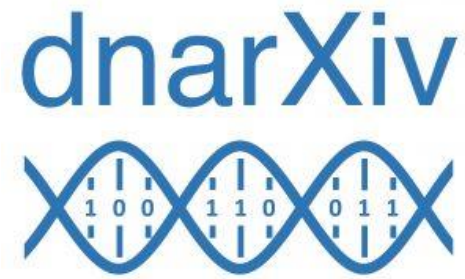




IMT Atlantique
Bretagne-Pays de la Loire
École Mines-Télécom

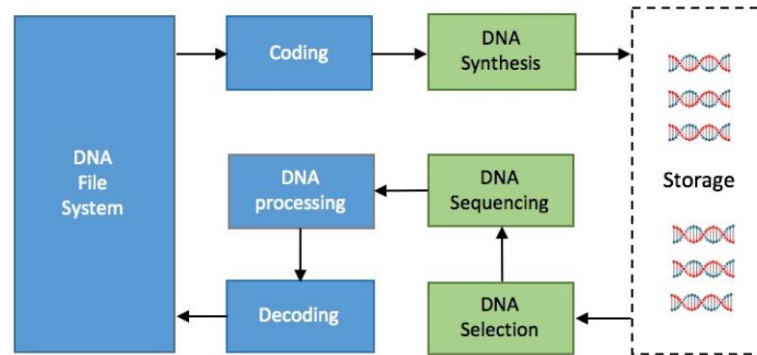


Security of the DNA data storage chain

Chloé Berton, Gouenou Coatrieux

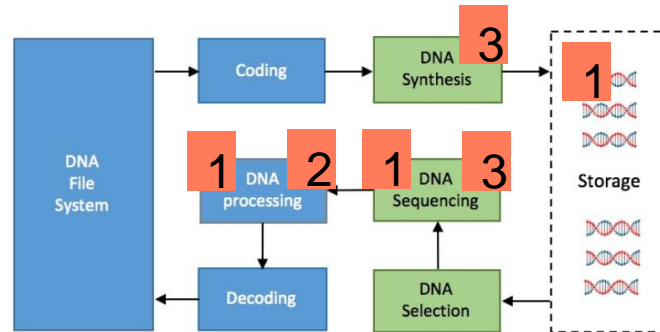
Context and motivations

- 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

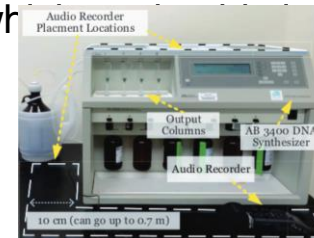


State-of-the-art

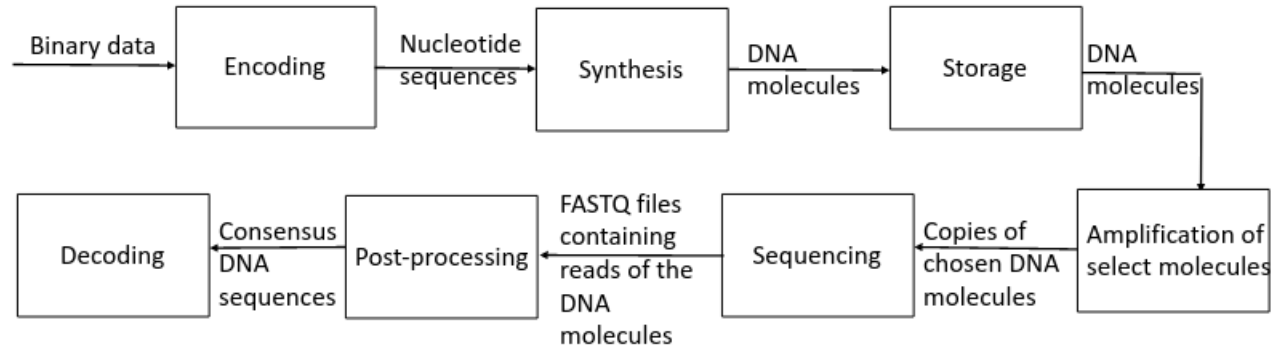
- Peter Ney et al., 2017.
- Exploit of a vulnerability of multiplex sequencing. Synthetic DNA is created from malicious shellcode. The DNA molecules are sequenced and as a result, the computer reads malicious fastQ files that take over the computer.



