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# Secure data storage into DNA molecules compliant with biological constraints: Ensuring the confidentiality of data stored into DNA molecules

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# Secure data storage into DNA molecules compliant with biological constraints

## Ensuring the confidentiality of data stored into DNA molecules

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### Projet

dnarXiv



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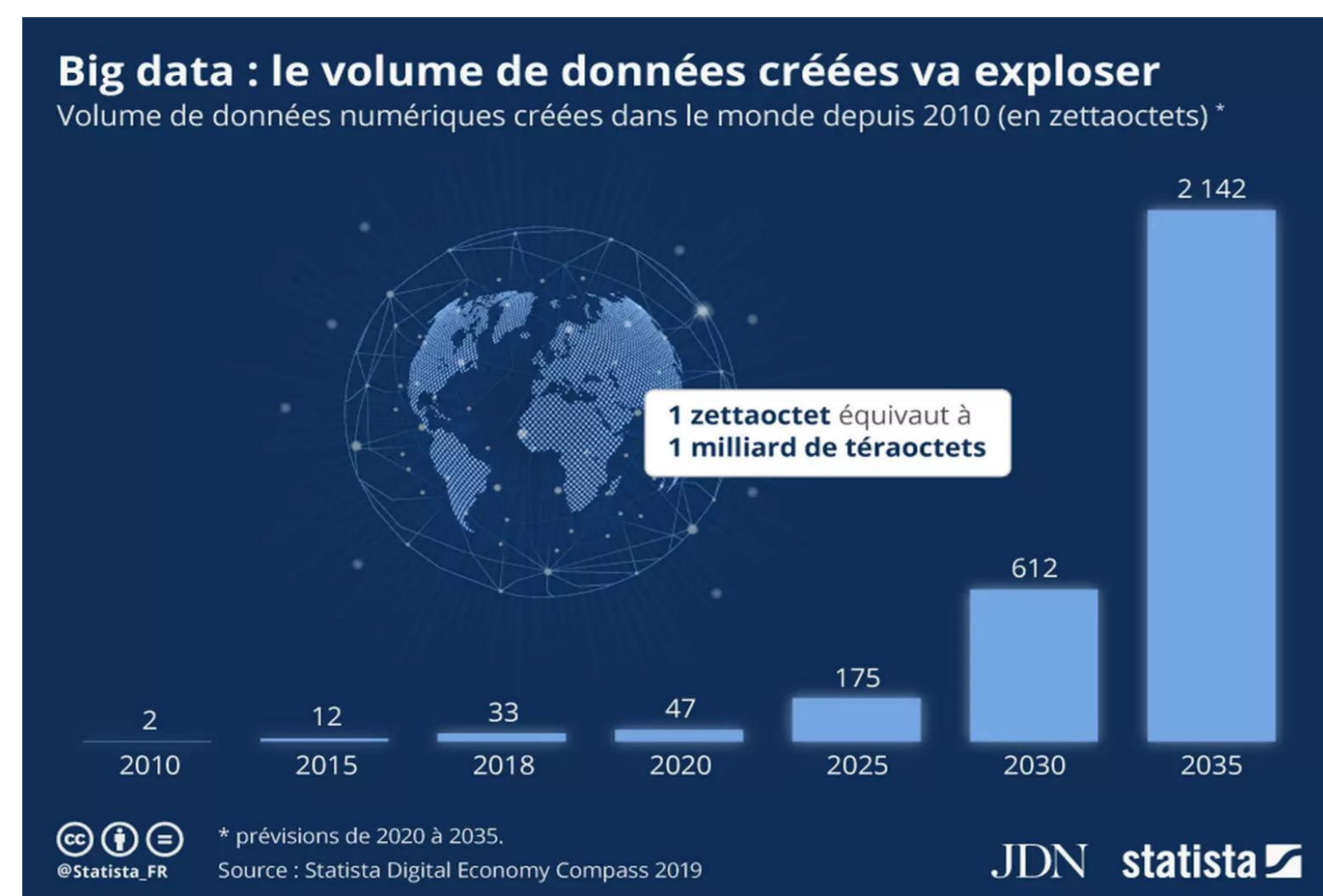
Lab-STICC

### References

[1] Rydning, D. R. J. G. J. (2018). The digitization of the world from edge to core. Framingham: International Data Corporation, 16.

