SECURE DATA STORAGE INTO DNA MOLECULES COMPLIANT WITH BIOLOGICAL CONSTRAINTS

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SUMMARY

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Tomorrow's data storage needs

➢ Data production rises exponentially [RGR18]

➢ **Advantages of DNA storage** [DSG16]:

- Density of 10^{21} bytes in one gram (10^6 times more compact than hard disks)
- Durability for centuries
- Energy cost close to zero (molecules kept at room temperature with no maintenance)

Global Data Creation is About to Explode
Actual and forecast amount of data created worldwide 2010-2035 (in zettabytes)

1 zettabyte is equal to **1 billion terabytes**.

2	12	33	47	175	612	2,142
2010	2015	2018	2020	2025	2030	2035

@StatistaCharts   Source: Statista Digital Economy Compass 2019

statista

Volume of data created or replicated in the world, projection for 2020 to 2035 - Source : Statista
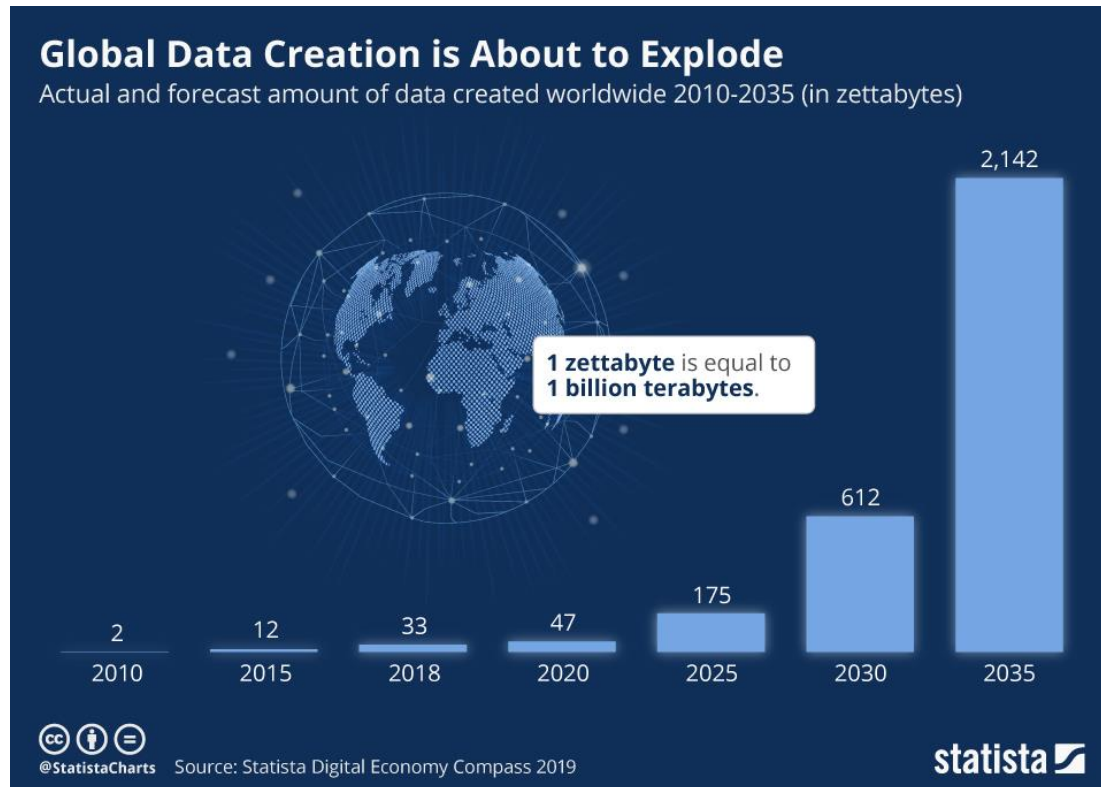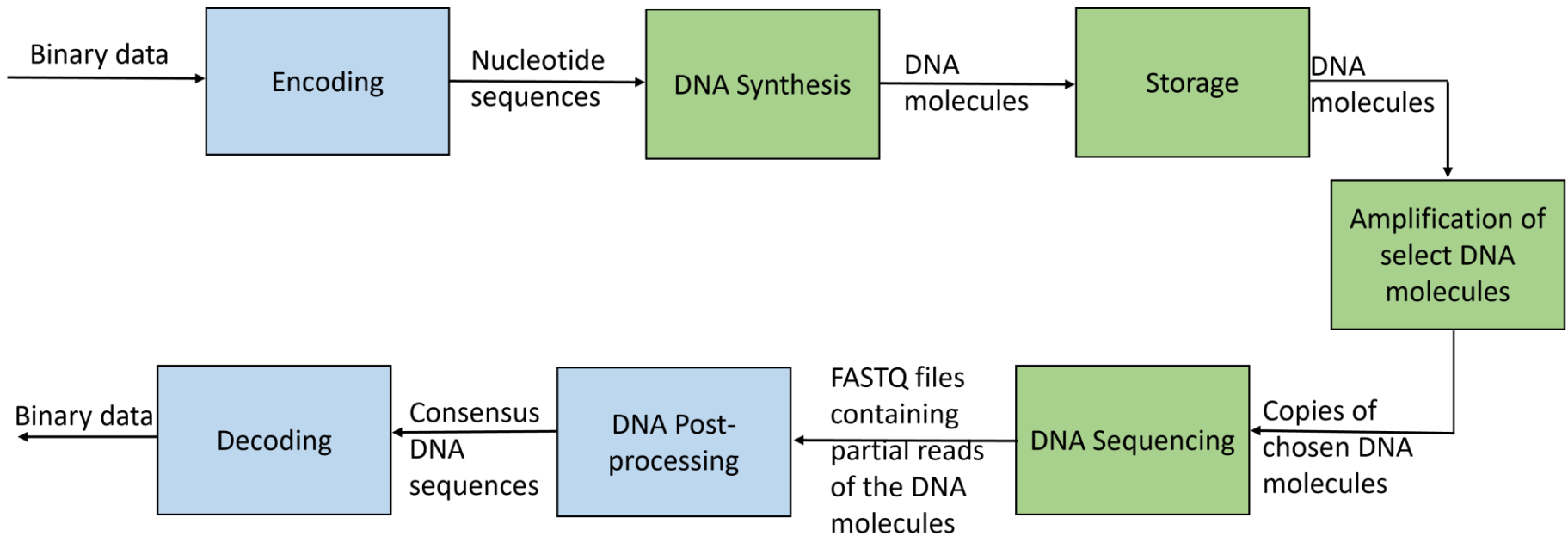
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STORING DATA ON DNA MOLECULES
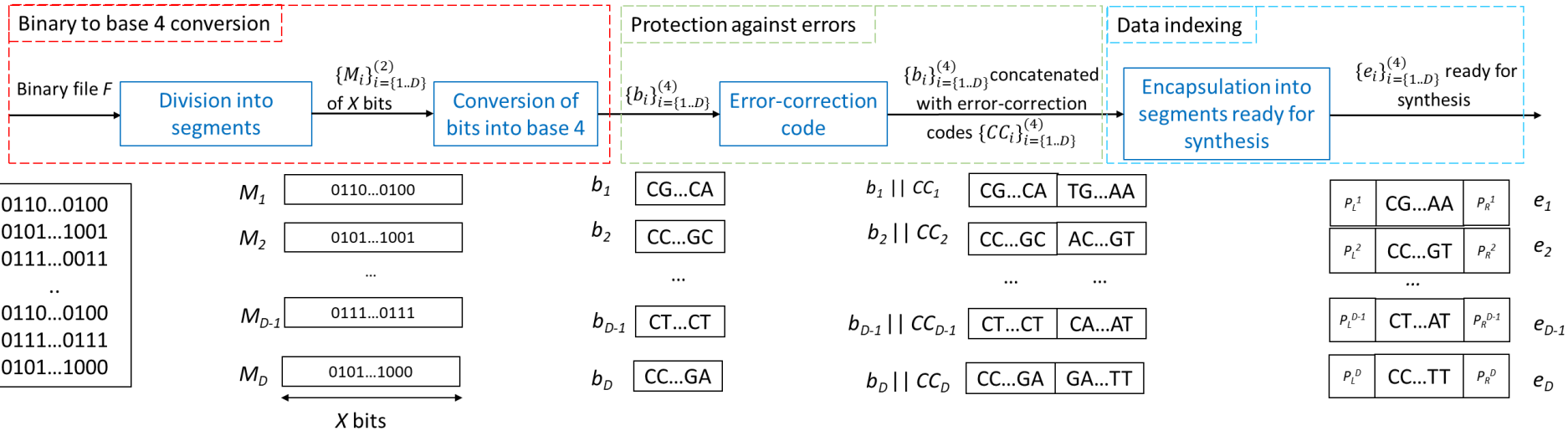
DNA data storage chain

