P) \in \mathbb{C}^{Q \times Q},
\]

\[
J_{\theta \sigma} = 2 \text{Re}[\hat{C}^H R^{-1} \hat{C}]^* \cdot \text{diag}(\hat{C}^H R^{-2} C) \in \mathbb{C}^{Q \times Q},
\]

\[
J_{pp} = \text{diag}(\hat{C}^H R^{-2} C) \in \mathbb{C}^{Q \times 1},
\]

\[
J_{\sigma\sigma} = \text{tr}(R^{-2}) \text{ and } \hat{C} = \left[ \frac{\partial a(\omega_1)}{\partial \omega_1} \frac{\partial a(\omega_2)}{\partial \omega_2} \ldots \frac{\partial a(\omega_Q)}{\partial \omega_Q} \right].
\]

The CRB(\( \hat{\theta} \)) can be obtained by inverting FIM. However, the expression of CRB(\( \hat{\theta} \)) is rather complicated by directly inverting \( J \). Here, the accurate CRB(\( \hat{\theta} \)) expression will be approximated by the simple one when certain condition is satisfied. The analysis of approximated CRB(\( \hat{\theta} \)) will be started from one source case.

Proposition 1: Under the condition of \( Q = 1 \) and high SNR \( \sigma \),

\[
\text{CRB}(\hat{\theta}) = \frac{1}{L} J^{-1}_{\theta\theta} \approx \frac{6}{(K + 1)(1 + 3u)a^2u^2(1 - u)^3N^2\text{SNR}}
\]

(20)

where \( uN = N_1, (1 - u)N = N_2 \) and \( 0 < u < 1 \).

Proof: See Appendix A

Proposition 2: Under the conditions of \( Q > 1 \) and high SNR, when the off-diagonal elements in \( \hat{C}^H C \), \( \hat{C}^H \hat{C} \) and \( \hat{C}^H \hat{C} \) are all negligible compared with their diagonal elements,

\[
\text{CRB}(\hat{\theta}) = \frac{1}{L} J^{-1}_{\theta\theta} \approx \frac{6}{(K + 1)(1 + 3u)a^2u^2(1 - u)^3N^2 \times \sigma^{-1}} \in \mathbb{C}^{Q \times Q}.
\]

(21)

Proof: See Appendix B

Note that under both conditions, CRB(\( \hat{\theta} \)) of multi-level DNA is in inverse proportion to \( K + 1 \) and \( a^2 \), which means that multi-level DNA with larger \( a \) and \( K \) enjoys lower CRB(\( \hat{\theta} \)). In addition, by comparing the CRB expression in [35] with the expression here, we can find that the CRB(\( \hat{\theta} \)) of multi-level DNA with \( a = 1 \) is \( K + 1 \) times lower than that of NA even they possess nearly the same UDoFs. When multiple sources exist, the CRB(\( \hat{\theta} \)) is rather complicated and is difficult to be approximated by a simple expression. However, when the matrices \( \hat{C}^H C \), \( \hat{C}^H \hat{C} \) and \( \hat{C}^H \hat{C} \) approach the diagonal matrices, the CRB(\( \hat{\theta} \)) can be expressed in a simple form. In addition, by differentiating the denominator of the approximated expression with respect to \( \mu \), we can obtain

\[
\frac{\partial}{\partial \mu} \left[ (1 + 3u)a^2(1 - u)^3 \right] \approx u(1 - u)^2(-18u^2 + 4u + 2).
\]

(22)

For simplicity, some constants irrelevant to \( \mu \) are neglected. Let (22) be zero, the maximum value of \( (1 + 3u)a^2(1 - u)^3 \) can be achieved when \( u \approx 0.46 \) (0 < \( u < 1 \)). As a consequence, we can find that although multi-level DNA can achieve its maximum DoFs when \( \mu = 0.5 \), its lowest CRB(\( \hat{\theta} \)) is achieved when \( \mu \approx 0.46 \).
For achieving the consecutive difference co-array, the maximum $a$ obtained in two-level DNA is 5 and that in DNA is 3.

