

Mathematical Model
on
“Secure Data Storage On Multi-Cloud Using DNA Based
Cryptography”

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Chapter 1

Mathematical Model

Laboratory Assignments on Project Analysis of Algorithmic Design

1.1 Embedding Data

In order to explain embedding phase, separating the phases into some successive and vivid sub-phases, is the best way of proposing current method. In below, sub-phases have been shown, respectively.

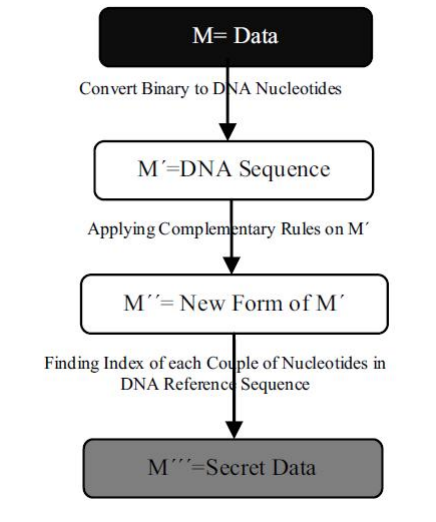


Figure 1.1: Embedding secret data

The first sub-phase is, converting by DNA base pairing rules. The product is M. M contains nucleotides sequences. **The next (second) sub-phase is**, applying complementary rules. Increasing the

complexity is the real and exact purpose of this step. By applying the complementary rules, the new form of the M which is M emerges.

When all the indexes have been extracted, M has been made, properly. M is precisely the secret data with some changes through the embedding phase.

- DNA Reference Sequence:

AT₁CG₂AA₃TT₄CG₅CG₆CT₇GA₈GT₉CA₁₀CA₁₁AT₁₂TC₁₃GC₁₄GC₁₅TG₁₆AG₁₇TG₁₈AA₁₉CC₂₀

- Let The Message Be M.

M = 100111000011

- Sub-phase1_(A=00,T=01,C=10,G=11) :

$M' = CTGAAG$

$M' = \Sigma_{start}^{eof}(encode1(d));$

where eof \rightarrow End Of File

encode1 \rightarrow function returning DNA nucleotide for set d

d = (d1,d2) | d1 and d2 are two consecutive digits in the file

M' is phase 1 encryption message.

- Sub-phase2_{((AC)(CG)(GT)(TA))} :

$M'' = GATCCT$

$M'' = \Sigma_{start}^{eof}(encode2(x));$

encode2 \rightarrow function returning DNA nucleotide compliment for set 'x'

x = {A,T,C,G}

M', is phase 2 encryption message.

- Sub-phase3 (Indexes):

$M''' = 8137$

$M''' = \Sigma_{start}^{eof}(encode3(g));$

encode3 \rightarrow function returning indexes for DNA pair

g = (g1,g2) | DNA Pair from M''

M''' is phase 3 encryption message.

Now, embedding phase is finally completed. Then, sender sends 8,13,7 to the cloud. In the next section, the client 2 will apply the extracting phase for extracting the original data by using three consecutive phases.

1.2 Extracting Original data

the secret data in form of some numbers. For the purpose of extracting the original data from DNA reference sequence, phase two with its sub phases will extract the original data, correctly.

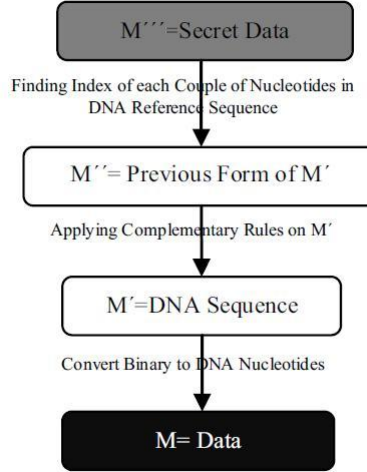


Figure 1.2: Extracting original data

- DNA Reference Sequence:

AT₁CG₂AA₃TT₄CG₅CG₆CT₇GA₈GT₉CA₁₀CA₁₁AT₁₂TC₁₃GC₁₄GC₁₅TG₁₆AG₁₇TG₁₈AA₁₉CC₂₀

- Sub-phase 1 (Indexes):

$$M = 8137$$

$$M'' = \Sigma_{start}^{eof}(\text{decode3}(g));$$

decode3 → function returning DNA pair for indexes

g = index from *M'''*

M'' is phase 31 extracted message.

- Sub-phases 2_{((AC)(CG)(GT)(TA))} :

$$M = GATCCT$$

$$M'' = \Sigma_{start}^{eof}(\text{decode2}(x));$$

decode2 → function returning DNA nucleotide compliment for set '*x*'

$$x = \{A, T, C, G\}$$

M', is phase 2 extracted message. Sub - phase 3_(A=00,T=01,C=10,G=11) :

$$M = CTGAAG$$

$$M' = \Sigma_{start}^{eof}(\text{decode1}(d));$$

decode1 \rightarrow function returning binar digits for DNA nucleotided = DNA Nucleotide From $M''M'$ is original message

- $M = 100111000011$

1.3 Throughput

$$\mu = (\Sigma_{i=0}^n D_n)/T$$

where ,

$\mu \rightarrow$ Throughput.

D_n is data upto n bits.

T is Average time consumed.

1.4 Time Complexity Conclusion (NP Hard/Complete, P)

The Mathematical model obtained gives the solvable output for proposed system. But the time depends on the positions of the base pairs in the reference string. So we conclude that our system lies in NP-complete.