A common DNA data storage chain

STORING DATA ON DNA MOLECULES

A classic way to store data

Encoding of a file *F*:

➤ Conversion and indexing of a binary file *F* into a nucleotide sequence
➤ **Output**: nucleotide sequences ready for synthesis

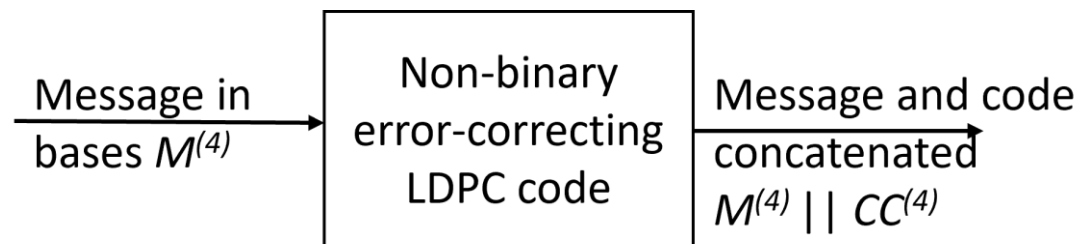*Encoding of a binary file F into DNA sequences $\{e_i\}_{i=\{1..D\}}^{(4)}$ ready for synthesis*

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A classic way to store data

Non-binary LDPC error-correction code (ECC) [HDCCL21]

➤ Low Density Parity Check (LDPC) codes: linear capacity-approaching block codes

➤ Able to correct substitution and deletion errors

Example: A (6,3)- LDPC code can correct one error

➤ Codes applied with the quaternary base alphabet

Message in bases $M^{(4)}$ → Non-binary error-correcting LDPC code → Message and code concatenated $M^{(4)} || CC^{(4)}$

$CC^{(4)}$: redundancy bases of LDPC error correction codes

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DNA STORAGE AND SECURITY THREATS

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Data security ?

➢ *Security properties of data*
- ▪ Confidentiality
- ▪ Availability
- ▪ Integrity
- ▪ Traceability

➢ *Deployment of security*
- ▪ Information systems are secured accordingly a Plan-Do-Check-Act procedure (ISO 2700X)
- ▪ Usually based on a risk analysis to identify security requirements in terms of CAIP (E-BIOS, STRIDE, …).