[2] De Silva, P. Y., & Ganegoda, G. U. (2016). New trends of digital data storage in DNA. BioMed research international, 2016.

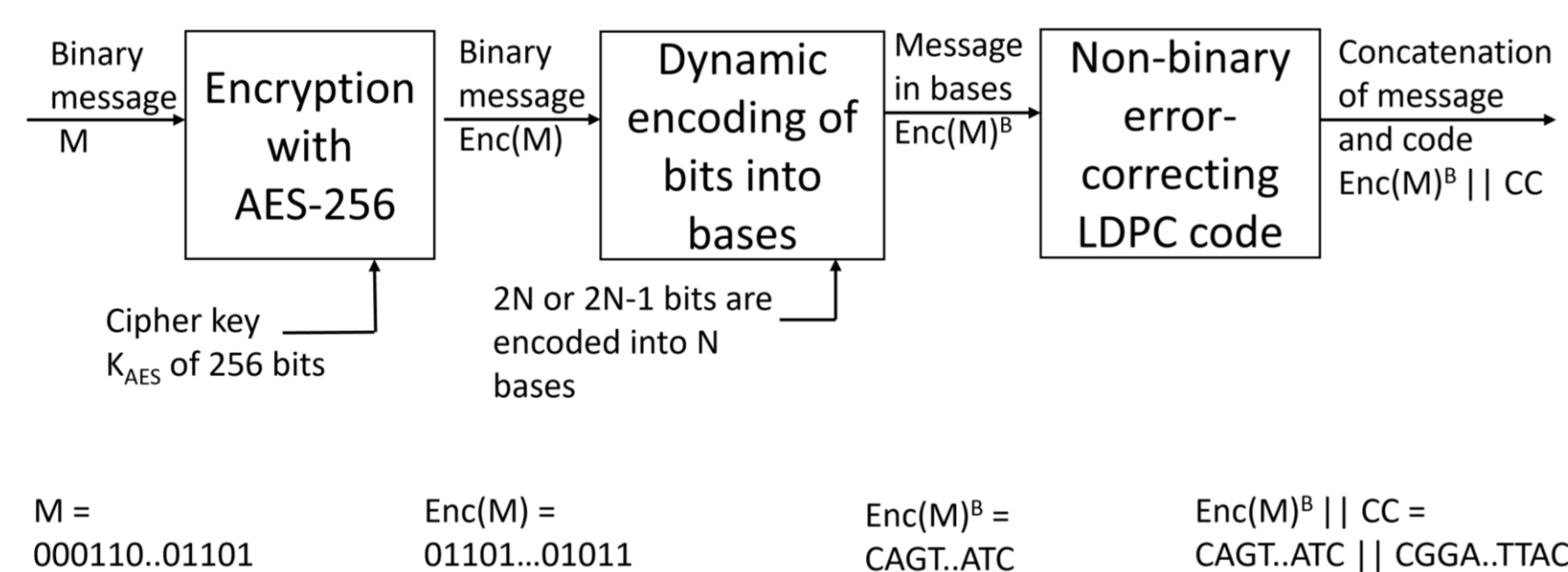
[3] Hamoum, B., Dupraz, E., Conde-Canencia, L., & Lavenier, D. (2021, August). Channel Model with Memory for DNA Data Storage with Nanopore Sequencing. In 2021 11th International Symposium on Topics in Coding (ISTC) (pp. 1-5). IEEE.



