An Enhanced DNA-based Steganography Technique with a Higher Hiding Capacity

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Abstract: DNA-based Steganography is one of the promising techniques to secure data exchange, where data is hidden into a real DNA sequence. For the sake of security, some steganography techniques encrypt data before hiding it which strengthen the technique's steganalysis. One of the widely used encryption techniques is the DNA-based playfair cipher. This technique intensively requires a long list of preprocessing steps in addition to extra bits which must be added to guarantee successful decryption. Nevertheless, the succeeding hiding step suffers from a limited capacity, which turns this current DNA-based Steganography technique into a complex, inefficient, and time consuming process. In this paper, we propose a new DNA-based Steganography algorithm to simplify the current technique as well as achieve higher hiding capacity. In the proposed algorithm, we enhance the commonly used playfair cipher by defining a novel short sequence of preprocessing steps and getting rid of the extra overhead bits. We also utilize a more efficient technique to enhance the hiding phase. The proposed approach is not only simple and fast but also provides a significantly higher hiding capacity with a high security. The conducted extensive experimental studies confirm the outstanding performance of the proposed algorithm.

1 INTRODUCTION

In the world where information and communication become indispensable, it becomes a must for research to find out solutions for data protection, integrity and accuracy. Recently, DNA-based Steganography becomes one of the promising techniques to secure data exchange, where data is hidden into a real DNA sequence. The complexity of the DNA structure and the randomness of its data are the main drivers of its outperformance in comparison with other traditional Steganography methods (Smith, 2003),(Alberts and Johnson, 2008),(Adleman, 1994). For the sake of security, some DNA-based Steganography approaches encrypt the data first through a ciphering technique and then hide it into a real DNA sequence. This paper focuses on such approach as it leads to a more confusion to the attacker and strengthen the technique's steganalysis [1].

The 5x5 playfair cipher is one of the well known and commonly used substitution ciphering techniques that uses a 5x5 grid containing the English alphabet in an ascending order from A to Z, where 24 letters occupies 24 cells and the remaining 2 letters -usually I & J- occupy the remaining cell. The sender and the receiver should agree on a specified keyword to rearrange the ordering of its cells to guarantee the uniqueness of the 5x5 grid each time the key is changed as shown in Fig1. Recently, this ciphering technique is used to encode DNA-based data due to its strong encrypting capability in comparison with the other encryption techniques (Atito, A. et al., 2012). However, such technique come up with long list of preprocessing steps that, in our point of view, do not decrease the cracking probability but complicate the implementation process and increase the processing time. Nevertheless, it also decreases the hiding capacity as we will prove in the rest of this paper. All these issues contradicts with the fact of the DNA's huge storage capacity.

In the current DNA-based 5x5 playair cipher implementation (Khalifa and Atito, 2012), the target message passes through a long sequence of transformations: from letters to binary, from binary to DNA

[1] Study of identifying the existence of data and detecting it.

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letters[2], from DNA letters to protein sequence presented by English letters [3], where ciphering technique takes place. Then the resulted ciphered English letters are again transformed to DNA letters with extra overhead bits, which is generally known as the ambiguity bits. Finally, the resulted DNA letters are concealed into a real DNA sequence through a hiding technique. The whole process is then reversed again at the receiver's node to extract the original message. As we can easily note, the whole process is a set of complicated long steps that only consume a lot of the computational effort without a real addvalue to the security strength.

In this paper, we propose an enhanced DNA-based Steganography algorithm that is much more efficient and faster than the current technique with a higher hiding capacity. In the proposed algorithm, we enhance the commonly used playfair cipher by defining a novel sequence of preprocessing steps and getting rid of the overhead. We also utilize a more efficient technique to enhance the hiding process (Khalifa and Atito, 2012). The proposed algorithm has redefined the whole process in a much smarter and straight forward mechanism resulting in a better performance and low execution time with a higher hiding capacity. Moreover, The security strength has been carefully checked and proved through the calculation of the cracking probability. The outstanding performance of our proposed algorithm is demonstrated through extensive experimental studies.