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➢ Common security threats

- Spoofing
- Tampering
- Repudiation

- Information Disclosure
- Denial of Service
- Elevation of Privilege

➢ Attacks from the literature

- **Exploit of a vulnerability of multiplex sequencing** [Ney2017]. Synthetic DNA sequences of malicious shellcode are produced. The sequencing reads the malicious fastQ files leading to an error and the pirate takes over the computer.

- **Acoustic side channel attack** [Faezi 2019]. A smartphone left in proximity to a synthesis device can guess which nucleotide is synthesized by listening to the machine, with 88 % accuracy.

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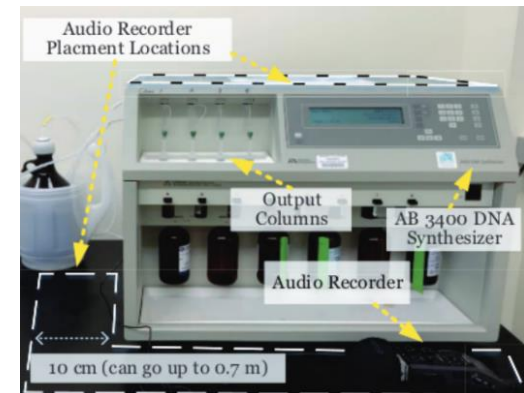
THREATS ANALYSIS ON DNA STORAGE

A short overview
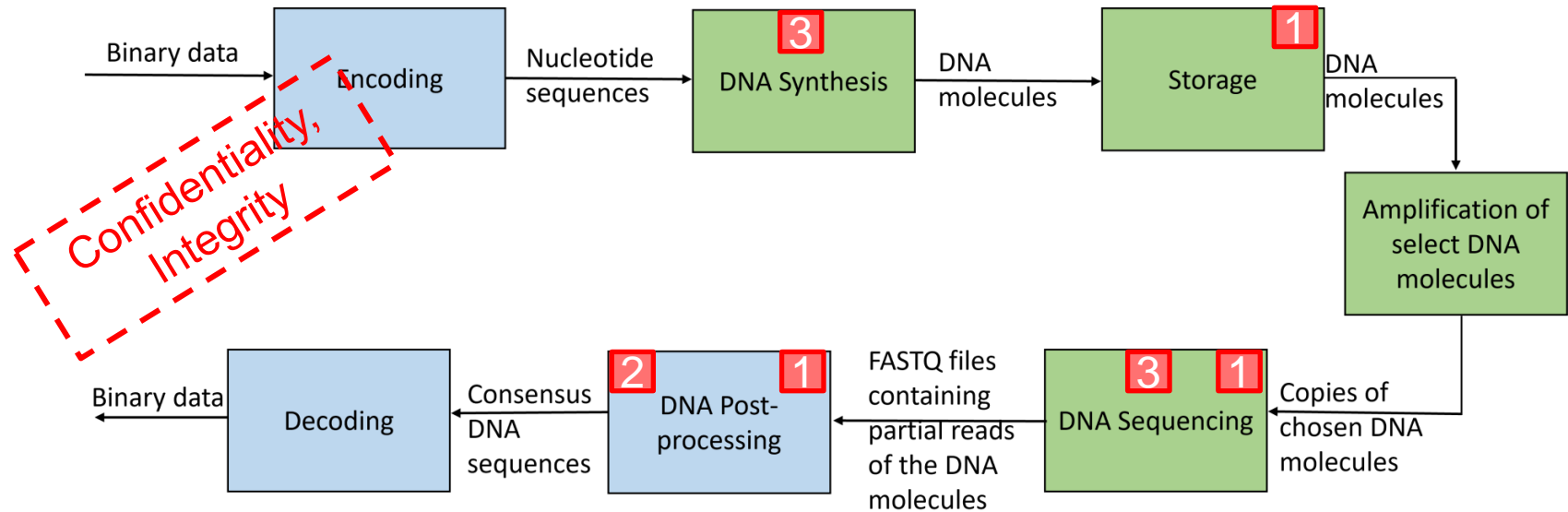
1 ► Theft or cloning (of molecules, fastQ files, sequencing devices): **Threat on availability, Confidentiality**

2 ► Denial of service attack by adding fake DNA sequences to confuse sequencing: **Threat on availability, integrity**

3 ► Spying the sequencing or synthesis device: **Threat on confidentiality**

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Data security and DNA : some of state-of-the-art methods

➢ DNA Cryptography – Use of DNA in encryption process
  ▪ [GLR03]: One Time Pad (OTP) encryption of base-4 data with a same-sized random DNA sequence.
  ▪ [CQWZ08]: For a secure data exchange, base-4 data are encrypted using an asymmetric encryption algorithm and are stored into DNA.
  ▪ [GHSD20]: Encryption of data with a key generated from human genome. (*Note*: this protocol has been tested on DNA molecules).

➢ DNA based steganography – Use of DNA to hide or secretly convey sensitive data (Spying)
  ▪ [WZWC13]: DNA sequences are encapsulated by primers, based on which it is possible to retrieve a sequence by amplification (Polymerase Chain Reaction PCR).

