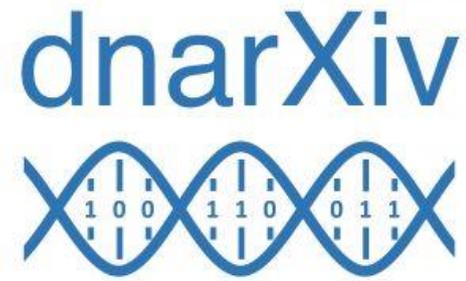




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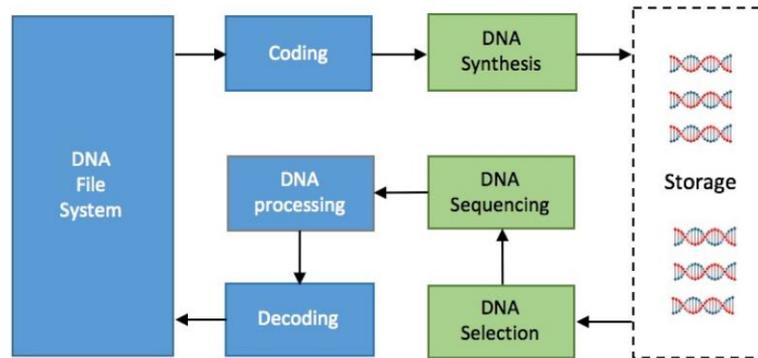


# Security of the DNA data storage chain

Chloé Berton, Gouenou Coatrieux

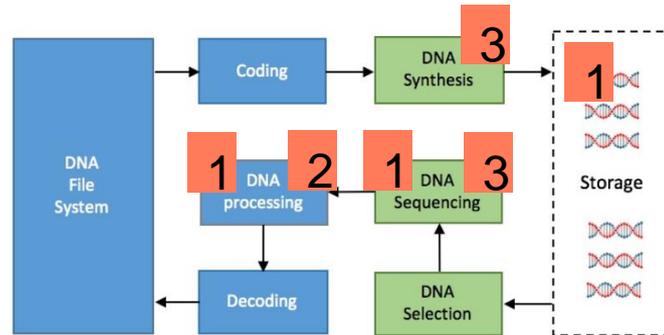
# Context and motivations

- Ensuring the confidentiality and integrity of the data stored in DNA molecules
- Integrating security at the biological level



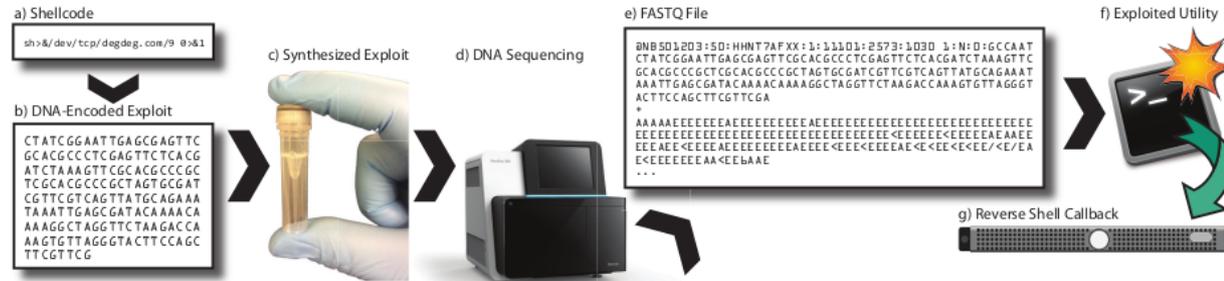
# Threats on the DNA storage chain

- 1 Theft or cloning (of molecules, fastQ files, sequencing devices)
- 2 Addition of DNA to confuse the sequencing device (Denial of service attack)
- 3 Spying the sequencing or synthesis device