- 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

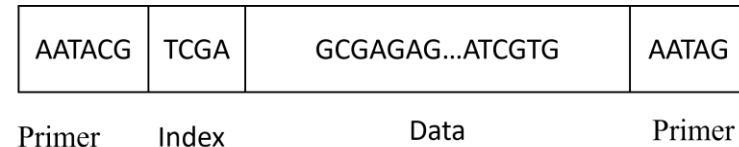
- Confidentiality of a message in the entire chain
- Coding solution taking into account the constraints of biological technologies (synthesis, sequencing)

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



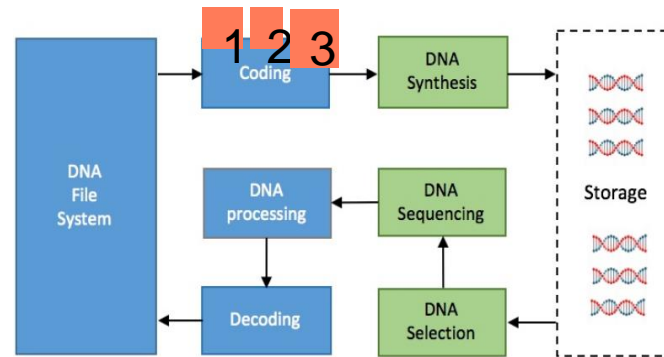
2nd issue : Errors

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

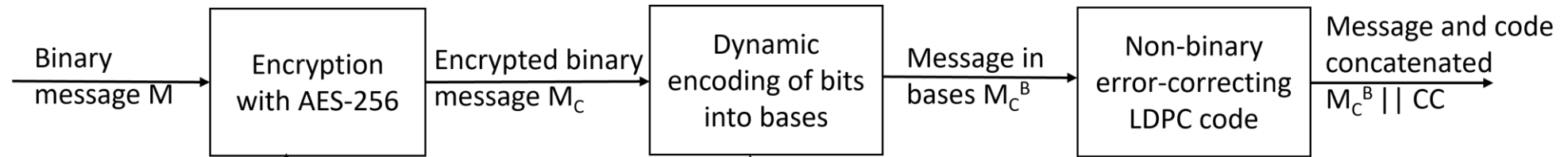
Proposed solution

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

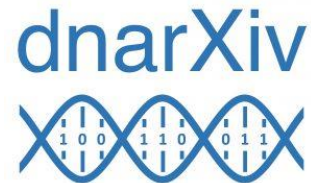
010010110..10101

CATCAGT..ATC

CATCAGT..ATC || CGGA..TAG

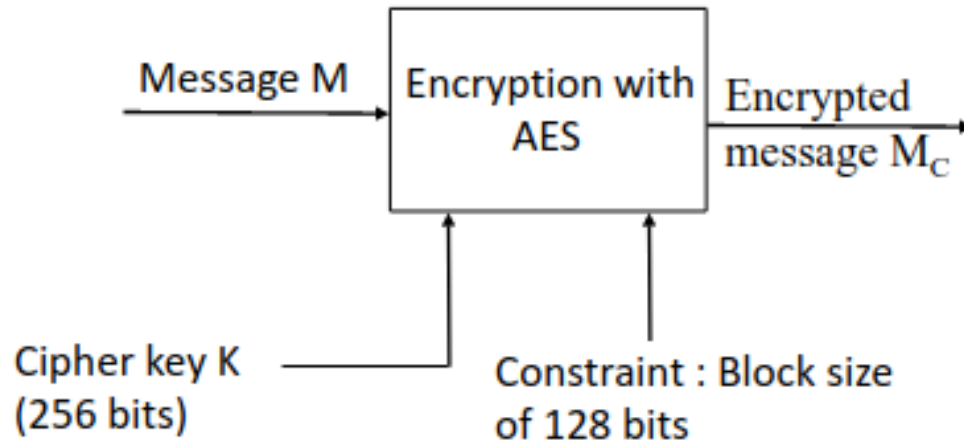


IMT Atlantique
Bretagne-Pays de la Loire
École Mines-Télécom



Step 1 : Encryption

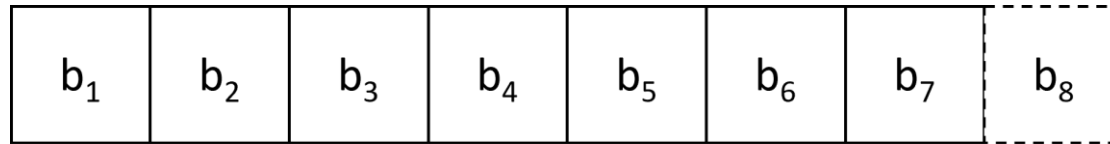
- Input : Blocks of binary message M
- Output : Encrypted message M_C uniformly- distributed