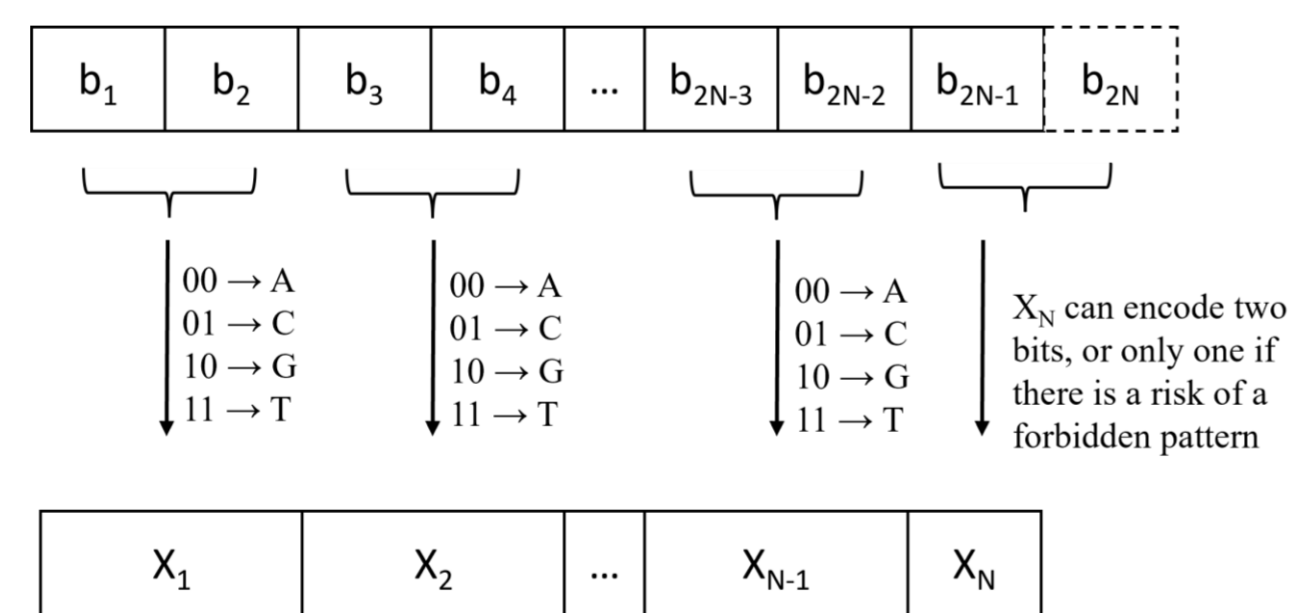
Volume of data created or replicated in the world, projection for 2020 to 2035 - Source : Statista

## DNA data storage - A new storage medium

- **Principle** – [WRITING] Encode binary data into 4-base sequences following the DNA structure, transfer this data into synthetic DNA molecules. [READING] Amplify encoded sequences of interest and get several reads of them with a sequencing device. Reads are then processed and decoded back to binary data
- **Constraints** – i) Biological DNA synthesis and sequencing are imperfect and introduce errors. ii) devices have structural DNA requirements when generating 4-base sequences
- **Vulnerabilities** – This chain is notably vulnerable to: theft or cloning of molecules; spying attacks on the sequencing or synthesis devices; DDoS attack by adding fake DNA sequence to confuse sequencing



Encoding solution to ensure data confidentiality in the entire DNA data storage channel