➔ Securing the whole DNA chain is still an open issue

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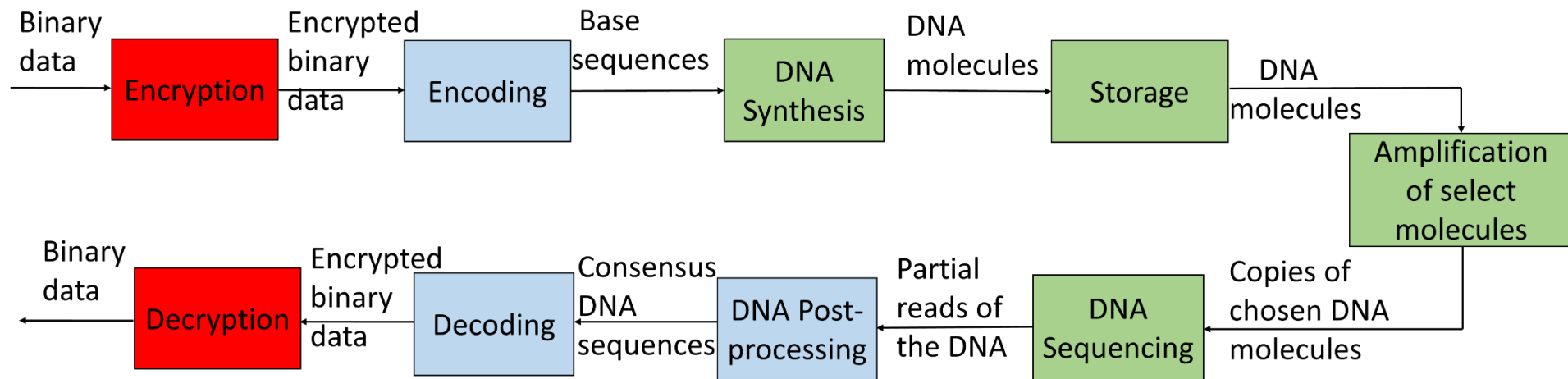Bretagne-Pays de la Loire
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DYNAMIC ENCODING OF ENCRYPTED DATA UNDER BIOLOGICAL CONSTRAINTS

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DYNAMIC ENCODING AND ENCRYPTION
The common way to ensure confidentiality of data …

DNA Data Storage chain including encryption before encoding of bits into bases

Example: use of the Advanced Encryption Standard AES

► Security verified by NIST, light and fast
► Encrypt a message *M* by blocks of 128 bits, Key size of 256 bits
► Encrypted message M_C uniformly distributed

Encryption key K_{AES}

Binary Block B → AES-256 Encryption → Encrypted Block B_e
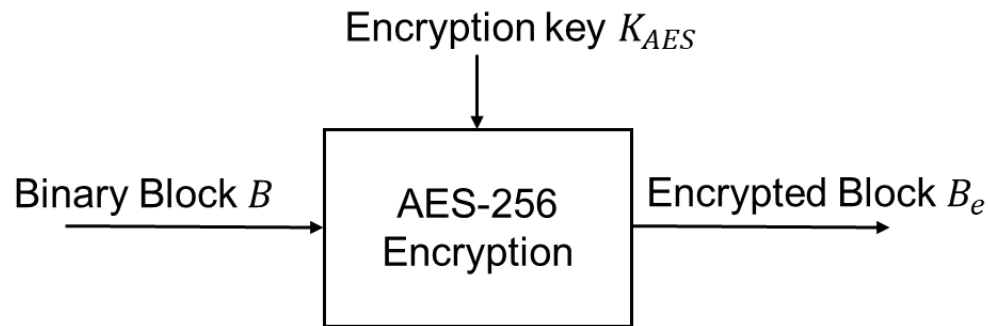
➔ **Considering AES as a perfect cryptosystem – encrypted data are uniformly distributed – may cause problems with synthesis and sequencing processes.**

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► **Homopolymers** N, long repeats of the same base, cause synchronization issues during sequencing.
Example: The MinION, a nanopore sequencing device, usually fails to identify the length of the repeat. ➔ $N \leq 4$.
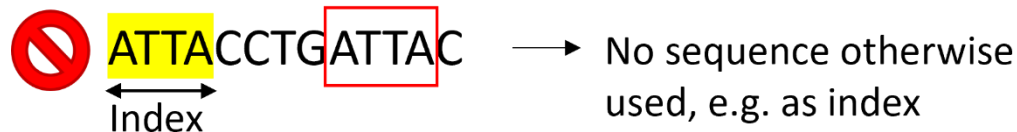
🚫 ATTA[GGGGG]CAA ⟶ No repeats longer than 4

► **G-C content** must be balanced, 40-60%, to facilitate synthesis and limit sequencing errors

🚫 ATTACTTAGATTAT ⟶ G-C content must be balanced

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Biological and data indexing constraints

▶ **Unwanted pattern:** No interferences with sequence indexing (primers)

▶ **Quality validation:** Use of an analyzer to determine whether the structure of a sequence is ready for synthesis. This includes a balanced G-C content, absence of long homopolymers, no repetitions of subsequences longer than 20 bases, *etc*.

Examples of analyzer tools: *GeneArt Instant Designer* by ThermoFisher Scientific, *gBlocks Gene Fragments Entry* by IDT.

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Overview of our module

► Objective: no homopolymers longer than *N* nor unwanted patterns.

