Cryptanalyzing a Medical Privacy Protection Scheme based on DNA Coding and Chaos

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Abstract—Recently, a medical privacy protection scheme (MPPS) based on DNA encoding and chaos was proposed in [IEEE Trans. Nanobioscience, vol. 16, pp. 850–858, 2017]. This paper reports some properties of MPPS and proposes a chosen-plaintext attack on it. In addition, the other claimed superiorities are questioned from the viewpoint of modern cryptography. Both theoretical analysis and experimental results are provided to support the feasibility of the attack and other security defects. The proposed cryptanalysis will promote proper application of DND encoding in protecting multimedia data including DICOM image.

Index Terms—cryptanalysis, chaotic cryptography, DNA encoding, image security, privacy protection.

I. INTRODUCTION

DNA (Deoxyribonucleic acid) encoding is widely used in medical image encryption and privacy protection in the past two decades [1], [2]. The first one is proposed in 2004 [3]. Unfortunately, some encryption schemes based on DNA encoding were reported to insecure of different extents [4]–[13].

The development of transmission and sensing technologies promote remote diagnosis (telediagnosis) and remote surgery (telesurgery). The concerns on security and privacy on the medical images transmitted on public channels are becoming more and more serious. Due to the bulky size of medical image and special storage format, the traditional text encryption standards are not efficient [14]. The directly optimized way is to reduce the size of encryption object by automatically detecting the region of interest (ROI) and leaving the region of non-interest (RONI) as plain-form. As the equivalent counterpart of cryptography, the object of cryptanalysis is to obtain the information on secret-key and/or plaintext under a given attacking scenario [15]–[18].

The randomness of the pseudo-random number sequences generated by iterating a chaotic map in digital computer may be very weaker than that of the counterpart obtained in infinite domain [19]. As reviewed in [20], various methods were proposed to counteract the dynamics degradation of digital chaotic maps: selecting state and control parameters; increasing the arithmetic precision; perturbing states; perturbing the control parameters; switching among multiple chaotic maps; cascading multiple chaotic maps [21], [22]. The review on chaotic cryptology can be found in [23]–[25].

In [26], a medical privacy protection scheme (MPPS) based on DNA and chaos was proposed. The images stored as DICOM (Digital Imaging and Communications in Medicine) standard are encrypted with DNA encoding and PRNSs generated by iterating two Coupled Chaotic Systems (CCS).

This paper focuses on security analysis of MPPS. Some properties on its essential structure are found and proved, which is then used to support an efficient chosen-plaintext attack. The metrics on validating security performance of MPPS are convincingly questioned.

The rest of the paper is structured as follows. Section II concisely present the medical privacy protection scheme under study. Detailed cryptanalyses are given in Sec. III with experimental results. The last section concludes the paper.

II. THE CONCISE DESCRIPTION OF MPPS

As specified in [26, Sec. III], MPPS can protect DICOM image data with two modes: partial and full encryption. If the former is adopted, only the significant areas for diagnosis are encrypted to considerably reduce the size of the encryption object. Except the difference on selected portions of the plain-image, MPPS works exactly the same under the two modes. Without loss of generality, the encryption object of MPPS is assumed to be a RGB color image I = \{I_r, I_g, I_b\} of size M × N for either mode, which can be represented with three two-dimensional 8-bit integer matrices: I_r = \{I_r(i, j)\}_{i=1,j=1}^{M,N}, I_g = \{I_g(i, j)\}_{i=1,j=1}^{M,N} and I_b = \{I_b(i, j)\}_{i=1,j=1}^{M,N}.

Accordingly, I' = \{I_r', I_g', I_b'\} is the cipher-image, where I_r' = \{I'_r(i, j)\}_{i=1,j=1}^{M,N}, I_g' = \{I'_g(i, j)\}_{i=1,j=1}^{M,N} and I_b' = \{I'_b(i, j)\}_{i=1,j=1}^{M,N}. Then, the basic parts of MPPS can be described as follow:

- The secret key is composed of six sets of initial value and control parameter \((\{y_m(0), \mu_m\}_{m=1}^{6}) = \{K_m\}_{m=1}^{6}\). The sub-keys \(K_1\) and \(K_2\) are the initial values and control parameters of Coupled Logistic-Sine (CLS) map

\[
g = f(x) + \frac{1}{4} \cdot (4 - \mu) \cdot \sin(\pi x) \mod 1,
\]

where

\[
f(x) = \mu \cdot x \cdot (1 - x)
\]

1To make the description more concise and complete, some details and symbols in [26] are modified under the precondition its security performance is kept unchanged.

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is the Logistic map. The other sub-keys, $K_2$, $K_4$, $K_5$ and $K_6$, are sets of the initial values and control parameters of Coupled Logistic-Tent (CLT) map

\[
y = \begin{cases} 
  f(x) + \frac{1}{2}(4 - \mu) \cdot x \mod 1 & \text{if } x < 0.5; \\
  f(x) + \frac{1}{2}(4 - \mu) \cdot (1 - x) \mod 1 & \text{if } x \geq 0.5,
\end{cases}
\]

where $x \in [0, 1]$, and $\mu \in [0, 4]$.