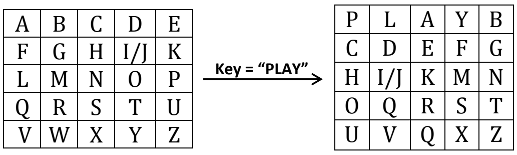
The rest of this paper is organized as follows. Section 2 overviews the background and related work on the current Steganography techniques. Section 3 presents the proposed technique in detail. Section 4 discusses its performance analysis. Finally, the paper is concluded in Section 5.

2 BACKGROUND

In this section, we provide a brief review on the DNA and the related work. In addition, we discussed in detail the main problems of the current DNA-based Steganography techniques and their problems.

2.1 DNA Overview

DNA is the magic code for life (Smith, 2003), it contains the genetic instructions used in the development and functioning of all living organisms. Inspired from nature, the fact that DNA molecule carries all the genetic information, evolves the idea of using DNA itself as a data carrier. The information in DNA is stored as a code made up of four chemical bases named as nucleotides: adenine (A), guanine (G), cytosine (C), and thymine (T). The sequence of these four bases encodes the genetic information (Alberts and Johnson, 2008). Each of the three nucleotides is called a codon, therefore in nature there are 64 codons since there are (4x4x4) letter combinations.



A	B	C	D	E
F	G	H	I/J	K
L	M	N	O	P
Q	R	S	T	U
V	W	X	Y	Z

P	L	A	Y	B
C	D	E	F	G
H	I/J	K	M	N
O	Q	R	S	T
U	V	Q	X	Z

Figure 1: 5x5 Playfair Cipher Grid before and after using the Key.

DNA has two main advantages that make it efficient for data hiding and transmission. First of all its high storage capacity; as proved by(Adleman, 1994). Secondly, the simplicity of converting data to DNA sequence makes it a good choice for data encryption within it. By exploiting the advantages of a DNA as an efficient data carrier in addition to using a well-suited encryption technique, researches ended up by many solutions for secure data communication and transmission. DNA steganography is one of these promising solutions(Peterson, 2001), (Catherine et al., 1999),(Leier et al., 2000),(Shimanovsky et al., 2002),(SAEB et al., 2007).

2.2 Related Work

In 1999, (Catherine et al., 1999) started DNA steganography, where data is encrypted in DNA and hid into microdots. In 2000 (Leier et al., 2000) proposed a hiding technique where data can be encoded into DNA sequence, however the original data can be easily recovered once the primer sequence is known.

In 2001 (Peterson, 2001) proposed another new scheme for secret data hiding but unfortunately it had some concerns as it can be cracked through a frequency-based cryptanalysis technique. In 2010 (Shiu et al., 2010) proposed three reversible data hiding schemes based on DNA sequence, the most significant one was the substitution method, yet its hiding capacity is not efficient enough.

In May 2012 (Khalifa and Atito, 2012) proposed a Steganography technique, where data is encrypted using DNA-based playfair cipher, then hid in a real DNA sequence using a modified substitution technique to increase its hiding capacity. Although it achieved higher hiding capacity than the original sub-

[2] The DNA letters are A, G, C, and T.

[3] The protein sequence is composed of amino acids, each is abbreviated by an English letter.

Table 1: Example of mapping codons to characters.

Character	Codons
F	GCT, GCC, GCA
B	TAA, TGA, TAG
C	TGT, TGC
N	AAT, AAC
P	CCT, CCC,CCG
O	TTA, TTG
R	CGT, CGG,CGA, CGC
M	ATG

stitution method, yet this hiding capacity was not efficient enough as a result of the ambiguity problem.

In October of the same year, (Taur et al., 2012) proposed another modified substitution technique achieving a high hiding capacity but without encrypting data which minimized its security.

2.3 Ambiguity Problem

One of the most critical cons of the current technique is the ambiguity problem. Hereby, we are providing a brief description of such problem.