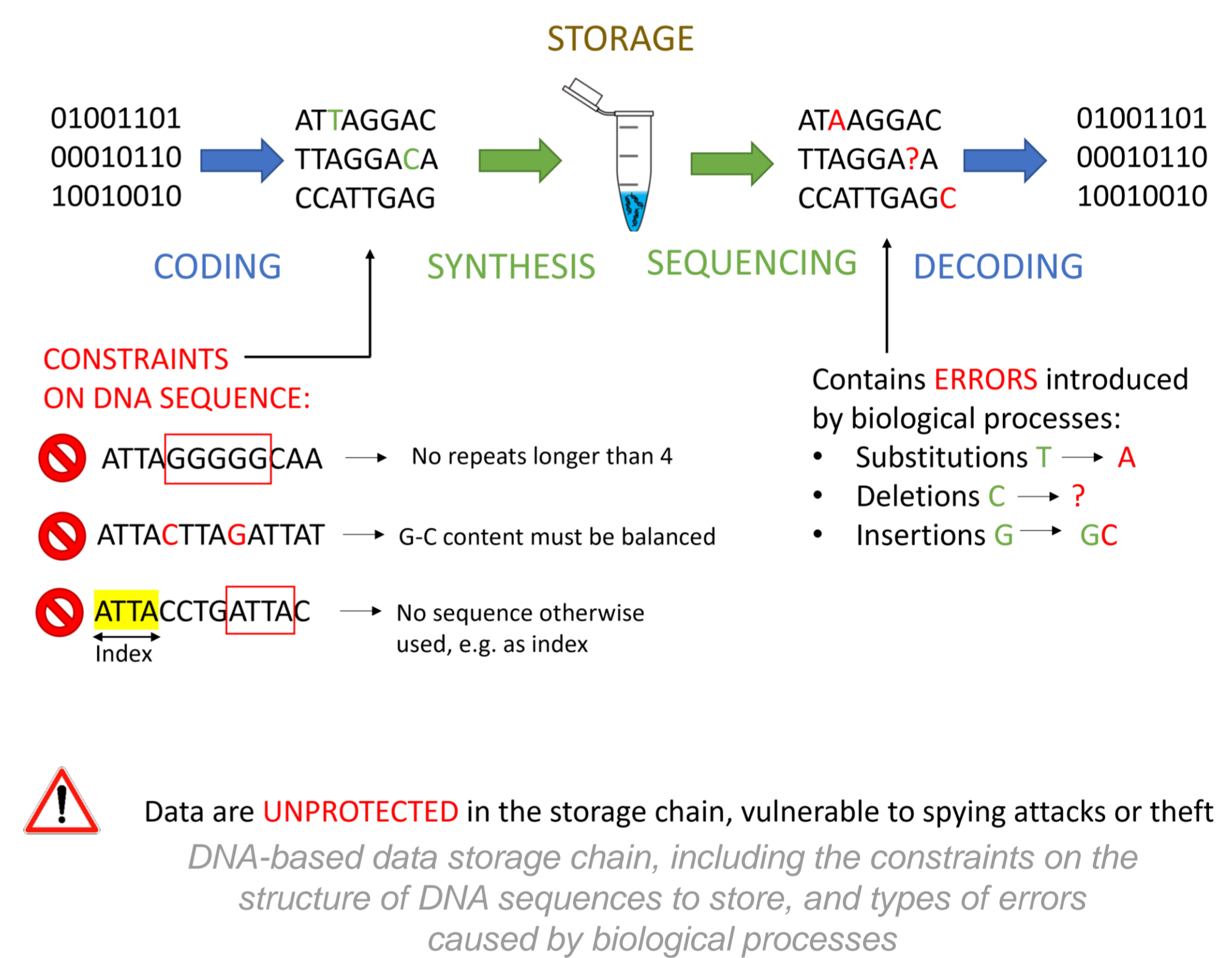
Dynamic information encoding into bases. In a block of N bases, each base  $X_i$  encodes two bits:  $b_{2i-1}$  and  $b_{2i}$ , except  $X_N$ , which encodes either  $b_{2N-1}$  only, or  $b_{2N-1}$  and  $b_{2N}$

## Experimental results

- **Simulation** of the biological processes using the simulator from [3]
- **Results:** no homopolymers longer than  $N$ , G-C content of 43-57%, data recovery without errors. For  $N=4$ , information rate of 1,875 bits per base.