**Initialization:**

1) **Generating index sequence:** iterate CLS map \(t_1\) times from the initial condition $Y_1(0)$ with control parameter $\mu_1$ to avoid the transient effect; iterate it $3 \cdot M \cdot N$ more times to obtain a chaotic state sequence $X_1 = \{X_1(i)\}_{i=1}^{3MN}$; sort $X_1$ in an ascending order to generate an index sequence $S_1 = \{S_1(i)\}_{i=1}^{3MN}$ satisfying that $X_1(S_1(i))$ is the \(i\)-th largest element of $X_1$.

2) **Determining DNA coding rules:** iterate the CLT map \(t_2\) times with control parameter $\mu_2$ from the initial condition $Y_2(0)$ $t_2 = 100$ times to avoid the transient effect; iterate it six more times to obtain a chaotic sequence $X_2 = \{X_2(i)\}_{i=1}^6$ and quantize it to get six random numbers $\{S_2(i)\}_{i=1}^6$ via

\[
S_2(i) = \lfloor X_2(i) \times 10^{14} \rfloor \mod 8,
\]

where $\lfloor \cdot \rfloor$ returns the nearest integers less than or equal to $x$.

3) **Constructing a pseudo-random number generator:** starting from the initial condition $Y_3(0)$, iterate CLT map \(t_3\) times with control parameter $\mu_3$; iterate the map $4 \cdot M \cdot N$ more times to obtain a chaotic state sequence $X_3 = \{X_3(i)\}_{i=1}^{4MN}$ and quantize to a binary random sequence $S_3 = \{S_3(i)\}_{i=1}^{4MN}$ by

\[
S_3(i) = \begin{cases} 
  0 & \text{if } 0 \leq X_3(i) \leq 0.5; \\
  1 & \text{if } 0.5 < X_3(i) < 1.
\end{cases}
\]

4) **Generating three keystreams $S_4$, $S_5$, $S_6$:** Similar to 1), set three sub-keys $K_4$, $K_5$ and $K_6$ as the control parameter and initial state of CLS map \(t_1\), generate three chaotic sequences $X_4 = \{X_4(i)\}_{i=1}^{4MN}$, $X_5 = \{X_5(i)\}_{i=1}^{4MN}$ and $X_6 = \{X_6(i)\}_{i=1}^{4MN}$, respectively. As above, the first \(t_1\) states are discarded for generating $S_m$, where \(m = 4, 5, 6\). Then, every element of such sequences is quantified by

\[
S_m(i) = \lfloor X_m(i) \cdot 10^{14} \rfloor \mod 256.
\]

**Encryption procedure:**

a) **Permutation:** the three matrices $I_r$, $I_g$ and $I_b$ are “placed” vertically to obtain a large image $P = \{P(i, j)\}_{i=1,j=1}^{3MN}$, where the elements of $\{P(i, j)\}_{i=1,j=1}^{3MN}$, $\{P(i, j)\}_{i=1,j=1}^{2MN}$ and $\{P(i, j)\}_{i=1,j=1}^{2MN}$ are set by that of $I_r$, $I_g$, and $I_b$ pixel by pixel, respectively. Then, produce a scrambled image $P^* = \{P^*(i, j)\}_{i=1,j=1}^{3MN}$ from $P$ by the index sequence $S_1$: $P^*(i, j) = P(u, v)$, where

\[
\begin{align*}
  u & = \left\lfloor S_1((i-1) \cdot N + j) / N \right\rfloor + 1; \\
  v & = S_1((i-1) \cdot N + j) \mod N + 1.
\end{align*}
\]

b) **DNA Encoding:** First, assign $E_i = X_2(i)$ for $i = 1 \sim 3$. Using function

\[
f(x) = (x_0, x_1, x_2, x_3)
\]

satisfying $\sum_{i=0}^{3} x_i \cdot 2^{2i} = x$ to transform every pixel of $\{P^*(i, j)\}_{i=1,j=1}^{3MN}$ and $\{P(i, j)\}_{i=2M+1,j=1}^{3MN}$ into four neighboring elements of 2-bit integer matrices of size $M \times 4N$, $I^*_r$, $I^*_g$, and $I^*_b$, respectively. Finally, convert $I^*_r$, $I^*_g$, and $I^*_b$ into DNA symbol matrices with the rules in the $E_1$-th, $E_2$-th, and $E_3$-th row of Table I respectively. Let $R$, $G$, and $B$ denote the corresponding results.

c) **Diffusion I with DNA complement:** Obtain matrix $R^* = \{R^*(i, j)\}_{i=1,j=1}^{M,4N}$ by

\[
R^*(i, j) = \begin{cases} 
  R(i, j) & \text{if } S_3(i) = 0; \\
  g(R(i, j)) & \text{if } S_3(i) = 1,
\end{cases}
\]

where

\[
g(x) = \begin{cases} 
  T & \text{if } x = \text{“A”}; \\
  C & \text{if } x = \text{“T”}; \\
  G & \text{if } x = \text{“C”}; \\
  A & \text{if } x = \text{“G”}.
\end{cases}
\]

d) **Diffusion II:** According to DNA addition operation rules given in the Table III calculate

\[
\begin{align*}
  R^{**}(i, j) & = R^*(i, j) \oplus B^*(i, j) \\
  G^{**}(i, j) & = G^*(i, j) \oplus R^*(i, j) \\
  B^{**}(i, j) & = B^*(i, j) \oplus G^*(i, j)
\end{align*}
\]

for $i = 1 \sim M$, $j = 1 \sim 4N$.