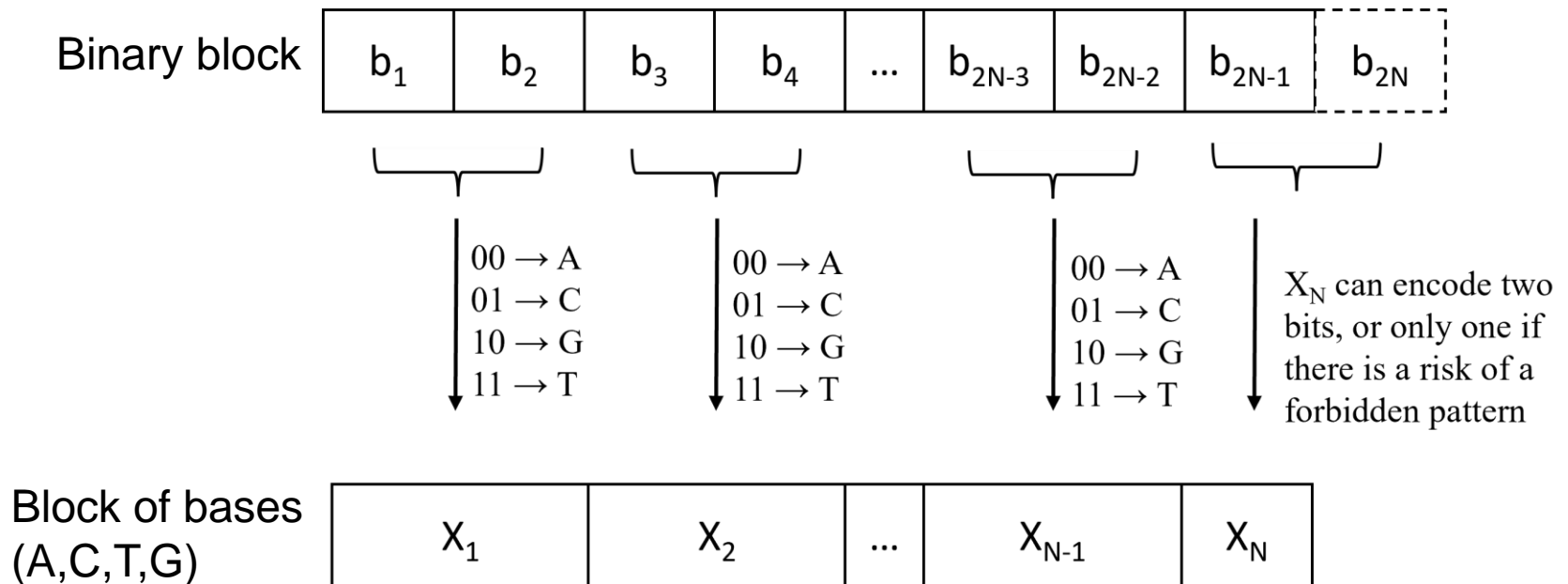► *Output*: a variable length encrypted message converted in bases M_e^4
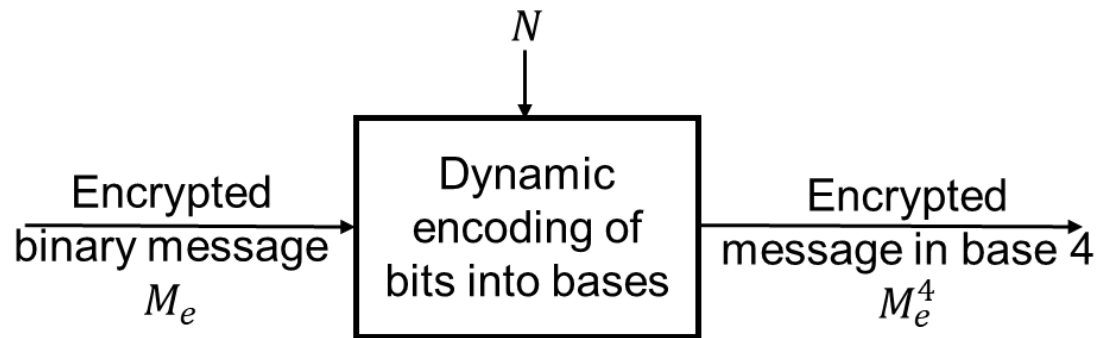
N : authorized maximum homopolymer length

Management of unwanted homopolymers

Encoding of a block of *N* bases:

► No unwanted patterns such as homopolymers longer than *N*

Binary block

b_1	b_2	b_3	b_4	...	b_{2N-3}	b_{2N-2}	b_{2N-1}	b_{2N}

$00 \rightarrow A$
$01 \rightarrow C$
$10 \rightarrow G$
$11 \rightarrow T$

$00 \rightarrow A$
$01 \rightarrow C$
$10 \rightarrow G$
$11 \rightarrow T$

$00 \rightarrow A$
$01 \rightarrow C$
$10 \rightarrow G$
$11 \rightarrow T$

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

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

X_1	X_2	...	X_{N-1}	X_N

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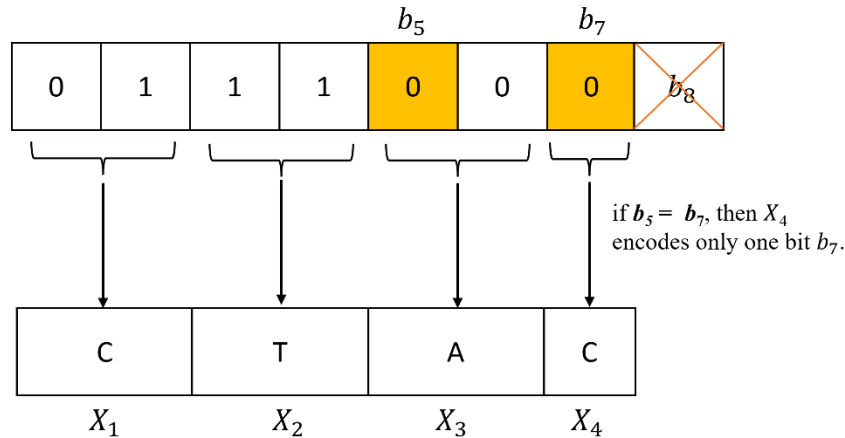
Example of a dynamic encoding

Homopolymer length $N = 4$

Case 1 : The last base X_4 encodes only one bit b_7.

if $b_5 = b_7$, then X_4 encodes only one bit b_7.