## Motivation - Considering the security of a promising storage medium

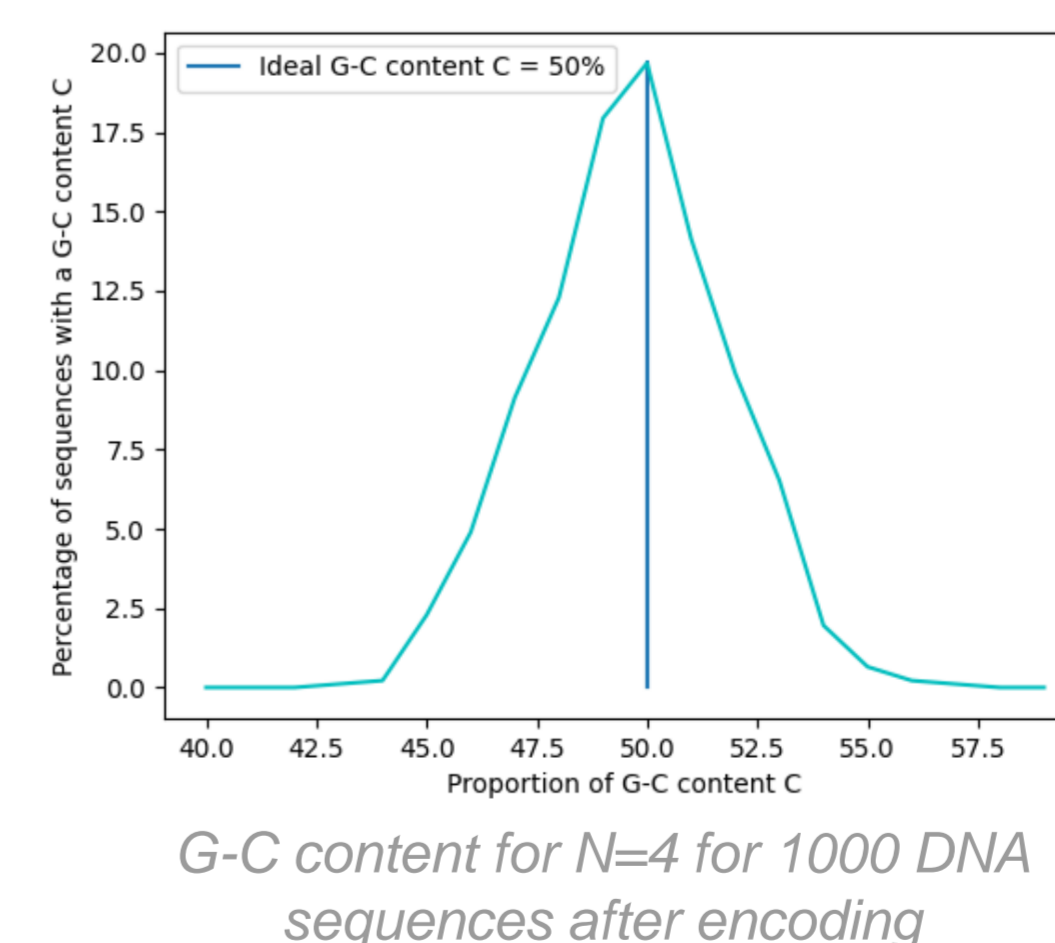
- **Context** – Actual storage technologies (flash memory, hard drives, magnetic tapes,..) are outpaced by the exponential rise of digital data production [1]
- **Advantages of DNA storage [2]** – Density of  $10^{21}$  bytes in one gram ( $10^6$  times more compact than hard disks), durability for centuries, energy cost close to zero (molecules kept at room temperature with no maintenance)
- **Motivation** – Introducing security to ensure the confidentiality of the data stored into DNA molecules