e) **DNA Decoding:** First, assign $D_i = X_2(i+3)$ for $i = 1 \sim 3$. Then, convert DNA symbol matrices $R^{**}$, $G^{**}$, and $B^{**}$ into 2-bit integer matrices with the rule in the $D_1$-th, $D_2$-th, and $D_3$-th rows of $B^{**}$, respectively. Accordingly, $B^{**}$, $B^{**}$, and $B^{**}$ are generated. Finally, transform $R^{**}$, $G^{**}$, and $B^{**}$ into $I^*_r$, $I^*_g$, and $I^*_b$, respectively. In such transforms, every four 2-bit integer elements are merged into one 8-bit integer with the inverse function of Eq. (7).

f) **Diffusion III:** Considering every 2-D matrix as a 1-D sequence by scanning it in the raster order, obtain $I'_r$, $I'_g$, $I'_b$ by calculating

\[
\begin{align*}
  I'_r(i) & = I_r(i-1) \oplus I^*_r(i) \oplus S_4(i) \\
  I'_g(i) & = I_g(i-1) \oplus I^*_g(i) \oplus I^*_r(i) \oplus S_5(i) \\
  I'_b(i) & = I_b(i-1) \oplus I^*_b(i) \oplus I^*_r(i) \oplus S_6(i)
\end{align*}
\]

| Rule number | (00)\(_2\) | (01)\(_2\) | (10)\(_2\) | (11)\(_2\) |
|-------------|-------------|-------------|-------------|-------------|
| 1           | A           | C           | G           | T           |
| 2           | A           | G           | C           | T           |
| 3           | T           | G           | C           | A           |
| 4           | T           | C           | G           | A           |
| 5           | C           | A           | T           | G           |
| 6           | C           | T           | A           | G           |
| 7           | G           | A           | T           | C           |
| 8           | G           | T           | A           | C           |

\[\text{Table I}

\text{Eight different DNA coding rules}
for \( i = 1 \sim MN \), \( \oplus \) denotes the bitwise exclusive OR operation, \( I'_r(0) = 0 \), \( I'_g(0) = 0 \) and \( I'_b(0) = 0 \).

• Decryption procedure: The decryption procedure is the inverse of the above encryption procedure. The DNA subtraction rules are shown in Table III.

### TABLE III
DNA SUBTRACTION RULES

| ⊕ | A | G | C | T |
|---|---|---|---|---|
| A | A | T | C | G |
| G | G | A | C | T |
| C | C | G | A | T |
| T | T | C | T | A |

III. CRYPTOANALYSIS OF MPPS

In this section, some properties related to MPPS and DNA coding are first analyzed. Then a detailed cryptanalysis under chosen-plaintext attack is proposed. Next attack process and simulation results are given. Evaluation on other attack analysis is finally presented.

A. Some properties of MPPS

Before the cryptanalysis, some properties of MPPS and DNA encoding/decoding are analyzed and summarized.

**Property 1.** Given two arbitrary cipher-images, \( C_u = [C_u(i)]_{i=1}^{3MN} \) and \( C_v = [C_v(i)]_{i=1}^{3MN} \), their difference \( \Delta C \) is independent of the keys or equivalent keys \( K_4 (S_4), K_5 (S_5) \) and \( K_6 (S_6) \), where \( \Delta C = C_u \oplus C_v = [C_u(i) \oplus C_v(i)]_{i=1}^{3MN} \).

**Proof:** Observing Eq. (11), one has

\[
\begin{align*}
\Delta C_r(i) \oplus \Delta C_r(i-1) &= \Delta C_r(i); \\
\Delta C_g(i) \oplus \Delta C_g(i-1) &= \Delta C_g(i) \oplus \Delta C_g(i); \\
\Delta C_b(i) \oplus \Delta C_b(i-1) &= \Delta C_b(i) \oplus \Delta C_b(i),
\end{align*}
\]

where \( \Delta \varphi = \varphi_u \oplus \varphi_v \) and \( \varphi \in \{C_r(i), C_g(i), C_b(i), \bar{C}_r(i), \bar{C}_g(i), \bar{C}_b(i)\} \). Hence the property is proved.

For convenience, here we define two composite functions \( F_{i,j}(x) = f_j^{-1}[f_i(x)] \) and \( G_{i,j}(x) = f_j^{-1}[g_i(x)] \), where \( f_i(x) \), \( f_j^{-1}(x) \) and \( g(x) \) are the DNA coding, decoding and transformation mentioned in the previous section, where \( x \in Z_4 \) and \( i, j \in Z_8 \).

**Property 2.** If \( x_1, x_2 \in x \) and \( x_1 \oplus x_2 = (11)_2 = 3 \),

\[
F_{i,j}(x_1) \oplus F_{i,j}(x_2) \neq G_{i,j}(x_1) \oplus G_{i,j}(x_2).
\]

**Proof:** Considering the complementary of DNA (i.e., A and T, C and G), for \( i \in Z_8 \), there exists

\[
(f_i(x_1), f_i(x_2)) \in \{(A, T), (T, A), (C, G), (G, C)\}.
\]

According to Eq. (9), one has

\[
(g[f_i(x_1)], g[f_i(x_2)]) \in \{(T, C), (C, T), (G, A), (C, G)\}.
\]

For \( i, j \in Z_8 \), if \( x_1 \oplus x_2 = (11)_2 = 3 \), then

\[
\begin{align*}
F_{i,j}(x_1) \oplus F_{i,j}(x_2) &= (11)_2, \\
G_{i,j}(x_1) \oplus G_{i,j}(x_2) &= (10)_2 \text{ or } (01)_2.
\end{align*}
\]

Obviously, \( F_{i,j}(x_1) \oplus F_{i,j}(x_2) \neq G_{i,j}(x_1) \oplus G_{i,j}(x_2) \).

