INSTITUTO DE PESQUISAS TECNOLÓGICAS

COMUNICAÇÃO TÉCNICA

Nº 179057

Challenges of encoding digital data into DNA sequences and decording it back to digital

Andre Guilherme da Costa Martins

Palestra apresentada na disciplina de Biologia Molecular do Programa de Pós-graduação Multicêntrico em Bioquímica e Biologia Molecular, do Campus Centro-Oeste Dona Lindu-UFSJ

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Challenges of encoding digital data into DNA sequences and decoding it back to digital

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What is a CODEC?

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Storaged DNA molecules

DNA Synthesis

DNA Sequencing

Original Binary data

ATGCTAGCA
AGGCGTGCA
Encoded DNA

ATGCTAGCA
AGGCGTGCA
Sequenced DNA

Recovered Binary data

ENCODING

DECODING

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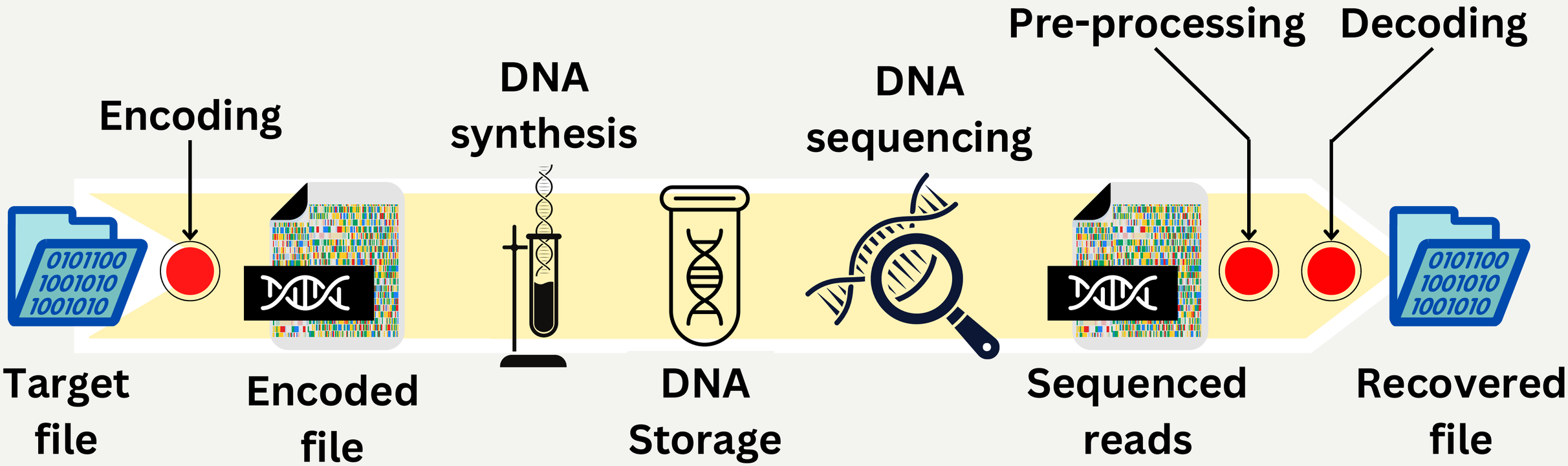
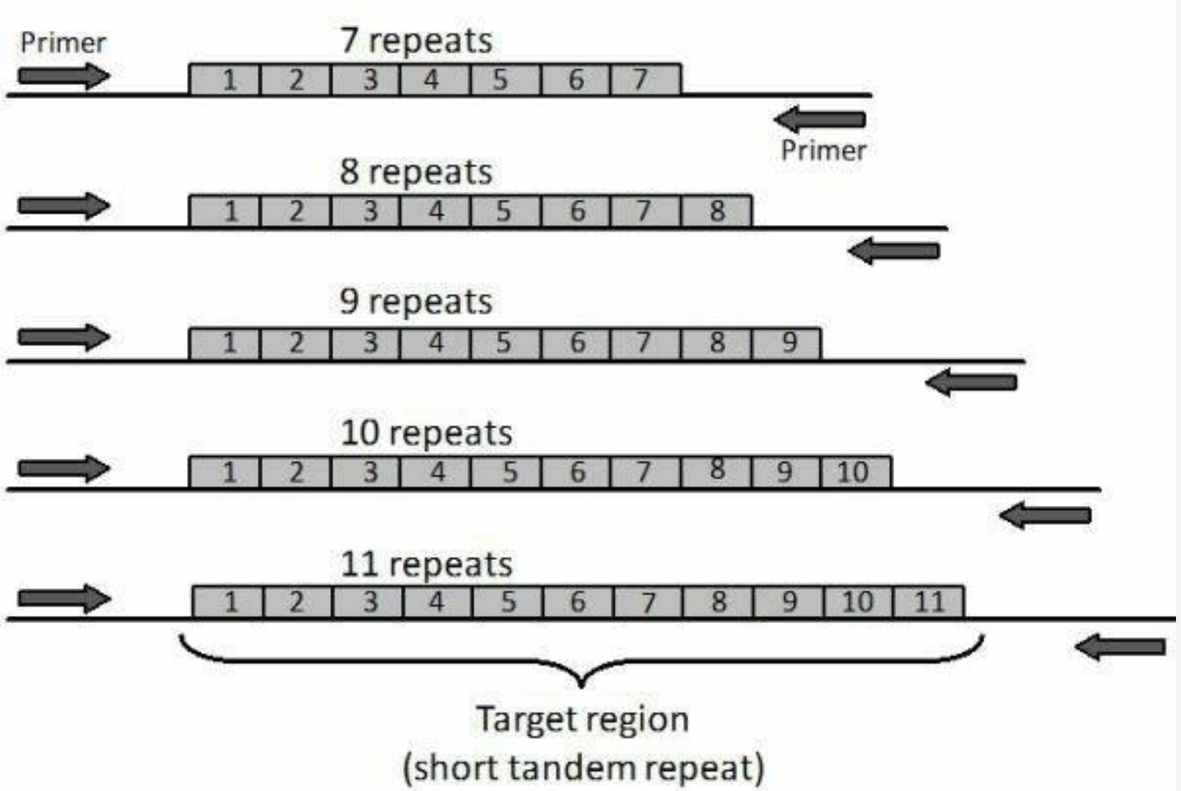
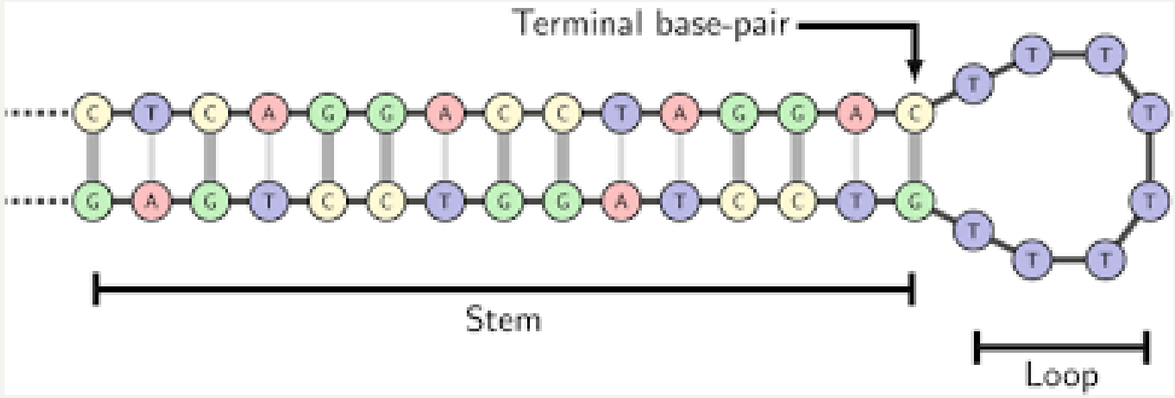
The workflow