In nature, each codon in a DNA sequence is converted to one of the 20 amino acids forming a protein sequence that is responsible for a certain functionality. Each amino acid is abbreviated by an English letter, i.e. ”Alanine” is an amino acid abbreviated with letter ”A”. Since We have 64 codons and 20 amino acids, each amino acid maps to at most 4 codons leading to the ambiguity problem. (Sabry et al., 2010) solve this problem by adding two extra bits next to each amino acid identifying which codon it represents. (Table 1) is an example showing the mapping of 8 characters to codons. For clarification assume that we have DNA sequence composed of two codons: ” GCC AAT”. This sequence when converted to characters using (Table 1), it will be: ” F N ” .

In the decryption process when converting from characters to DNA sequence, we will not know which codon does character ”F” represent. This is solved by adding 2 extra bits that represent a DNA base as clarified in (Table 2), to identify which codon does the character represent. Assume that base ”A” represents the 1st codon, ”G” for the 2nd codon, ”C” for the 3rd and ”T” for the fourth codon. so instead of having ”F N” we will have ”FG NA” , where ”G” is an ambiguity base refers to second codon and ”A” refers to first codon.

2.4 Hiding using 5x5 Playfair Cipher Technique

In this subsection we explain the currently used encryption and decryption process using DNA-based 5x5 playfair cipher as well as the recent substitution process used for DNA hiding mentioned in (Khalifa and Atito, 2012).

2.4.1 Encryption and Decryption using the Current DNA-based 5x5 Playfair Cipher Technique :

The encrypting process works as follows:

1. Convert message text to the binary form where each character is presented by 8 bits.
2. Transform the binary form into DNA letters using (Table 2).
3. The DNA form is transferred to the Amino acids letters representation according to the new alphabet distribution with the corresponding new codons used in (Sabry et al., 2010), taking into consideration two ambiguity bits for each Amino acid letter.
4. Separate the ambiguity bits from the amino acids sequence.
5. Use the key of Upper case letters to generate the 5X5 grid.
6. Apply the traditional Playfair cipher process.
7. Encrypted amino acids letters are transferred back to DNA sequence form.
8. Concatenate the DNA sequence with the saved ambiguity bits. Eventually we got an encrypted DNA sequence.

The decryption process:

Given the key and the encrypted DNA sequence

1. Separate the ambiguity bits from the encrypted DNA sequence.
2. Convert encrypted DNA sequence to amino acids letters.
3. Use the key to generate the 5x5 playfair cipher grid.
4. Perform the inverse of the playfair cipher process.
5. Use the ambiguity bits to get the correct DNA sequence.
6. Convert DNA sequence to binary form.
7. Convert the binary form to the original plaintext.

Table 2: DNA letter representation of binary bits.

DNA letter	Binary representation
A	00
G	01
C	10
T	11

Although this 5x5 DNA-based playfair cipher technique encodes encrypted data efficiently it suffers from two drawbacks. First is the ambiguity problem, which means that for every codon we are enforced to add 2 more bits to solve the ambiguity problem i.e. 3/4 of the ciphered DNA is real data while 1/4 is for solving the ambiguity problem, which minimizes the hiding capacity. Second, the long list of unnecessary complicated iterations consume a lot of computational resources especially when dealing with large data sizes.

2.4.2 Implemented Substitution Process

The above mentioned encryption technique uses a modified substitution method to achieve the Steganography goal. This technique is mentioned in detail in (Khalifa and Atito, 2012), it proved to be better than the original one mentioned in (Shiu et al., 2010). It assumes that the length of cover DNA sequence is the same as the message itself (S), and according to the 5x5 playfair cipher explained above, only 3/4 of these bases represent the actual message bits, since the remaining 1/4 are reserved for the ambiguity bits. The hiding capacity is measured in terms of the number of hidden bits per neuclotide[4] (bpn). Since each DNA base actually represents two bits of the binary message (M), therefore the hiding capacity is represented by the following equation:

$$Capacity = \frac{Sizeofmessageinbits}{Sizeofcoverinbases} \quad (1)$$

$$= \frac{\frac{3}{4} * |S| * 2}{|S|} = \frac{3}{2} bpn \quad (2)$$

From the previous equation we got that the hiding capacity of the current hiding technique using the DNA-based 5x5 playfair cipher is 3 bits per 2 neuclotides.