A. WEIGHT FUNCTION AND MUTUAL COUPLING COMPARISON

First of all, the weight functions $w(m)$ (defined as the number of array element pairs that lead to a co-array index [25]) of two-level DNA with different $a$ are demonstrated in Fig. 3. In general, $w(m)$ indicates the UDoFs and redundant degree of the difference co-array. Apparently, as $a$ increases, the UDoFs of two-level DNA improves while the redundant degree of it drops. Specially, as shown in Fig. 3(d), when $a = 6 > 2K + 1 = 5$, the difference co-array of two-level DNA is not hole-free any more, which is satisfied with Property 2. Therefore, two-level DNA with $a = 5$ can obtain the highest UDoFs and the lowest redundant degree. The original mutual coupling matrix, which represents the interference between array elements, is complicated. Here, the simplified version is adopted, namely

$$
\langle C \rangle_{n_1,n_2} = \begin{cases}
    c_{|n_1 - n_2|}, & \text{if } |n_1 - n_2| \leq B \\
    0, & \text{otherwise}
\end{cases}
$$

(25)

where $n_1, n_2 \in \mathcal{P}_O$ and coupling coefficients satisfy $1 = c_0 > c_1 > \ldots > c_B$ [27]. In the simulation, $c_1 = 0.3e^{j\pi/3}$ and $c_i = c_1e^{-j(i-1)\pi/8}$ for $2 \leq i \leq B$.

The distributions of $\text{abs} \left( (C)_{n_1,n_2} \right)$ for different sparse arrays are displayed in Fig. 4. According to the definition of mutual coupling matrix, the amplitude of its off-diagonal components characterizes the amount of mutual coupling. Conceptually speaking, two-level DNA with larger $a$ exhibits small mutual coupling effect for the large interval between array elements, which corresponds to the results in Fig. 4. In addition, the coupling leakage coefficient $CL = \|C - \text{diag}(C)\|_F / \|C\|_F$, which denotes the degree of coupling leakage, decreases with the increase of $a$. In general, the smaller the $CL$ is, the less the mutual coupling is. Therefore, two-level DNA with larger $a$ can obtain less mutual coupling. In Fig. 5, $CL$ varies with $|c_1|$ for two-level DNA and DNA are illustrated. Evidently, when $|c_1|$ varies from 0 to 1, DNA with $a = 1$ suffers from the most serious mutual coupling effect while two-level DNA with $a = 5$ enjoys the least serious mutual coupling effect.
B. MUSIC SPECTRAL COMPARISON

In Fig. 6, the co-array MUSIC spectrals [24] of two-level DNA and DNA are compared, where 40 uncorrelated sources are considered and their positions are marked as the red dot lines. The SNR is 10dB. The DOA estimation mean-square error \( E = \sqrt{\frac{1}{Q} \sum_{q=1}^{Q} (\bar{\omega}_q - \omega_q)^2} \) with \( \omega_q \) being the true DOA of each source and \( \bar{\omega}_q \) being the estimated DOA of each source, which infers the bias between the estimated DOA and the true DOA, is also demonstrated. \( E \) represents the average estimated DOA error of each source when \( Q \) sources exist. Smaller \( E \) implies more accurate DOA estimation ability.

As shown in Fig. 6, two-level DNA with \( a = 5 \) and \( a = 4 \) can identify all the 40 sources while DNA with \( a = 3 \) fails. In addition, two-level DNA with \( a = 5 \) can acquire the best estimation accuracy since its UDoFs is the maximum. Since DNA with \( a = 3 \) fails to identify the DOAs of some sources, its \( E \) is not exist.

C. DOA CRB COMPARISON

In this simulation part, the DOA CRBs of two-level DNA and DNA are demonstrated. Initially, DOA CRB varying with respect to SNR is shown in Fig. 7, where two conditions including fewer sources than array elements and more sources than array elements are both considered. Apparently, DOA CRB decreases with the increase of SNR for each array. Under both conditions, two-level DNA with larger \( a \) possesses lower DOA CRB. It can be noted that when more sources than array elements exists, the DOA CRB curve will cease to decrease at a certain SNR, which is consistent with the results shown in [35].