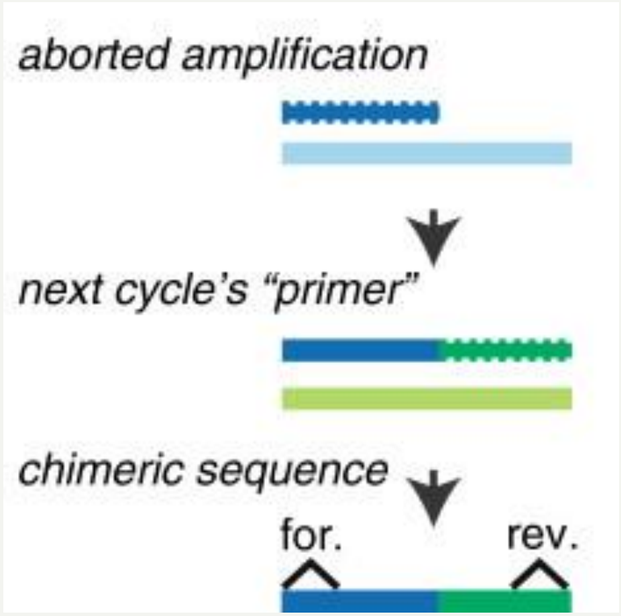
Challenges of encoding



Repetitive segments



DNA hairpins



Interspecific similarity

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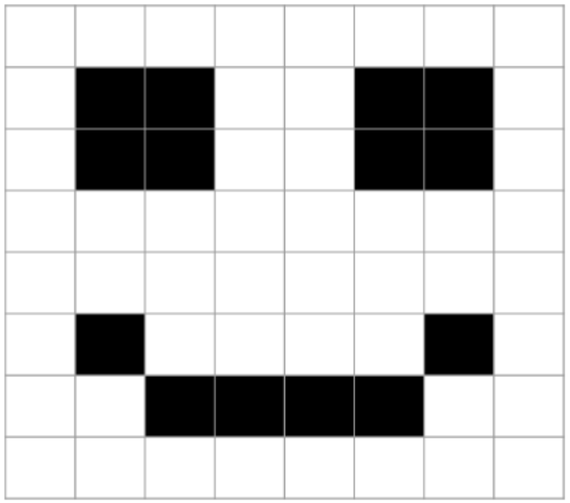
Challenges of encoding

IPT - Main gate

Bitmap image



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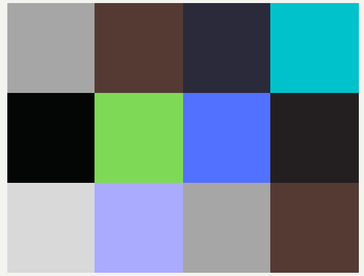
0	1	1	0	0	1	1	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0
0	0	1	1	1	1	0	0
0	0	0	0	0	0	0	0