# State-of-the-art

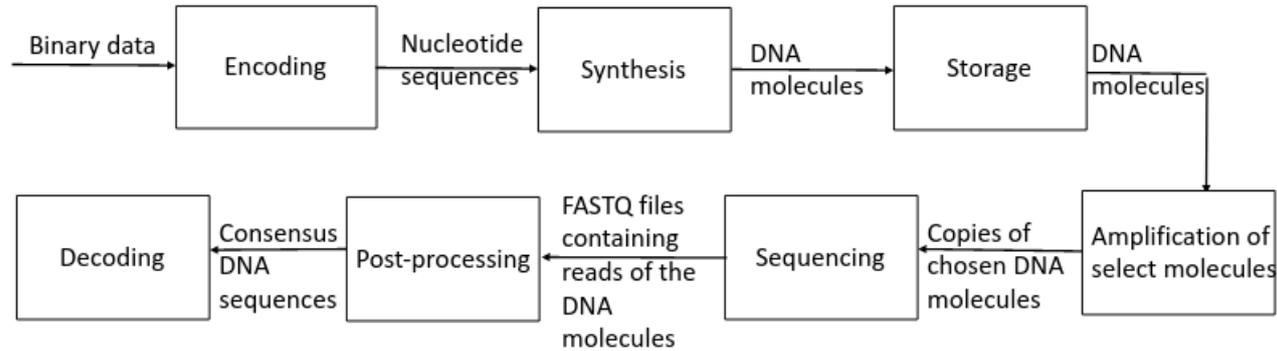
- Peter Ney et al., 2017.
- Exploit of a vulnerability of multiplex sequencing. Synthetic DNA is created from malicious shellcode. The DNA molecules are sequenced and as a result, the computer reads malicious fastQ files that take over the computer.



- Sina Faezi et al., 2019.
- A smartphone left in proximity to a synthesis device can guess what was synthesized by listening to the machine, with 88 % accuracy.



# Detailed DNA data storage chain



## Objectives

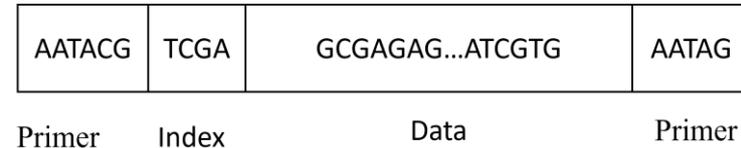
- Confidentiality of a message in the entire chain
- Coding solution taking into account the constraints of biological technologies (synthesis, sequencing)

# First issue : biological constraints

- Homopolymers (longer than 4) are forbidden in the sequence because they cause errors during sequencing and synthesis.
- The rate of G-C nucleotides must be balanced, ideally at 50-55 %.
- Some sequences are forbidden, for example primers and indexes (an index signals the placement of a sequence in a file).

ACGGATTTTTAGC

ACGATTTAATAGA



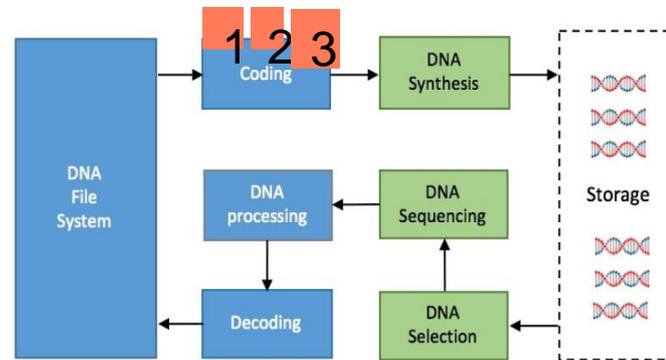
# 2nd issue : Errors

- Insertions, deletions and substitutions appear in the sequence during synthesis and sequencing.
- The error-correcting code must not contain unwanted motifs such as homopolymers.