**Property 3.** The composite functions \( F_{i,j}(x) \) and \( G_{i,j}(x) \) are bidirectional maps defined in domain \( Z_4 \), and they only have 8 and 16 different maps, respectively.

**Proof:** First, since \( f_i(x) \) and \( f_j^{-1}(x) \) for \( i, j \in Z_8 \) and \( g(x) \) are fixed bidirectional maps in domain \( Z_4 \), \( F_{i,j}(x) = f_j^{-1}[f_i(x)] \) and \( G_{i,j}(x) = f_j^{-1}[g_i(x)] \) are also fixed bidirectional maps. Considering the constraints of Eq. (14), one can determine the number of satisfied maps of \( F_{i,j}(x) \) and \( G_{i,j}(x) \) is \( C_2^1 C_2^1 C_2^1 = 8 \) and \( C_4^1 C_2^1 C_2^1 = 16 \), respectively. ■

**Property 4.** If \( i_1, i_2 \in i, j_1, j_2 \in j \), there are two different maps \( F_{i_1,j_1}(x) \), \( F_{i_2,j_2}(x) \) satisfying

\[
F_{i_1,j_1}(x) \oplus F_{i_2,j_2}(x) = \lambda
\]

for \( x = 0, 1, 2, 3 \), where \( \lambda = 1, 2 \) or 3.

**Proof:** The above proposition is equivalent to another proposition: if \( F_{i,j}(x) \) is one of maps of \( F_{i,j}(x) \), then \( F_{i_2,j_2}(x) = F_{i_1,j_1}(x) \oplus \lambda \) is another map. Since \( F_{i_2,j_2}(x_1) \oplus F_{i_2,j_2}(x_2) = F_{i_1,j_1}(x_1) \oplus F_{i_1,j_1}(x_2), x_1, x_2 \in x \), according to Property 2, \( F_{i_2,j_2}(x_1) \) is another map of \( F_{i,j}(x) \).

**Property 5.** If \( i_1, i_2 \in i, j_1, j_2 \in j \), there are two different maps \( G_{i_1,j_1}(x) \neq G_{i_2,j_2}(x) \) satisfying

\[
G_{i_1,j_1}(x) \oplus G_{i_2,j_2}(x) = \lambda
\]

for \( x = 0, 1, 2, 3 \), where \( \lambda = 1, 2 \) or 3.

**Proof:** The proof is similar to that of Property 4 ■

### TABLE IV
THE ORIGINAL KEYS AND THE CORRESPONDING EQUIVALENT KEYS OF MPPS.

| Original keys | Corresponding equivalent keys | Related information |
|---------------|-------------------------------|---------------------|
| \( K_1 \)     | \( S_1 \)                     | Permutation index sequence |
| \( K_2 \)     | \( E_1, E_2, E_3 \) and \( D_1, D_2, D_3 \) | DNA coding and decoding rules |
| \( K_3 \)     | \( S_3 \)                     | Binary sequence |
| \( K_4 \)     | \( S_4 \)                     | Keystream of \( r \) plane |
| \( K_5 \)     | \( S_5 \)                     | Keystream of \( g \) plane |
| \( K_6 \)     | \( S_6 \)                     | Keystream of \( b \) plane |
B. Breaking MPPS under chosen-plaintext attack

The corresponding equivalent keys and related information of the six keys of MPPS are shown in Table IV. The goal of cryptanalysis of the paper is to reveal these equivalent keys under chosen-plaintext attack.

First, we choose a group of color plain-images whose all pixel values are equal, represented as a set of images \( \mathcal{P} = \{ P_0, P_1, \ldots, P_{255} \} \) where \( P_0 = \{ 0, 0, 0, \ldots, 0 \} \), \( P_1 = \{ 1, 1, 1, \ldots, 1 \} \) and \( P_{255} = \{ 255, 255, 255, \ldots, 255 \} \). Suppose their corresponding cipher-images set is \( \mathcal{C} = \{ C_0, C_1, \ldots, C_{255} \} \). Obviously, these images before and after the permutation are unchanged, that is, the corresponding images satisfy \( P_0 = P_0, P_1 = P_1, \ldots, P_{255} = P_{255} \). Hence, we only need to focus on all intermediate states from the permutation-images to the cipher-images. Recall the description of MPPS, the DNA coding and diffusion operations after the permutation are carried out in the \( r \), \( g \) and \( b \) planes of the images respectively. To reveal the keys of these planes, a divide-and-conquer strategy is adapted in the cryptanalysis as follows.