3 PROPOSED TECHNIQUE

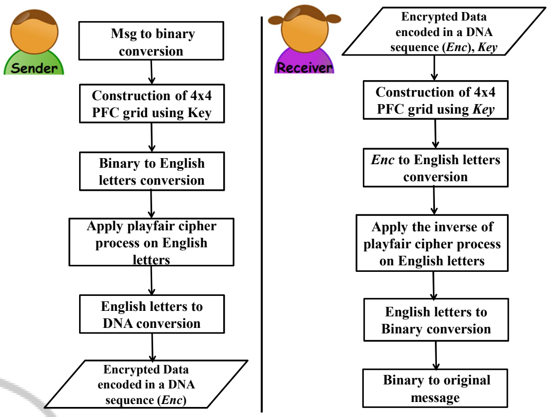

Sender
Msg to binary conversion
Construction of 4x4 PFC grid using Key
Binary to English letters conversion
Apply playfair cipher process on English letters
English letters to DNA conversion
Encrypted Data encoded in a DNA sequence (*Enc*)
Receiver
Encrypted Data encoded in a DNA sequence (*Enc*), *Key*
Construction of 4x4 PFC grid using *Key*
Enc to English letters conversion
Apply the inverse of playfair cipher process on English letters
English letters to Binary conversion
Binary to original message

Figure 2: Overall Ciphering and Deciphering processes of the proposed technique.

Table 3: Example of 16 randomly generated English letters -Playfair cipher grid-.

H	C	M	U
D	G	Z	B
I	A	X	J
Q	V	W	F

The proposed DNA-based Steganography technique consists of two phases, First the ciphering phase, where we used 4x4 playfair cipher grid as a modified version to the current 5x5 playfair cipher grid (Sabry et al., 2010), (Khalifa and Atito, 2012), (Atito, A. et al., 2012) to avoid all its drawbacks, Figure 2 shows a short, illustrative diagram to the overall proposed ciphering and deciphering processes. Second, the hiding phase using the modified substitution process in (Khalifa and Atito, 2012). As a result of modifying the ciphering process we succeeded in achieving higher hiding capacity than (Khalifa and Atito, 2012). In the following subsections we discuss in detail the proposed Steganography algorithm from both the sender and receiver side, followed by a step-by-step illustrative example.

3.1 Ciphering

In our proposed ciphering algorithm we used 4x4 playfair cipher grid. Since the English alphabet consists of 26 letters, we will use the *Key*'s ASCII value as a seed number for generating 16 unique random English letters to be represented by the 4x4 playfair

Table 4: 4x4 Binary grid.

0000	0001	0010	0011
0100	0101	0110	0111
1000	1001	1010	1011
1100	1101	1110	1111

[4] the nucleoide is the same as the DNA-base

Table 5: 4x4 DNA grid.

AA	TC	CG	TG
GC	TT	TA	GT
GG	AT	CT	CC
CA	AC	AG	GA

cipher grid as the example shown in (Table 3). Another 4x4 grid will be used, called the 4x4 binary grid where each cell contains one of the 4-bit possible combinations as shown in (Table 4), where the values in this grid are ordered in an ascending manner. Again we will construct another 4x4 grid, called the 4x4 DNA grid that contains the 16 possible 2-DNA letters combinations, the initial order of these combinations is shown in (Table 5). Then the encryption process done by the sender is implemented as follows:

Preprocessing (Key)

1. Use the *Key* as a seed value for generating 16 random English letters to form the 4x4 playfair cipher grid.
2. Use the *Key* to shuffle the 4x4 binary grid and the 4x4 DNA grid.

Encryption (Msg, 4x4-pfc-grid, ShuffledBG, ShuffledDG)[a]

1. Convert *Msg* to its binary form *B*.
2. Transform *B* to English letters *E* by mapping each value in *ShuffledBG* to its corresponding position in *4x4-pfc-grid*.
3. Perform playfair cipher technique on *E* to get a ciphered text *C*.
4. Map positions of *C* in *4x4-pfc-grid* to its corresponding DNA letters in *ShuffledDG* lying in the same cell position, to get the final encrypted DNA sequence *Enc*.