In Fig. 8, DOA CRB varying with the number of sources, from which the identifiability of an array can be observed, is evaluated. The DOA CRB curve of each array will diverge at a certain number of sources, which is corresponding to the UDoFs of each array. Certainly, two-level DNA with \( a = 5 \) can identify the most number of sources while DNA with \( a = 1 \) can identify the least number of sources.
DOA CRB varying with the number of array elements under one source case, which verifies the approximated expression in Section 4, is depicted in Fig. 9. The solid line represents the DOA CRB calculated by directly inverting (19) while the dotted line represents the DOA CRB calculated by the approximated expression in (20). As shown in Fig. 9(a), although there exists obvious deviation between the accurate DOA CRB and the approximated one when the number of array elements is small, the deviation becomes negligible when the number of array elements approaches large. However, when SNR is low, the deviation between the accurate DOA CRB and the approximated one is always large no matter how many array elements are deployed. In Fig. 10, three sources with \( \text{SNR} = [-20 \ 0 \ 20] \) dB are considered to verify the approximated DOA CRB expression of multiple sources in (21). The matrices \( \hat{C}H \hat{C} \) are all regarded as the diagonal matrices. As the results show, when the number of array elements approaches large, the approximated DOA CRB suitably follows the accurate one for the high SNR source.

Finally, Fig. 11 shows the variation of accurate DOA CRB with \( \mu \), where \( N = 40 \) and \( \text{SNR} = 10 \) dB. Clearly, the lowest bound of accurate DOA CRB is achieved around 0.46, which satisfies the result derived from the approximated DOA CRB expression.
VI. CONCLUSION

A generalized NA structure in moving platform called multi-level DNA that further extends the original DNA to the general situation and improves the DOA estimation performance is proposed. By using only $N$ array elements, multi-level DNA can generate as many as $O(2KN^2)$ UDoFs, which is several times higher than DNA. For the closed-form element position, multi-level DNA can be easily implemented. The performance of multi-level DNA has been verified by several simulation experiments. However, the difference co-array generated by multi-level DNA is a bit more redundant than that generated by NA. Therefore, in the future work, a more ingenious design will be performed over multi-level DNA to further reducing its redundancy. It should be noted that the NA in the designed approach can also be replaced by other well known sparse arrays, such as CA and super NA, and the results are similar.

APPENDIXES

APPENDIX A

PROOF OF PROPOSITION 1

Here, the equation in Proposition 1 will be derived in detail. Since the items in FIM are all related to $\mathbf{C}$, $\dot{\mathbf{C}}$, $\mathbf{R}^{-1}$ and their combinations, we first study their expressions when one source is considered. For the one source case, the manifold vector in multi-level DNA with $N = N_1 + N_2$ array element is given by $\mathbf{c} = [\mathbf{a}_1^T, \mathbf{a}_2^T, \ldots, \mathbf{a}_K^T]^T \in C^{(K+1)N_1 \times 1}$, where $\mathbf{a}_k = [e^{-j2\pi(a+k)\omega}, \ldots, e^{-j2\pi(N_1a+k)\omega}, \ldots, e^{-j2\pi(N_2a+k)\omega}, \ldots, e^{-j2\pi(N_1+N_2)a+k)\omega}]^T$. (26), (27) and (28) can be obtained when $N$ approaches infinity