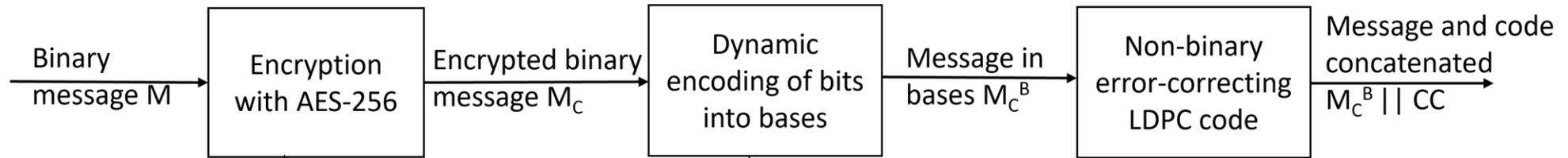
# Proposed solution

## Encryption and encoding of the message before synthesis

- 1 Encryption of the binary data using AES-256.
- 2 Dynamic encoding of the binary data into nucleotides
- 3 Error-correcting code : non-binary LDPC code



# Our encoding solution in three steps



Cipher key  
 $K_{AES}$  of 256 bits

$2N$  or  $2N-1$  bits are  
encoded into  $N$   
bases

010011111110..10011

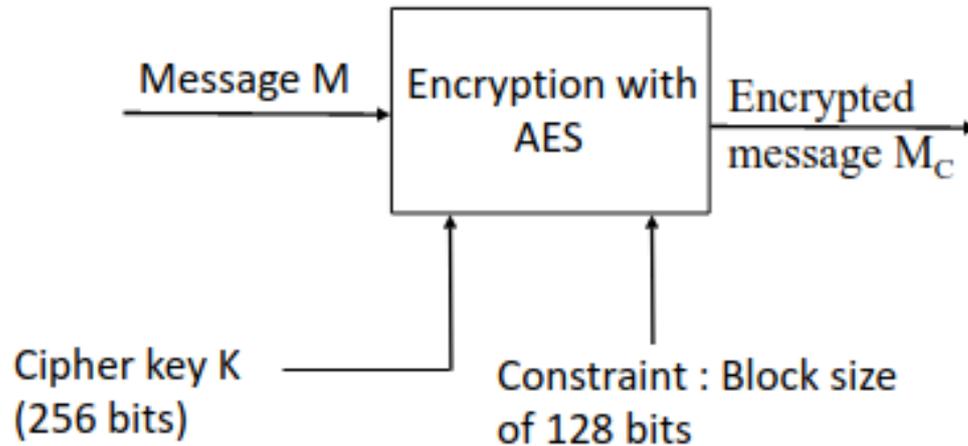
010010110..10101

CATCAGT..ATC

CATCAGT..ATC || CGGA..TAG

# Step 1 : Encryption

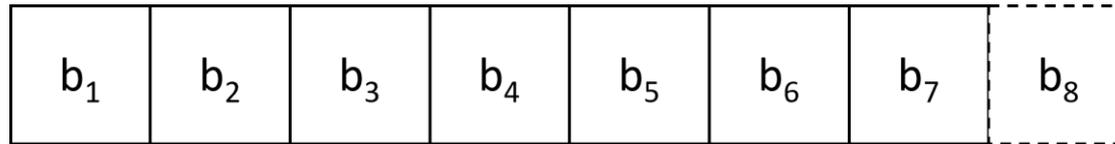
- Input : Blocks of binary message  $M$
- Output : Encrypted message  $M_C$  uniformly- distributed



# Step 2 : Dynamic encoding

- Objective : No homopolymers longer than 4, so  $X_4 \neq X_3$  always
- Input : Encrypted binary message  $M_C$
- Output : Encrypted message converted in bases  $M_C^B$

Block of bits  
(0,1)