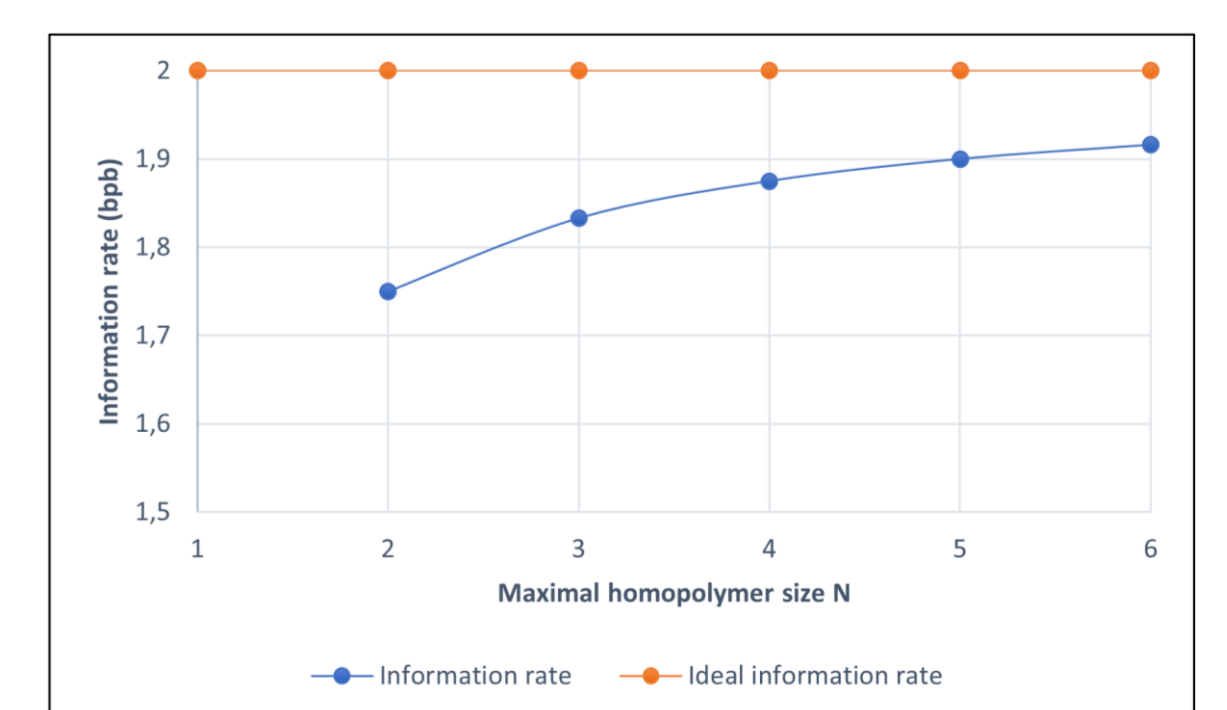
⚠ Data are UNPROTECTED in the storage chain, vulnerable to spying attacks or theft DNA-based data storage chain, including the constraints on the structure of DNA sequences to store, and types of errors caused by biological processes

## Dynamic encoding - a solution for confidentiality

- **Challenge** - Ensure confidentiality under biological constraints while approaching the ideal rate of 2 bits of information per base
- **Solution** – A three step coding process that includes encryption, dynamic data encoding and error-correction code
  - **Step 1:** Encryption with AES-256 to ensure confidentiality and to regulate the G-C base rate and homopolymers
  - **Step 2:** Dynamic encoding to manage unwanted base patterns; encoding based on the addition or not of one bit of data every  $N$  bases to avoid homopolymers longer than  $N$
  - **Step 3:** Non-binary LDPC error-correction code to correct any base substitutions, deletions or insertions



G-C content for  $N=4$  for 1000 DNA sequences after encoding



Information rate (bits per base) depending on  $N$ , the maximal homopolymer size

## Conclusion and future work

- **Confidentiality** in the entire storage chain that takes into account **biological constraints**
- Encoding solution **independent** from encryption algorithm and error-correction code, **adaptable** to the size of unwanted patterns
- Extend the approach to other synthesis and sequencing technologies

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