1) Cracking the \( r \) plane: In this plane, we will reveal the equivalent keys \( E_1, D_1, S_3 \) and \( S_1 \). First, choose two special images \( P_{o1}, P_{o2} \), which satisfy \( P_{o1}, P_{o2} \in \mathcal{P} \) and \( P_{o1} \oplus P_{o2} = P_{255} \). Obviously, there are \( (C_2)^4 = 256 \) plain-image pairs in set \( \mathcal{P} \) that meet. As mentioned earlier, their permutation-images are unchanged, i.e., \( P_{o1} = P_{o1} \) and \( P_{o2} = P_{o2} \). Subsequently, in the \( r \) plane of \( P_{o1} \) and \( P_{o2} \), each of two-bit elements (denoted as \( x_1 = a1 \mod 4 \) and \( x_2 = a2 \mod 4 \)) is DNA encoded \( f(x_k) \), transformed (Eqs. (89)) and decoded \( f_j^{-1}(x_k) \), then the output \( I_{R1}(k) \) can be represented in two forms

\[
I_{R1}(k) = \begin{cases} F_{i,j}(x_k), & \text{if } S_3(k) = 0 \\ G_{i,j}(x_k), & \text{if } S_3(k) = 1 
\end{cases}
\]

(18)

where \( x_1, x_2 \in x_k, k \sim 4 MN \) and \( i, j \in Z_8 \). From Property [2] and Eq. (14), the differential \( \Delta I_{R1}(k) \) satisfies

\[
\begin{align*}
F_{i,j}(x_1) &\oplus F_{i,j}(x_2) = (11)_2, & \text{if } S_3(k) = 0 \\
G_{i,j}(x_1) &\oplus G_{i,j}(x_2) = (01)_2 \text{ or } (10)_2, & \text{if } S_3(k) = 1
\end{align*}
\]

(19)

According to the above equation, if the output \( \Delta I_{R1}(k) \) is known, then \( S_3(k) \) can be uniquely determined. Fortunately, by Property [1] and Eq. (12), \( \Delta I_{R1}(k) \) can be obtained by dividing \( \Delta C_r(i) \) into two four-bit elements, and the differential pixel \( \Delta C_r(i) \) is available from \( \Delta C_r(i) \). So the binary sequence \( S_3 \) is revealed.

The next goal is to obtain \( E_1, D_1 \) and \( S_4 \). Since the key space of \( E_1 \) and \( D_1 \) is very small, only \( 8 \times 8 = 64 \), we design an effective exhaustive search method for the keys, as summarized in Algorithm [1]. The main idea is that we reveal same \( S_4 \) for different plain-images when the exhaustive key \( E_1 \) and \( D_1 \) are correct. Also, considering \( x \in Z_4 \) for \( F_{E_1,D_1}(x) \) and \( G_{E_1,D_1}(x) \), so we choose only four special image pairs \( \{ P_0, C_0 \}, \{ P_{255}, C_{255} \}, \{ P_{255}, C_{170} \}, \) and \( \{ P_{255}, C_{255} \} \), which correspond to different plain-pixel values \( \{ 00000000 \}, \{ 01010101 \}, \{ 10101010 \} \) and \( \{ 11111111 \} \), respectively. Before Algorithm [1] is executed, the plain-image \( C_u \) will be converted to an intermediate image \( CC_{u,u} = \{ 0, 1, 2, 3 \} \). Formula (11) first can be converted to

\[
\begin{align*}
C_r(i) &\oplus C_r(i-1) = \overline{C_r}(i) \oplus S_4(i) \\
C_g(i) &\oplus C_g(i-1) = \overline{C_g}(i) \oplus \overline{C_g}(i) \oplus S_2(i) \\
C_b(i) &\oplus C_b(i-1) = \overline{C_b}(i) \oplus \overline{C_b}(i) \oplus S_6(i)
\end{align*}
\]

(20)

Furthermore, one has

\[
\begin{align*}
C_{R_r}(i) &\oplus C_{R_r}(i-1) = \overline{C_{R_r}}(i) \oplus S_4(i) \\
C_{G_s}(i) &\oplus C_{G_s}(i-1) = C_{R_r}(i) \oplus C_{R_r}(i-1) \oplus C_{B_r}(i) \oplus C_{B_r}(i-1) \\
C_{B_r}(i) &\oplus C_{B_r}(i-1) = \overline{C_{B_r}}(i) \oplus S_4(i) \oplus S_5(i) \oplus S_6(i)
\end{align*}
\]

(21)

The above equation shows that one can obtain three sub-images from \( C \), i.e., \( C_r(i) \oplus S_4, C_g(i) \oplus S_2 \oplus S_6, C_b(i) \oplus S_4 \oplus S_6 \) without the keys. The joint of the sub-images is defined as the intermediate cipher-image \( CC_{u,u} \).

Interestingly, the values \( E_1, D_1 \) and \( S_4 \) searched by the Algorithm [1] are not unique. In other words, there are four equivalent classes in the table, and each class has 16 different equivalent keys, as listed in Table VII. For example, suppose MPPS encrypts the \( r \) plane with \( E_1 = 0 \) and \( D_1 = 0 \), then the remaining 15 elements of the equivalent key class II be used to decrypt. The reasons for the results are as follows:

- \( F_{i,j}(x) \) and \( G_{i,j}(x) \) are two kind of transformations of the \( r \) plane. From Property [3] there are 8 and 16 satisfied maps of \( F_{i,j}(x) \) and \( G_{i,j}(x) \), respectively, rather than the expected \( 8 \times 8 = 64 \). Hence, there are several maps that are equivalent for different \( i, j \in Z_8 \).

- \( S_4 \) also has multiple equivalent keys. \( S_4^{(1)} \) and \( S_4^{(2)} \) are different equivalent keys only if \( F_{i,j}(x) \oplus S_4^{(1)}(k) = F_{i,j}(x) \oplus S_4^{(2)}(k) \) and \( G_{i,j}(x) \oplus S_4^{(1)}(k) = G_{i,j}(x) \oplus S_4^{(2)}(k) \) for \( x = 0, 1, 2, 3 \), are holds, where \( x \in Z_4, i, j, i', j' \in Z_8 \) and \( k = 1 \sim 4 MN \). The above proposition is equivalent to Properties [1] and [2].