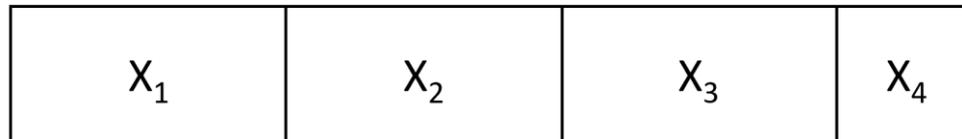
00 → A  
01 → C  
10 → G  
11 → T

00 → A  
01 → C  
10 → G  
11 → T

00 → A  
01 → C  
10 → G  
11 → T

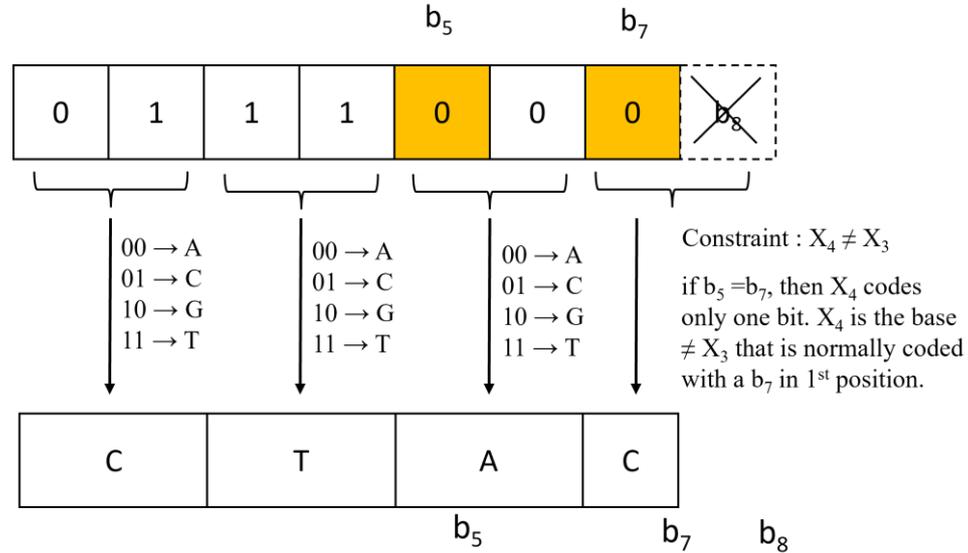
$X_4$  can encode two bits, or only one if there is a risk of a forbidden pattern

Block of bases  
(A,C,T,G)