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)



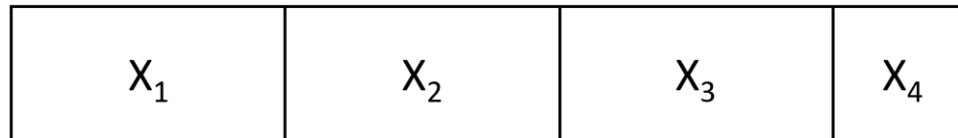
00 → A
01 → C
10 → G
11 → T

00 → A
01 → C
10 → G
11 → T

00 → A
01 → C
10 → G
11 → T

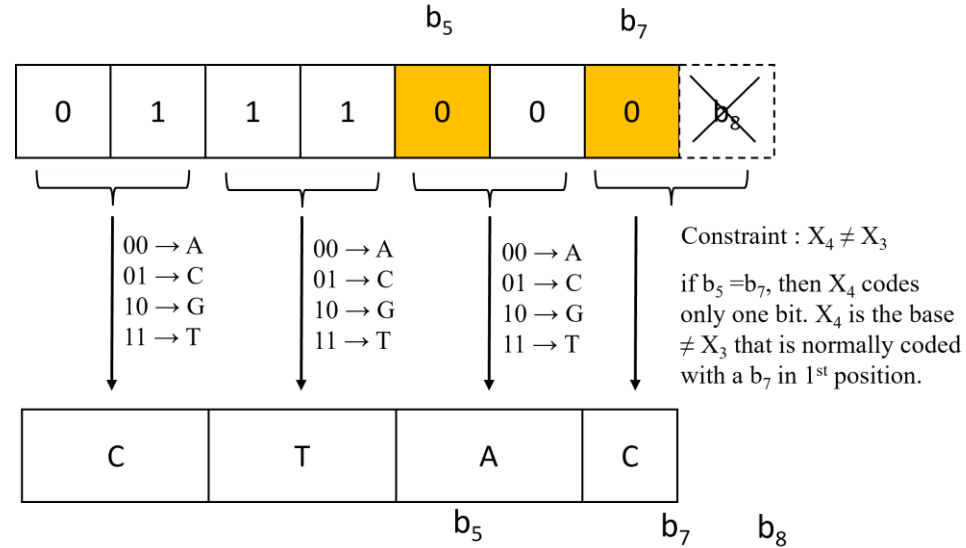
X_4 can encode two bits, or only one if there is a risk of a forbidden pattern