Note that these equivalent key sets in Table VII are not finalized, because DNA encoding rule \( f_{E_1} \) is constrained by Eq. (10), and we will further filter to obtain the correct keys in the next subsection.

2) Cracking the green and blue planes: This subsection we will crack the \( g \) and \( b \) planes and further determine a correct set of equivalent keys for \( r \) plane.

First, in the \( g \) plane, we also apply the exhaustive search method with the same four plain-images and intermediate cipher-image, which is similar to Algorithm [1]. But the exhaustive algorithm needs to consider the DNA coding rules \( f_{E_1} \) since the \( g \) plane is related to \( r \) plane. Overall, it needs to search \( 8 \times 8 \times 8 = 512 \) times. Then we will reveal an equivalent set of \( \{ (E_1, E_2, D_2, S_3 \boxplus S_4) \} \) and further filter a new equivalent key set of \( r \) plane.

Similarly, we will obtain another equivalent key set of \( \{ (E_2, E_3, D_3, S_0 \boxplus S_1) \} \) plane and the existing equivalent key sets of \( g \) is refined. Finally, we confirm the right sets of \( S_0 \) and \( S_3 \) [2].
TABLE V
FOUR DIFFERENT EQUIVALENT KEY CLASSES FOR \((E_1, D_1, S_4)\)

| Equivalent key classes I | Equivalent key classes II | Equivalent key classes III | Equivalent key classes IV |
|---------------------------|---------------------------|---------------------------|---------------------------|
| \( (0, 0, S_4^{(1,1)}) \) | \( (0, 1, S_4^{(1,1)}) \) | \( (1, 1, S_4^{(1,1)}) \) | \( (1, 0, S_4^{(1,1)}) \) |
| \( (0, 2, S_4^{(1,2)}) \) | \( (0, 3, S_4^{(1,2)}) \) | \( (1, 3, S_4^{(1,2)}) \) | \( (1, 2, S_4^{(1,2)}) \) |
| \( (0, 4, S_4^{(1,3)}) \) | \( (0, 5, S_4^{(1,3)}) \) | \( (1, 5, S_4^{(1,3)}) \) | \( (1, 4, S_4^{(1,3)}) \) |
| \( (0, 7, S_4^{(1,4)}) \) | \( (0, 6, S_4^{(1,4)}) \) | \( (1, 6, S_4^{(1,4)}) \) | \( (1, 7, S_4^{(1,4)}) \) |
| \( (2, 0, S_4^{(2,1)}) \) | \( (2, 1, S_4^{(2,1)}) \) | \( (3, 1, S_4^{(2,1)}) \) | \( (3, 0, S_4^{(2,1)}) \) |
| \( (2, 2, S_4^{(2,2)}) \) | \( (2, 3, S_4^{(2,2)}) \) | \( (3, 3, S_4^{(2,2)}) \) | \( (3, 2, S_4^{(2,2)}) \) |
| \( (2, 4, S_4^{(2,3)}) \) | \( (2, 5, S_4^{(2,3)}) \) | \( (3, 5, S_4^{(2,3)}) \) | \( (3, 4, S_4^{(2,3)}) \) |
| \( (2, 7, S_4^{(2,4)}) \) | \( (2, 6, S_4^{(2,4)}) \) | \( (3, 6, S_4^{(2,4)}) \) | \( (3, 7, S_4^{(2,4)}) \) |

\( S_4^{(i,j)} \) represents the \( j \)th different keystream \( S_4 \) in the \( i \)th equivalent classes, where \( i \in \{1, 2, 3, 4\} \), \( j \in \{1, 2, \ldots, 8\} \). Since the value of \( S_4^{(i,j)} \) depends on the original key \((Y_4(0), \mu_4)\), only more general relationships between them are given here.

Fig. 1. Attack framework for obtaining all equivalent keys.

3) Revealing permutation key: Except for permutation index \( S_1 \), now we obtain all the equivalent keys or equivalent key sets in Table [V]. So, we can recover the permutation-image \( P \) for any cipher-image \( C \). Then it becomes a classic cryptanalysis of permutation-only cipher problem, which has been studied in depth in [27], [28]. The general way is to use the multi-fork tree optimization method [27]. To attack MPPS, only \( \lceil \log_{256}(3MN) \rceil \) plain-images are extra chosen, here \( \lceil x \rceil \) returns the nearest integers more than or equal to \( x \).

C. Attack process and simulation results

The above theoretical analysis demonstrates that MPPS is successfully broken with only \( \lceil \log_{256}(3MN) \rceil + 4 \) chosen plain-images. Here, a complete attack example to verify the proposed cryptanalysis method will be given.

For better presentation, assume that MPPS processes a RGB color image of size \( 2 \times 2 \times 3 \), and the pixel value of each plane range from 0 to 255. In the following simulation, set the initial iteration of CLS or CTS map \( t_0 = 500 \) and six original keys of MPPS as listed in the second column of the Table [VI]. Accordingly, the equivalent key corresponding to each original key is calculated by an Initialize procedure of MPPS.