[a] pfc-grid stands for playfair cipher grid, ShuffledBG is the shuffled Binary Grid, and ShuffledDG is the shuffled DNA grid.

Note that, the values in the 4x4 binary grid and the 4x4 DNA grid are initial values which must be shared between the sender and the receiver. The sender will use the *Key* to shuffle these grids, where the resultant shuffled grids will be used for encrypting the binary data into DNA-based encrypted data.

3.2 Hiding Phase

After encryption, we applied the recent substitution method (Khalifa and Atito, 2012) for hiding data to achieve the goal of Steganography. By using equation(1) with the proposed encryption technique, we will achieve higher hiding capacity as proved by the following equation:

$$= \frac{|S| * 2}{|S|} = 2bpn \qquad (3)$$

From the previous equation, we can see the great impact of our proposed encryption technique on the substitution method. It has a significant higher hiding capacity, as a result of the ambiguity problem removal. In other words, the hiding capacity is improved by 25% since in (Khalifa and Atito, 2012) it was $3/2$ bits per nucleotide, while in our proposed technique it is 2 bits per nucleotide.

3.3 Extraction

The extraction process is formed by the receiver, to extract the hidden encrypted DNA sequence. In our technique we used the extraction process in (Khalifa and Atito, 2012).

3.4 Deciphering

The receiver will receive the encrypted DNA sequence and the *Key* through a secure channel. Then s/he will use the *Key* to be able to shuffle the 4x4 binary grid and the 4x4 DNA grid to decrypt the extracted encrypted DNA sequence. Ultimately, same key must be used by the sender and the receiver. The following is the proposed decryption algorithm which is the reverse of the aforementioned *Encryption* algorithm. It will be used by the receiver to retrieve the original data from the encrypted DNA sequence.

Decryption(Enc, Key)

1. Perform the *Preprocessing* function mentioned before the encryption step to obtain the *4x4-pfc-grid*, *ShuffledBG* and the *ShuffledDG*.
2. Map the positions of each 2 letters of the encrypted DNA sequence *Enc* in *ShuffledDG* to its corresponding positions in *4x4-pfc-grid* to get English text *C*.
3. Perform the inverse of playfair cipher technique on *C* to get *E*.
4. Map *E* to *ShuffledBG* to get its binary form *B*.
5. Convert *B* to the original message *Msg*.

Our proposed algorithm allows the message and the key to be of any type. The used 4x4 matrix eliminates the ambiguity problem that was presented in the previous algorithms(Sabry et al., 2010), (Khalifa and

Table 6: 4x4 Shuffled Binary grid.

0111	0010	1100	0011
0110	0001	1000	0000
1001	0101	1010	1110
0100	1111	1011	1101

Atito, 2012). Additionally, it provides more simplicity with no redundancy in the processes, which leads to higher remarkable performance and lower execution time.

Moreover, as mentioned in the steps of our algorithm, we use the numeral value of the key to generate random English letters to construct the playfair cipher grid, which makes the playfair cipher technique more confusing to the attacker than the traditional one; achieving higher security. On the other hand, any binary message can be encrypted in a DNA sequence of half its length as will be clarified in the illustrative example.

3.5 Illustrative Example

Assume the message: Hello and the Key : 2411
The Sender side:

1. Encryption process
   (a) Generate 16 random letters using the given key, (Table 3) will be generated.
   (b) Use the key to shuffle the initial values in (Table 4) and (Table 5), where (Table 6) and (Table 7) will be generated respectively.
   (c) Get the Binary form [B] of the message: 0100100001100101011011000110110001101111 (Binary sequence)
   (d) Get the English letters sequence by mapping the position of each 4 bits of B in (Table 6) to their corresponding positions in (Table 3): Q Z D A D M D M D V (Original English text)
   (e) Perform the playfair cipher process on the English text: W D G I Z H Z H G Q (Ciphered text)
   (f) Convert the ciphered text to a DNA sequence using (Table 3) and (Table 7), the resulted sequence: CCTATCATGGGTGGGTTCGC (Encrypted DNA sequence)

   Note: the Binary message consists of 40 bits, encrypted in a DNA sequence of 20 bases. i.e. half its length.