Bits	Bases
00	A
01	C
10	G
11	T

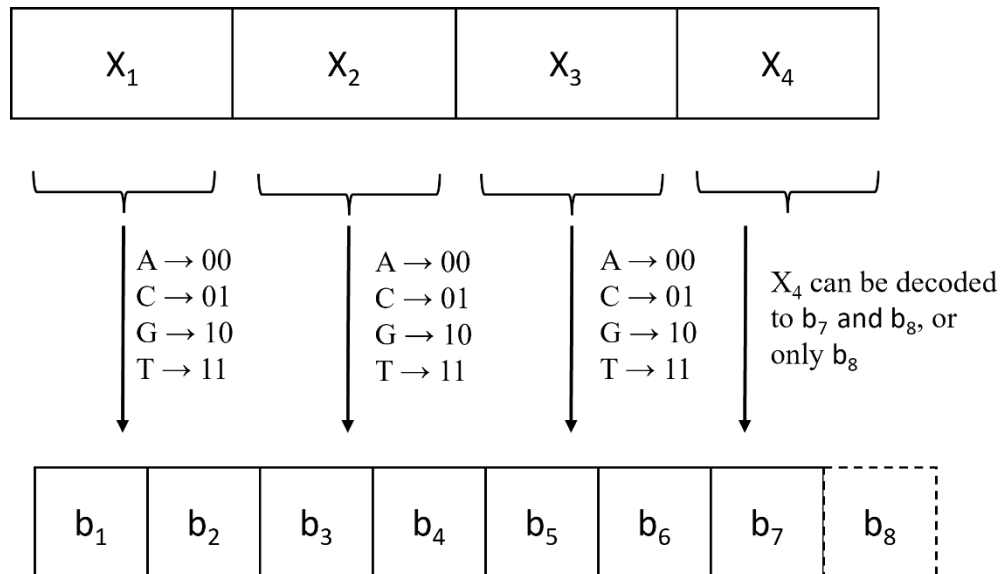*Case 2* : The last base X_4 encodes two bits b_7 and b_8

if $b_5 \neq b_7$, then X_4 encodes two bits.

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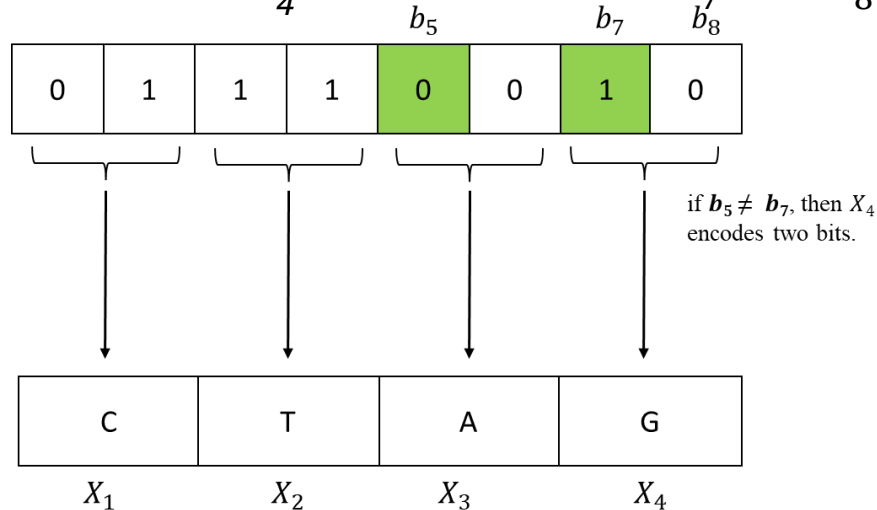
Informed dynamic encoding – the decoding step

Decoding of a message *M'*

► *Input:* Quaternary message *M'*, by blocks of *N=4* bases
► *Output:* binary message *M* of variable length

Decoding process

1. The first *N-1=3* bases are decoded with two bits each
2. The last base is decoded as follows:
   - If X_3 and X_4 are bases **encoding** the **same first bit** (A and C, G and T) ➔ X_4 encodes only one bit.
   - If X_3 and X_4 **encode** a **different first bit** ➔ X_4 encodes two bits.

X_1	X_2	X_3	X_4

$A \to 00$	$A \to 00$	$A \to 00$	X_4 can be decoded
$C \to 01$	$C \to 01$	$C \to 01$	to b_7 and b_8, or
$G \to 10$	$G \to 10$	$G \to 10$	only b_8
$T \to 11$	$T \to 11$	$T \to 11$	

b_1	b_2	b_3	b_4	b_5	b_6	b_7	b_8

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Gestion of homopolymers in the error-correcting code (ECC)

Addition of a module after the error-correcting code (ECC) :