\[ \mathbf{C} = (K + 1)N \]  
\[ j\dot{\mathbf{C}} = \mathbf{C} \Gamma \mathbf{C} = 2\pi \sum_{k=0}^{K} \sum_{i=1}^{N_1} (ia + k) \]
\[ + 2\pi \sum_{k=0}^{K} \sum_{i=1}^{N_2} [i(N_1 + 1)a + k] \]
\[ \approx \pi (K + 1)au(u - 1)N^3 \]  
\[ \mathbf{C} = \mathbf{C} \Gamma \mathbf{C} = 4\pi^2 \sum_{k=0}^{K} \sum_{i=1}^{N_1} (ia + k)^2 \]
\[ + 4\pi^2 \sum_{k=0}^{K} \sum_{i=1}^{N_2} [i(N_1 + 1)a + k]^2 \]
\[ \approx 4\pi^2(K + 1)N_1(N_1 - 1)[(2N_1 - 1)a^2 + a(2a + K)] \]
\[ \approx 4\pi^2(K + 1)au^2(1 - u)^3N^5 \]  
(28)

where $\Gamma = \text{diag}(\Gamma_0, \Gamma_1, \ldots, \Gamma_K) \in C^{(K+1)N \times (K+1)N}$ and $\Gamma_k = 2\pi[\text{diag}(a, k, \ldots, N_1a + k, \ldots, N_2(N_1 + 1)a + k)]$. According to the matrix inverse Lemma, $\mathbf{R}^{-1}$ can be expressed as

\[ \mathbf{R}^{-1} = \sigma^{-1}\mathbf{I} - \frac{\mathbf{C}\mathbf{C}^H}{\sigma^2 \sigma_s^{-1} + (K + 1)N^2} \]  
(29)

After obtaining the aforementioned approximated expressions, the items (30), (31) and (32) for calculating CRB$(\hat{\omega})$ can be achieved as the following form when $\sigma/\sigma_s = 1/SNR \ll N$

\[ \mathbf{C}^H \mathbf{C} = \sigma^{-1}[\mathbf{C}^H \mathbf{C} - \frac{\mathbf{C}^H \mathbf{C} \mathbf{C}^H \mathbf{C}}{\sigma^2 \sigma_s^{-1} + (K + 1)N}] \approx \sigma^{-1} \]  
(30)

\[ \dot{\mathbf{C}}^H \dot{\mathbf{C}} \approx -j\pi au(1 - u)^2N^2\sigma_s^{-1} \]  
(31)

\[ \ddot{\mathbf{C}}^H \dot{\mathbf{C}} \approx -\pi^2(K + 1)(1 + 3u)a^2u^2(1 - u)^3N^5 \]  
(32)

Keeping these relations in mind, the expression for $J_{\omega\omega}$ can be approximated as

\[ J_{\omega\omega} = 2\pi^2[(\dot{\mathbf{C}}^H \dot{\mathbf{C}} - \sigma_s^{-1}) + (\dot{\mathbf{C}}^H \dot{\mathbf{C}})]^2 \]
\[ = 2\pi^2[\sigma^{-1}\pi^2(K + 1)(1 + 3u)a^2u^2(1 - u)^3N^5] \]
\[ \approx 2\pi^2(K + 1)(1 + 3u)a^2u^2(1 - u)^3N^5SNR \]  
(33)

Evidently, $\ddot{\mathbf{C}}^H \dot{\mathbf{C}}$ and $\dddot{\mathbf{C}}^H \ddot{\mathbf{C}}$ are both purely imaginary while $\dot{\mathbf{C}}^H \dot{\mathbf{C}}$ is purely real, which infers that $J_{\omega\omega} = 0$ and $J_{\omega\sigma} = 0$. Therefore,

\[ \text{CRB}(\hat{\omega}) = \frac{1}{J_{\omega\omega}^{-1}} \approx \frac{3}{2\pi^2L(K + 1)(1 + 3u)a^2u^2(1 - u)^3N^5SNR} \]  
(34)

and the proof of Proposition 1 is completed.

APPENDIX B

PROOF OF PROPOSITION 2

When the off-diagonal elements in $\mathbf{C}^H \mathbf{C}$, $\dot{\mathbf{C}}^H \mathbf{C}$ and $\ddot{\mathbf{C}}^H \ddot{\mathbf{C}}$ can be neglected, they can be approximated by the following equations

\[ \mathbf{C}^H \mathbf{C} \approx (K + 1)N\mathbf{I} \]
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