DNA-store: ADVANCED CODING SCHEMES FOR DNA-BASED DATA STORAGE USING NANOPORE SEQUENCING TECHNOLOGIES

IAS, Lab-STICC, UBS
- L. Conde-Canencia
- B. Hamoum

GenScale, INRIA
- D. Lavenier
- E. Roux

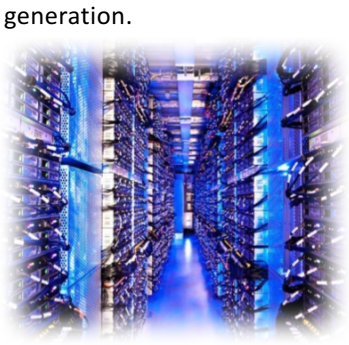
Introduction and objectives

Design of coding schemes that allow information to be efficiently stored on DNA molecules, and read back using very low cost sequencing devices based on nanopore technologies.

1. The first part of the project focused on developing codes adapted to the nanopore sequencing constraints.
2. Demonstrate the feasibility of the approach by
   (1) synthetizing DNA molecules encoded with the proposed coding schemes;
   (2) sequencing those DNA molecules on a MinION device;
   (3) correcting the output signal to retrieve the initial information..

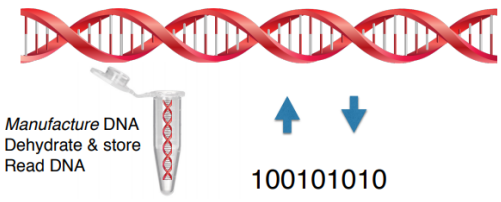
Motivation

The current data explosion era is bringing new challenges in data storage technologies and leading research to emerging fields.
The need to explore innovative solutions is now undeniable because the available data storage systems have grossly been outpaced by the ever-increasing data generation.



Microsoft Data Center, Chicago

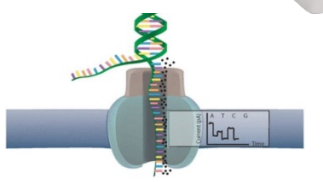
Principle and advantages

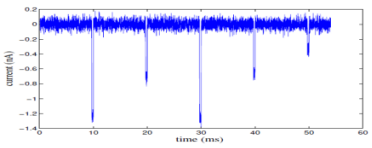


- 10^6 more compact than hard disks
- Capability for longevity > 100 years …
- Resistance to obsolescence
- Potential revolution in data centers

The MinION: a portable real-time device for DNA sequencing

- 100 g
- USB plug
- ~ 1000 $



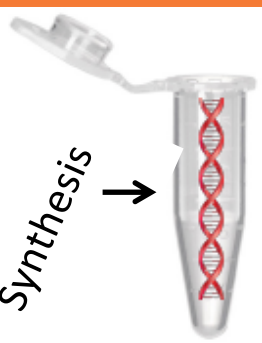


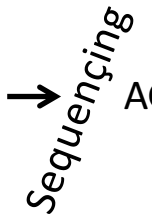
DNA-based data storage chain

writing

11011101 → AGCTATCA →

Oligonucleotide chemical synthesis

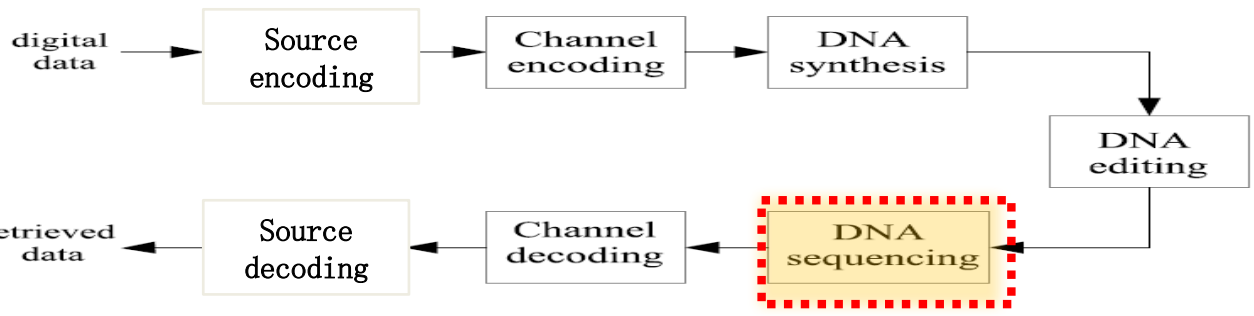




reading

AGCTATCA → 11011101

3rd generation sequencing: MinION



Source coding to avoid homopolymers and improve the MinION output signal

Synthesis and sequencing of real data sequences

Results: match rates and errors

- Simulation results obtained with deep learning tool: DeepSimulator
- Simulation vs. real synthesis and sequencing
- 3 types of errors: substitutions (or mismatches), insertions/deletions (*aka* gaps).
- 3 types of sequences:

"HP" sequence with homopolymers,
"NoHP" stands for the sequence without homopolymers
"Max" stands for the sequence without homopolymers and with maximized inter-*k*-mer distances (our proposed source coding)

- "NoHP" decrease error rates
- "Max" does not introduce gain

Conclusion and future work

We implemented a complete DNA-based data storage chain: we coded + synthesized + stored + retrieved the data. We analyzed error rates for 3 types of sequences to evaluate the effect of homopolymers and source coding.

This project was extremely enriching for the two partners. We have set the foundations for an interdisciplinary and fruitful collaboration. DNA-based data storage is a revolutionary technology but its success will only come by putting together the knowledge of bioinformatics, biology, information theory and coding.