As shown in Fig. 1, we select two group of images to obtain all the equivalent keys of MPPS. The first group includes four special plain-images and cipher-images as:

\[
\begin{align*}
&P_0 = \{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0\}, \\
&C_0 = \{198, 60, 216, 204; 107, 69, 102, 24; 49, 72, 224, 205\}; \\
&P_{255} = \{255, 255, 255, 255, 255, 255, 255, 255, 255, 255, 255, 255, 255, 255\}; \\
&C_{255} = \{51, 158, 39, 228; 148, 69, 153, 24; 110, 234, 181, 229\}; \\
&P_{55} = \{85, 85, 85, 85, 85, 85, 85, 85, 85, 85, 85, 85, 85, 85\}; \\
&C_{55} = \{108, 60, 114, 204; 59, 20, 51, 12; 49, 72, 224, 205\}; \\
&P_{170} = \{170, 170, 170, 170, 170, 170, 170, 170, 170, 170, 170, 170\}; \\
&C_{170} = \{153, 158, 141, 228; 145, 20, 153, 12; 110, 234, 181, 229\}.
\end{align*}
\]

From Eq. (20) [21], the diffusion between pixels can be eliminated and an intermediate image \( CC_u, u \in \{0, 255, 85, 170\} \) can be created:

\[
\begin{align*}
&CC_0 = \{198, 250, 228, 20; 156, 173, 111, 71; 247, 131, 76, 57\}; \\
&CC_{255} = \{51, 173, 185, 195; 201, 248, 58, 18; 93, 41, 230, 147\}; \\
&CC_{55} = \{108, 80, 78, 190; 102, 6, 193, 172; 93, 41, 230, 147\}; \\
&CC_{170} = \{153, 7, 19, 105; 102, 6, 193, 172; 247, 131, 76, 57\}.
\end{align*}
\]

The differential pixel sequence of \( r \) plane between \( CC_0 \) and \( CC_{255} \) is \{111101012, 010011112, 001111102, 110101112\}. By the inverse of Eq. (19), one can determine the value of the binary sequence

\[
S_3 = \{0, 0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 1, 0\}.
\]

(22)
Algorithm 1: Exhaustive search procedure for the keys

Input: Special plain-images $P_1, P_{S_8}, P_{170}$ and $P_{255}$ and intermediate cipher-images $CC_0, CC_{S_8}, CC_{170}$ and $CC_{255}$, DNA encoding and decoding rules $f_i, f_j^{-1}, i, j \in S_8$, the revealed key $S_3$

Output: Keys $E_1$, $D_1$ and $S_4$

function $Encrypt_{Rls}(P, S_3, i, j)$

1. $I_r \leftarrow$ obtain r plane of $P$
2. $I_{R_1} \leftarrow$ DNA encode $I_r$ with $f_i$
3. $I_{R_1'} \leftarrow$ DNA transform $I_r$ via Eqs. 8, 9
4. $CC_r \leftarrow$ DNA decode $I_{R_1'}$ with $f_j^{-1}$
5. return $CC_r$
6. $CC_0 \leftarrow$ obtain r plane of $CC_0$
7. $CC_{S_8} \leftarrow$ obtain r plane of $CC_{S_8}$
8. $CC_{170} \leftarrow$ obtain r plane of $CC_{170}$
9. $CC_{255} \leftarrow$ obtain r plane of $CC_{255}$

for $i \leftarrow 0$ to 7 do

for $j \leftarrow 0$ to 7 do

10. $K_0 \leftarrow Encrypt_{Rls}(P, S_3, i, j) \oplus CC_0$
11. $K_{S_8} \leftarrow Encrypt_{Rls}(P, S_3, i, j) \oplus CC_{S_8}$
12. $K_{170} \leftarrow Encrypt_{Rls}(P, S_3, i, j) \oplus CC_{170}$
13. $K_{255} \leftarrow Encrypt_{Rls}(P, S_2, i, j) \oplus CC_{255}$
14. if $K_0 == K_{S_8} == K_{170} == K_{255}$ then
15. $E_1 \leftarrow i$
16. $D_1 \leftarrow j$
17. $S_4 \leftarrow K_0$
18. Print keys $E_1$, $D_1$ and $S_4$

end

end

TABLE VI

| Original keys | Calculated equivalent keys |
|---------------|-----------------------------|
| $K_1 = (0.11, 3.91)$ | $S_1 = \{9, 1, 10, 2, 11, 5, 7, 3, 12, 6, 4, 8\}$ |
| $K_2 = (0.12, 3.92)$ | $S_2 = \{5, 6, 0, 2, 8, 7\}$ |
| $K_3 = (0.13, 3.93)$ | $S_3 = \{0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 0\}$ |
| $K_4 = (0.14, 3.94)$ | $S_4 = \{99, 172, 189, 190\}$ |
| $K_5 = (0.15, 3.95)$ | $S_5 = \{155, 45, 47, 189\}$ |
| $K_6 = (0.16, 3.96)$ | $S_6 = \{193, 122, 164, 238\}$ |

Then, input four pairs of images, $(P_0, CC_0), (P_{S_8}, CC_{S_8}), (P_{170}, CC_{170}), (P_{255}, CC_{255})$, into Algorithm 1 with $S_4$. As a result, the matching equivalent keys $E_1, D_1$ (DNA encoding/decoding rule index) are successfully searched, and the corresponding keystreams $S_4$ are also output. Similarly, multiple matching equivalent keys $(E_2, D_2, S_3), (E_2, D_3, S_4), (E_2, D_3, S_5)$ of $g$ and $b$ plane, can be obtained by the key search method, respectively, where $S_4 = S_4 \oplus S_5 \oplus S_6 \oplus S_7$, and $S_6 = S_6 \oplus S_4$. The corresponding results are shown in Table VII. Note that these searched keys need to be further filtered because some of them are wrong. For example, $E_2 = 2, 7, 1$ or $5$ are the wrong keys because they don’t appear in both key search results (the first and second columns).