▶ Adds a base of redundancy after every block of $N-1$=3 bases

▶ The added base X'_1 is always different from X_3
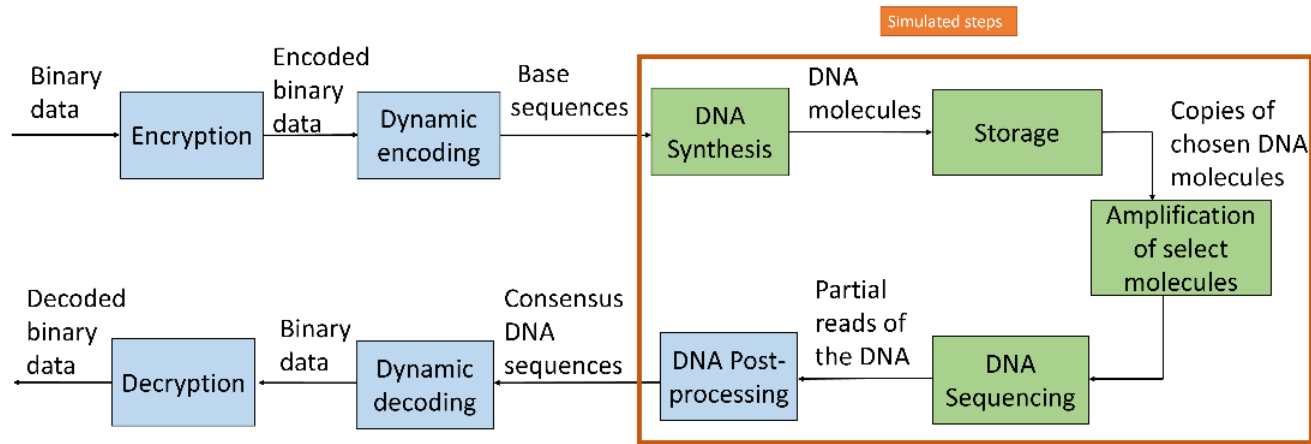
▶ Circular code with a dictionary

X_1	X_2	X_3	X_4	X_5	X_6

X_1	X_2	X_3	X'_1	X_4	X_5	X_6	X'_2
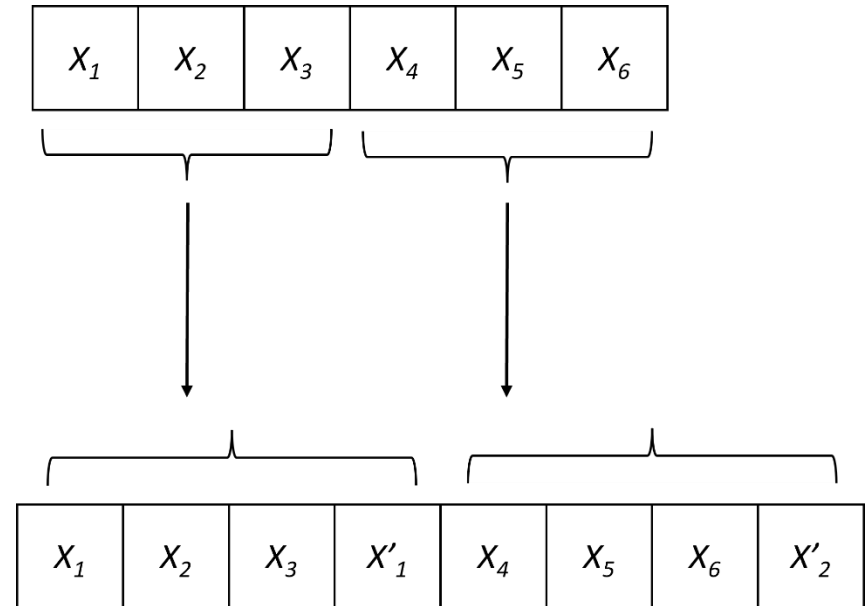
EXPERIMENTAL RESULTS

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Simulator and encoded data


DNA data storage chain with simulated biological steps

► Simulator of the biological processes proposed in [HDCCL21]

► Takes as input a DNA sequence S encapsulated by primers and the required number Z of reads of S by a nanopore sequencing machine.

► Outputs a consensus sequence with a post-processing algorithm [Lav21] from N partial reads of the DNA sequences.

Conducted experiments

► Encryption parameters: AES-256
  - Key size of 256 bits
  - Block size of 128 bits (padding if input does not conform)
  - AES in cipher block chaining mode (CBC) mode

► LDPC code (k, 2k) = (500,1000)

► Maximum homopolymer length N=4

► Input binary data from 256 to 6144 bits

► Tests on black-and-white images
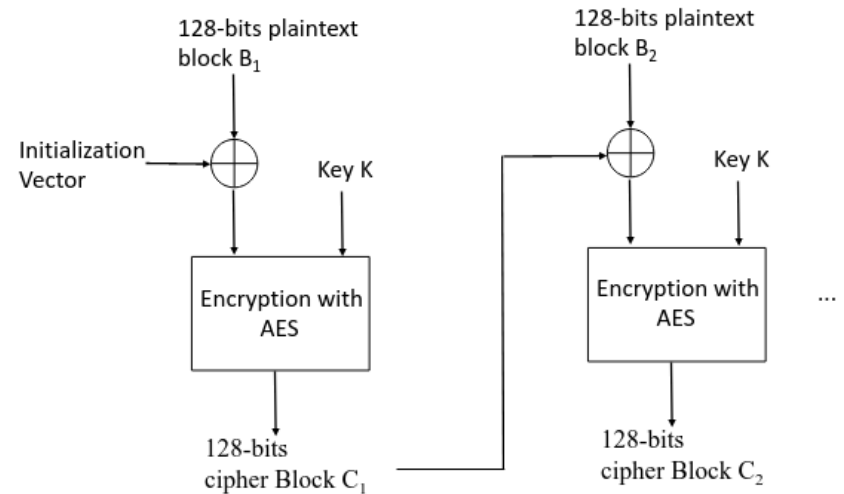
Experimental results