2. Hiding process
   (a) Use a suitable Reference DNA sequence from NCBI database (NCBI database).

Table 7: 4x4 Shuffled DNA grid.

GT	CG	CA	TG
TA	TC	GG	AA
AT	TT	CT	AG
GC	GA	CC	AC

   (b) Hide the Encrypted DNA sequence ”CCTATCATGGGTGGGTTCGC” in the chosen reference DNA sequence using the substitution process mentioned in (Khalifa and Atito, 2012).
   (c) The result is a fake DNA sequence.

The Receiver side:
Given the fake DNA sequence, the reference DNA sequence and the key.

1. Extraction process
   (a) Extract the hidden encrypted DNA sequence, using the reverse of the substitution process mentioned in (Khalifa and Atito, 2012).
   (b) The result is encrypted DNA sequence: ”CCTATCATGGGTGGGTTCGC”.
2. Decryption process
   (a) Generate 16 random letters using the given key, (Table 3) will be generated.
   (b) Use the key to shuffle (Table 4) and (Table 5), (Table 6) and (Table 7) will be generated.
   (c) Convert the encrypted DNA sequence to English letters by mapping their positions in (Table 7) to their corresponding positions in (Table 3): W D G I Z H Z H G Q (Ciphered text)
   (d) Perform the inverse of playfair cipher process Q Z D A D M D M D V (Original English text)
   (e) Map the positions of the English letters in (Table 3) to a binary form in their corresponding positions in (Table 6) 0100100001100101011011000110110001101111
   (f) Convert the Binary form to the original message ”Hello”

4 PERFORMANCE ANALYSIS

In this section we discuss the cracking probability as well as the experimental results on our algorithm implementation

4.1 Cracking Probability

Despite the fact of simplifying the recent DNA-based playfair cipher algorithm, the cracking probability of our proposed algorithm remains high and becomes even more confusing to the attacker. In case of both the recent technique and the proposed one, the attacker needs 4 types of information to decrypt a message, Binary representation, Reference DNA, the Complementary rule (Khalifa and Atito, 2012) and the ciphering technique. Probability to get the binary scheme b is:

$$P(b) = \frac{1}{4!} \tag{4}$$

Since we have 4 DNA bases, the number of possible binary schemes is 4!.

Probability to get the Reference DNA r:

$$P(r) = \frac{1}{1.6 * 10^8} \tag{5}$$

Since there exists $1.6 * 10^8$ DNA sequences on the DNA database(NCBI database).

Probability of the complementary rule c is:

$$P(c) = \frac{1}{16} \tag{6}$$

Therefore the overall cracking probability k is:

$$P(k) = P(b) * P(r) * P(c) = \frac{1}{24 * 1.6 * 10^8 * 16} \tag{7}$$

In case of the ciphering technique, there are 3 aspects that make our proposed DNA-based playfair cipher technique stronger than the traditional one.

1. We are using 4x4 grid instead of the traditional 5x5 playfair cipher grid, which means that the attacker might guess a sequence of English letters which are not in the grid.
2. We are not ciphering plaintext, but we are ciphering the binary form of the plain text. This means that we can cipher letters, numbers and even punctuation symbols.
3. The Key used in our modified playfair cipher technique is not restricted to characters only, it can be of any type since we get the numeral of the key and use it as a seed value for generating any 16 English letters to be presented by the grid.

All the above new aspects of our proposed modified DNA-based playfair cipher technique makes it more robust and its cryptanalysis becomes harder to break.

4.2 Experimental Results

Experimental results of our proposed DNA-based Steganography technique was compared with the results in(Khalifa and Atito, 2012) to confirm the superiority of our proposed algorithm regarding the maximum size of bits that can be embedded in the cover media named as the hiding capacity, as well as the percentage of the maximum hiding capacity needed to hide the message named as the actual payload and the execution time. Our algorithm was tested on the same used 8 benchmarks adopted from the (NCBI database). As shown in Figure 3, Figure 4 and Figure 5, the x-axis represents DNA sequences with different sizes used for hiding in terms of base-pairs(bp).