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

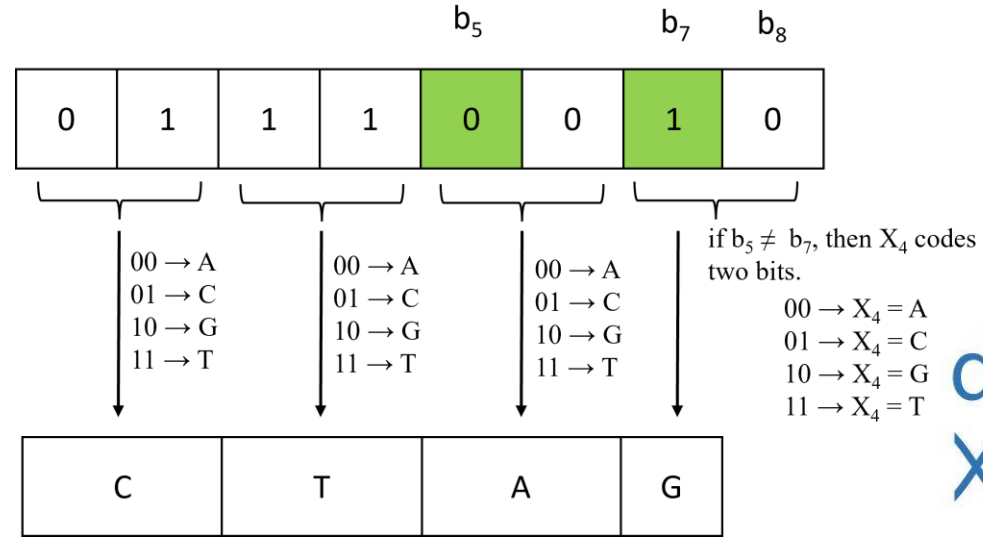


Step 2 : Dynamic encoding

Case 1 : The last base X_4 encodes only one bit

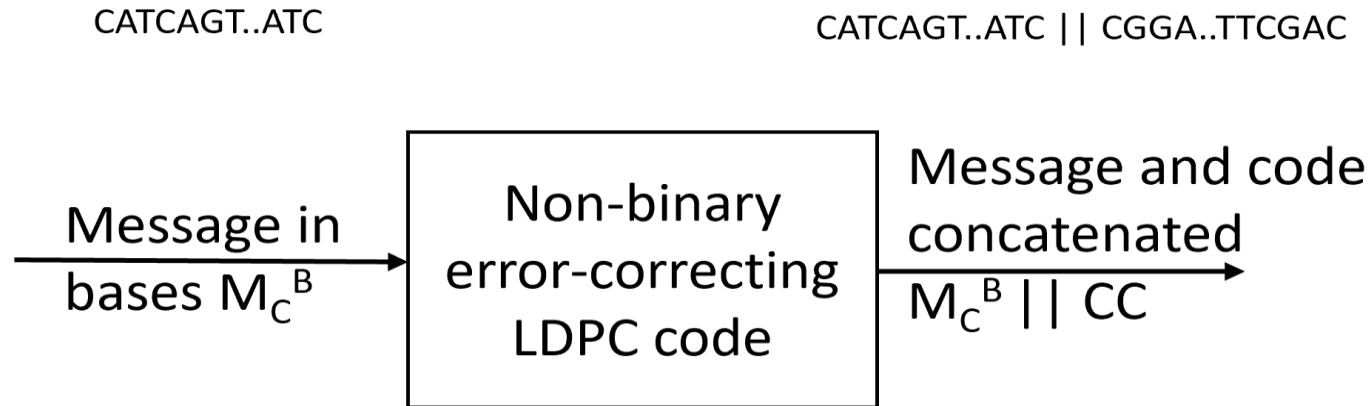


Case 2 : The last base X_4 encodes two bits



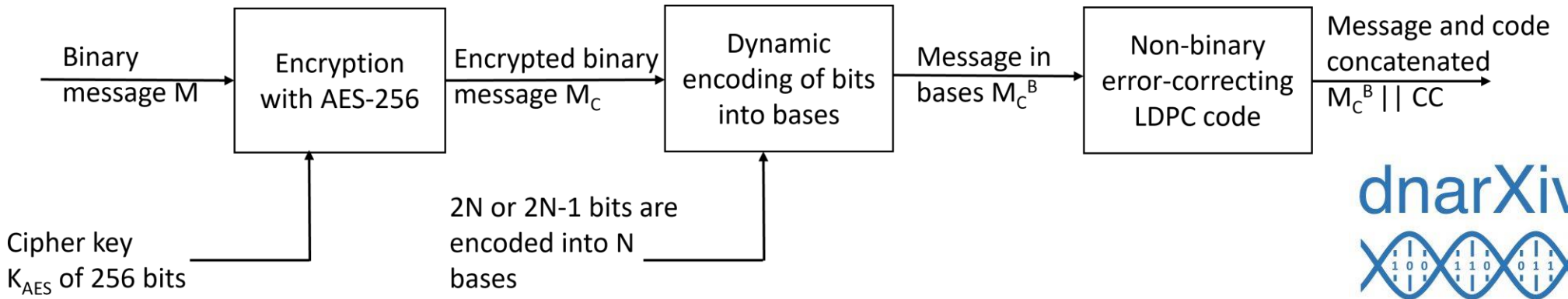
Step 3 : Error-correcting code

- 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.