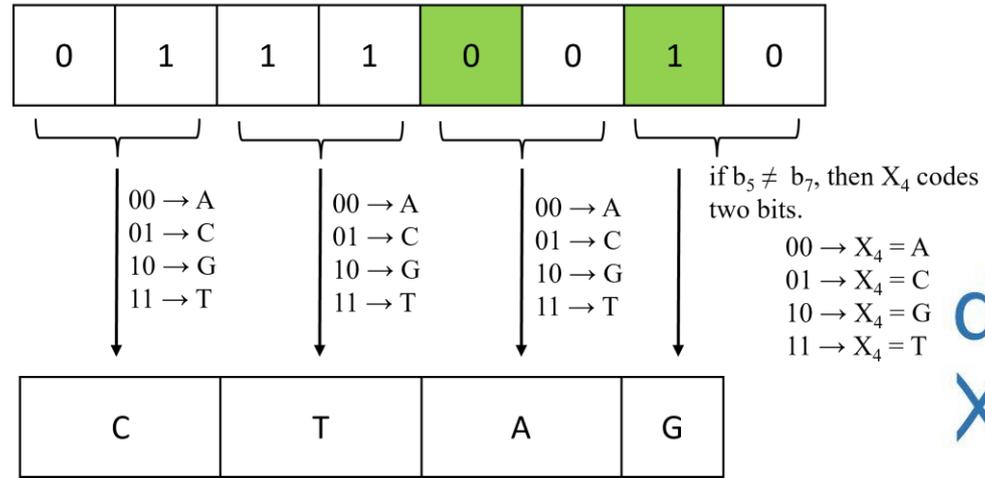


# Step 2 : Dynamic encoding

Case 1 : The last base  $X_4$  encodes only one bit

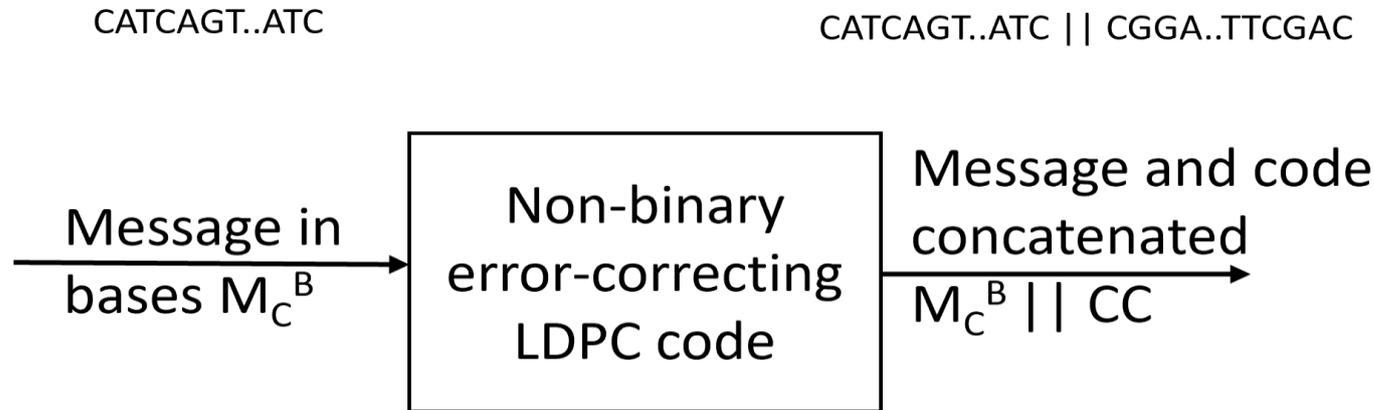


Case 2 : The last base  $X_4$  encodes two bits



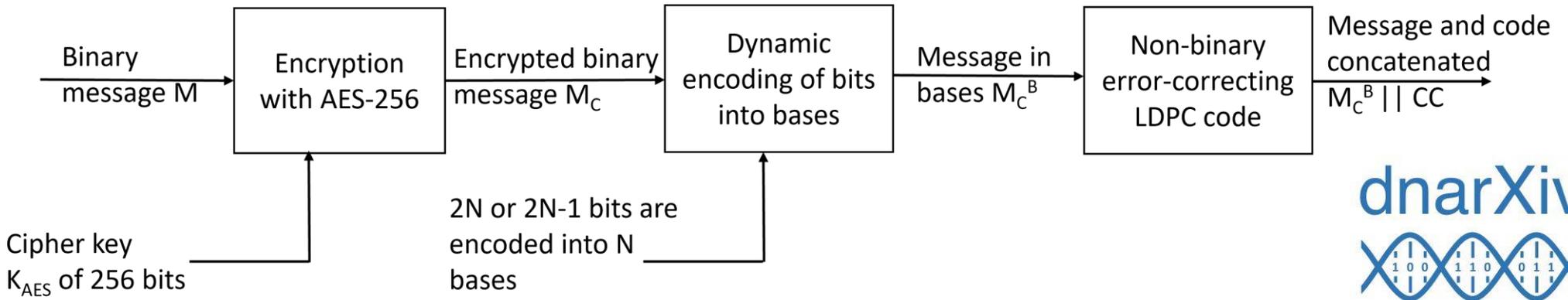
# Step 3 : Error-correcting code

- Input : Message  $M_C^B$  in bases
- Output : Concatenation of  $M_C^B$  and the error-correcting code CC



# Results

- Encryption outputs uniformly-distributed data, this ensures a balanced G-C content.
- To avoid homopolymers longer than 4, we encode blocks of 4 bases with 7 or 8 bits.
- Information rate on uniformly-distributed data : 1,87 bits per base.



# Experimentation

- Simulation of the biological processes
- The simulation outputs partial reads of the DNA sequences. Processing determines a consensus sequence by majority voting.
- The LDPC code corrects the remaining errors in the sequence, and the message is decoded back to binary.
- Sequences of size 500-2000 have been successfully retrieved with 100 partial reads.