- ➢ **Information rate –** rate of bits encoded in a base
  - ➢ 1,875 bits per base (*bpb*) for *N*=4 on data, and 1,833 bpb for *N*=3
  - ➢ Using the LDPC code, Information rate = 0,937 *bpb*
  - ➢ Compared to [GHSD20]: 1,77 *bpb* on data for *N*=3 and 1,18 (*bpb*) by applying turbocode ECC, but tested with other synthesis/sequencing technologies and a fixed encoding dictionary
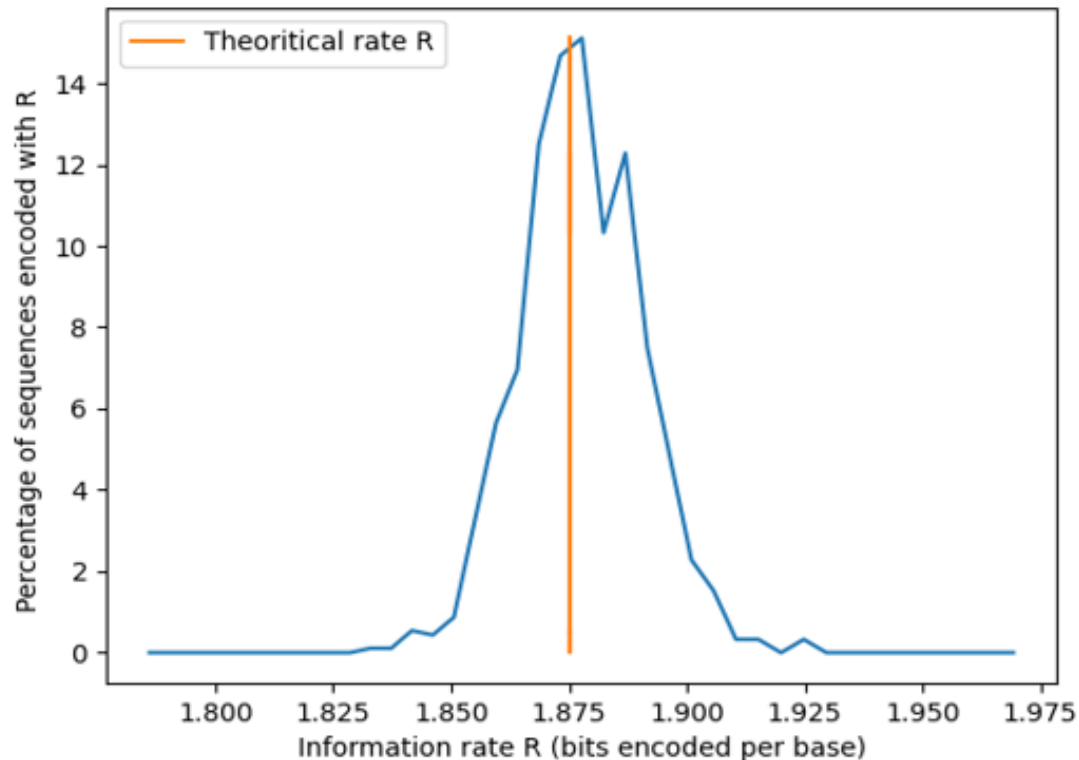
Information rate for 1000 sequences for an image encoded with N=4

Experimental results

- ➢ **Error rate**
  - ➢ Sequences of size 500-2000 have been successfully retrieved with 100 partial reads.

- ➢ **G-C content of 43-57%**
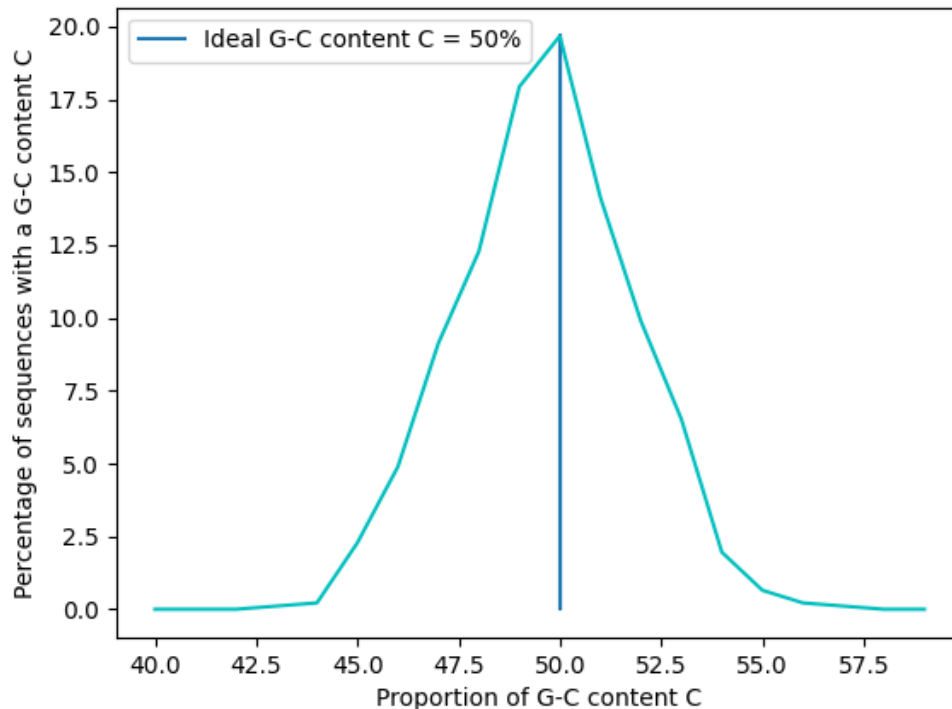
G-C content ratio for an image encoded with a maximal authorized length of homopolymers N=4

CONCLUSION

➢ We have proposed a dynamic encoding process that :

  ➢ Takes into account biological and indexing constraints

  ➢ Offers confidentiality control by encrypting data

  ➢ Uses a flexible encoding algorithm adaptable to the maximum length of homopolymers

  ➢ Trade-off between information rate and maximum homopolymer length

  ➢ Increases information rate up to 1,875 bpb on the data part

➢ Our proposal is independent from the encryption algorithm

➢ Future work will focus on how to increase the data rate even for the error correction codes

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