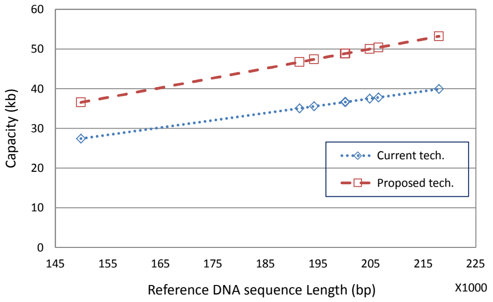


Figure 3: Capacity of the current technique Vs the proposed one.

In Figure 3, the y-axis presents the hiding capacity of the 8 reference DNA sequences. Despite the fact of our proposed technique simplicity, it improved the hiding capacity by 25% more than the current technique, since the current technique hides 3/2 bits per nucleotide, the proposed technique hides 2 bits per nucleotide; for example a reference DNA of size 149,884 bp can hide a message of length up to 27.44 Kb by using the current technique while the proposed one can hide up to 36.56 Kb.

The actual payload of the proposed technique is compared with that of the current one using a message of size 10 kb. As shown in Figure 4, the less actual payload percentage, the more data can be hidden. For example, the 10 Kb message occupies 26.45% in a reference DNA of length 206,488 bp using the current technique, while the same message occupies 19.83% in the same reference DNA using the proposed technique. In other words, the proposed technique can efficiently hide a larger messages in comparison with the current one, as illustrated by Figure 4. It is worth to note, that the hiding capacity of the proposed technique increases by an average rate of 25% in comparison with the current technique, while the actual payload decreases by almost the same rate.

In Figure 5, the y-axis represents the execution time. The two illustrated curves represent the performance of the current hiding algorithm and our proposed one. It is easily noted that the execution time of the proposed algorithm is significantly less than the current one as it get rid of the repetitive steps of the current technique.

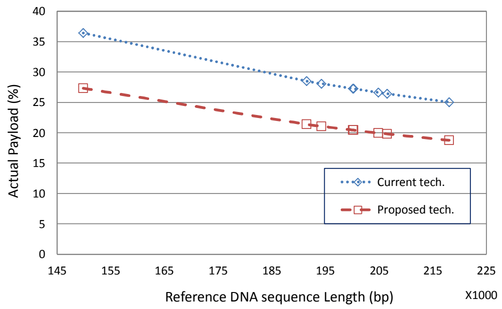


Figure 4: Actual payload of the current technique Vs the proposed one.

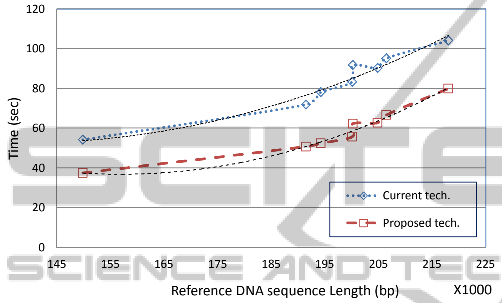


Figure 5: Execution time of the current technique Vs the proposed one.

5 CONCLUSIONS AND FUTURE WORKS

This paper proposed a new DNA-based Steganography algorithm to achieve a high hiding capacity. It's composed of two steps, firstly data encryption using enhanced DNA-base playfair cipher, Secondly utilizing the recent substitution technique for hiding. The proposed algorithm enhanced the commonly used playfair cipher and got rid of the overhead ambiguity bits. It proved that a message can be encrypted in a DNA sequence in half of its length. Moreover, the hiding capacity of the cover DNA sequence is improved by 25% where each 2 bits are hidden in one DNA base as a result of the playfair cipher modification. Additionally, we enhanced the security and achieved lower execution time as well. The conducted experimental studies proved the superiority of our proposed approach in terms of higher hiding capacity and better time performance in comparison with the current DNA-based Steganography algorithms.

Using DNA as a medium for Steganography is very promising, due to the fact of its huge storage capacity. As a future work, we should focus on imitating the DNA nature by developing algorithms with higher data hiding capacity.

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