Now we choose another group of images to obtain the permutation index $S_1$, it includes $\lceil \log_{256}(3 \times 2 \times 2) \rceil = 1$ image. Such as a pair of plain-image and cipher-image:

$p_{new} = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11\}$,

$c_{new} = \{202, 48, 210, 196, 99, 72, 106, 17, 60, 76, 231, 205\}$.

Select any group of keys from Table VII such as $(E_1, D_1, S_1) = (0, 1, \{201, 6, 23, 40\}). (E_2, E_3, D_3, S_3) = (0, 1, 0, \{147, 81, 156, 123\})$ and $(E_2, E_3, D_3, S_3) = (1, 1, 1, \{247, 131, 70, 57\})$. By Eq. 22 and keys $S_1, S_5, S_6$, one can obtain an intermediate image

$\hat{C}_{new} = \{169, 95, 86, 148; 172, 93, 90, 150; 84, 80, 92, 80\}$.

Then using DNA subtraction (the inverse of Eq. 10) and DNA decoding (the inverse of Eqs. 8 and 9), one can get a scrambled image

$\hat{P}_{new} = \{8, 0, 9, 1, 10, 4, 6, 2, 11, 5, 3, 7\}$.

By comparing the positions of the same pixels between $P_{new}$ and $P_{new}$, a permutation index sequence

$S_1 = \{9, 1, 10, 2, 11, 5, 7, 3, 12, 6, 4, 8\}$

can be obtained.

In general, by choosing five pairs of plain-images and cipher-images, we can uniquely determine the equivalent keys $S_1$ and $S_3$, which are consistent with Table VI. In addition, we have eight different $(E_1, D_1, S_4)$, eight $(E_2, D_2, S_5)$ and sixteen $(E_3, D_3, S_6)$, so there are $8 \times 8 \times 16 = 1024$ groups of equivalent keys in total, and one of them is the same as in Table VI. Therefore, the proposed attack is effective and feasible.

D. Evaluation on other attack analysis

In [26], Sec. IV, the performance of MPPS was analyzed from eight aspects. In this subsection, we question their credibility one by one as follows.

1) Key space: The statement “it can be evident that the coupled chaotic map achieves amplified chaotic range in the entire region of [0, 4]” in [26] is questionable. The size of each sub-figure in [26], Fig. 1 is about 0.9 inch by 0.9 inch. Assume that the adopted dpi (dots per inch) is 200, the number of the printed dots is only about 32,400. Observing [26], Fig. 1, one can see that the distribution is not uniform.

Since symmetry in fixed-point arithmetic domain for initial value of CCS and CLT (namely, the initial values $Y(0)$ and $(1 - Y(0))$ will generate the same dynamic behavior), the effective key space of the MPPS is reduced by half. On the other hand, the initial values $Y(0) = 0, 0.5$ or 1.0 are the fixed points of CCS and CLT, which correspond to some weak keys of the MPPS. In addition, the key space of $K_2$ is estimated to be $10^{28}$ in [26], but its actual key space is only $8^6 = 2^{18}$ since six kinds of DNA encoding/decoding rules. Further, considering DNA encoding properties (Property 2, Property 3), it will generate a part of weak keys and equivalent keys. In general, the key space of MPPS is far overestimated.

2) Key Sensitivity: As analyzed in [28–30], there are many equivalent secret-key due to the dynamics degradation of chaotic system in a finite-precision computer.

3) Statistical Attack: Histogram analysis and entropy are unrelated with any security performance of an encryption scheme [29, 30].
4) Differential Attack: According to Property 1 the difference of cipher-image is unrelated to the keys $S_4$, $S_5$, and $S_6$, which will greatly reduce the effective key space. Therefore, MPPS is vulnerable to differential attack.

5) Chosen-plaintext attack: One specific relationship between plain-image and the corresponding cipher-image is almost unrelated with the capability of an encryption scheme against chosen-plaintext attack.

6) Cropping Attack: If the encryption process is not related with the plain-image, any encryption scheme is robust against cropping attack.

7) Performance Comparison: As emphasize in [29], any encryption scheme should target at a specific application scenario. Otherwise, the balancing point among usability, security and efficiency is unclear.

E. Other defects

1) Practical consideration: In [29], Sec. III, it is stated that “selection of a region of interest and region of non-interest is solely left to the under the recommended physician”. In addition, MPPS “requires the user’s fee that specifies the number of rounds of operation”. So it requires professional training for the ordinary patients.

2) Efficiency: As analyzed in [29], conversion functions in [3] waste much computation on the discard bits. To generate a sequence of length six $X_2$, $t_2 = 100$ states are sacrificed.

IV. Conclusion

This paper analyzed security and practical performances of a medical privacy protection scheme based on DNA encoding and chaos. Some of its properties were derived and used to obtain the equivalent secret key of the scheme with some chosen plain-images. Much works need to be done to bridge the gap between DNA computing and multimedia security.

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