High complexity regions



Low complexity regions

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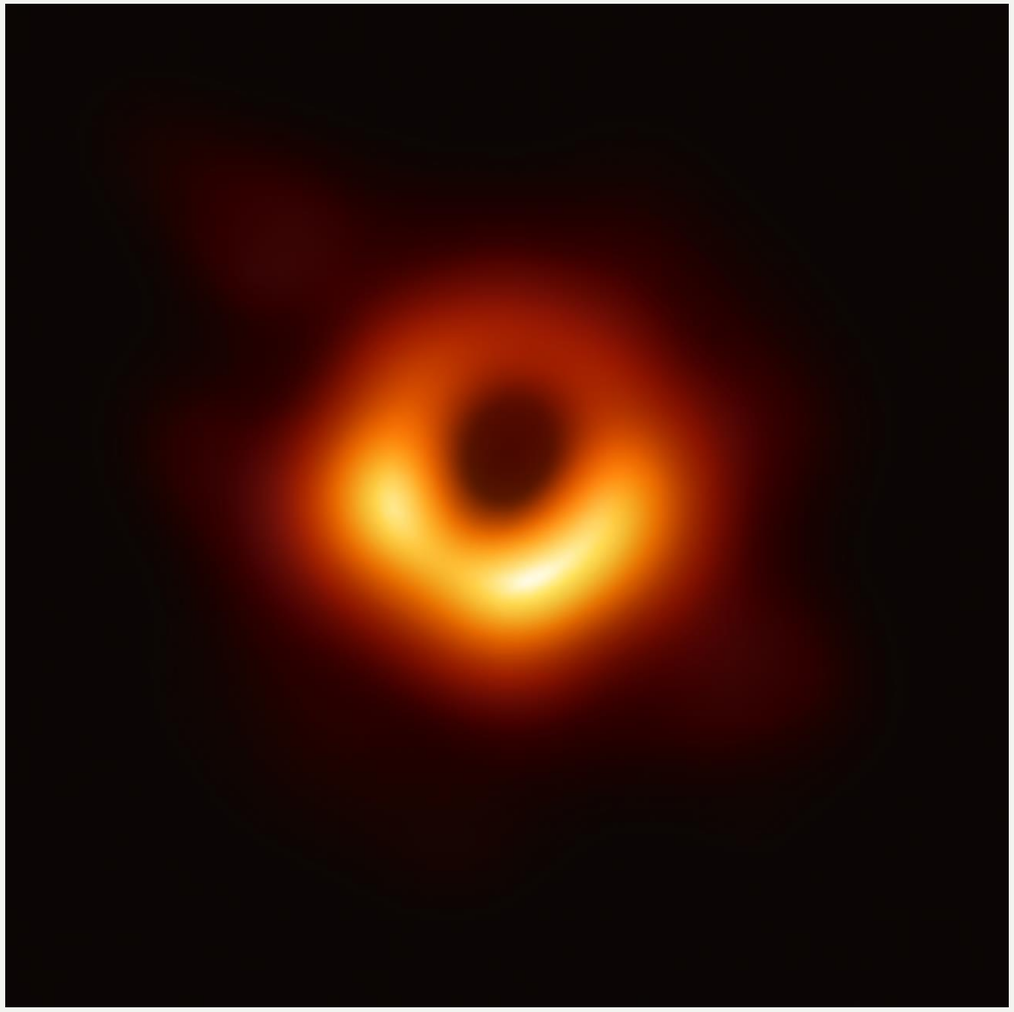
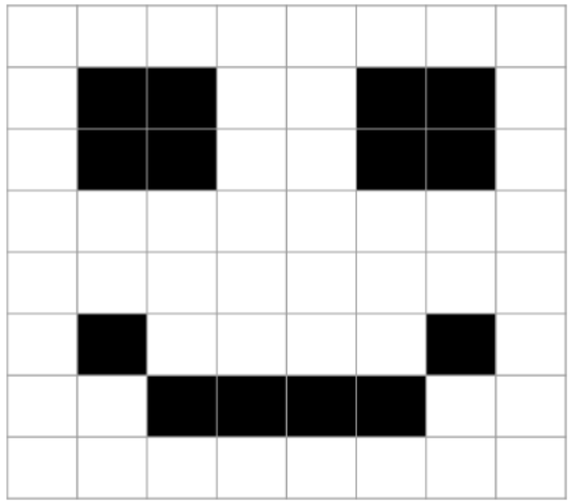
Challenges of encoding



M87* black hole, taken on 11 April 2017

Bitmap image



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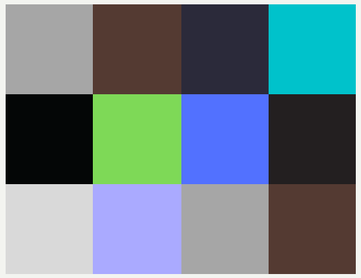
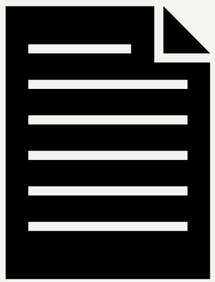
High complexity regions



Low complexity regions

Challenges of processing NGS reads

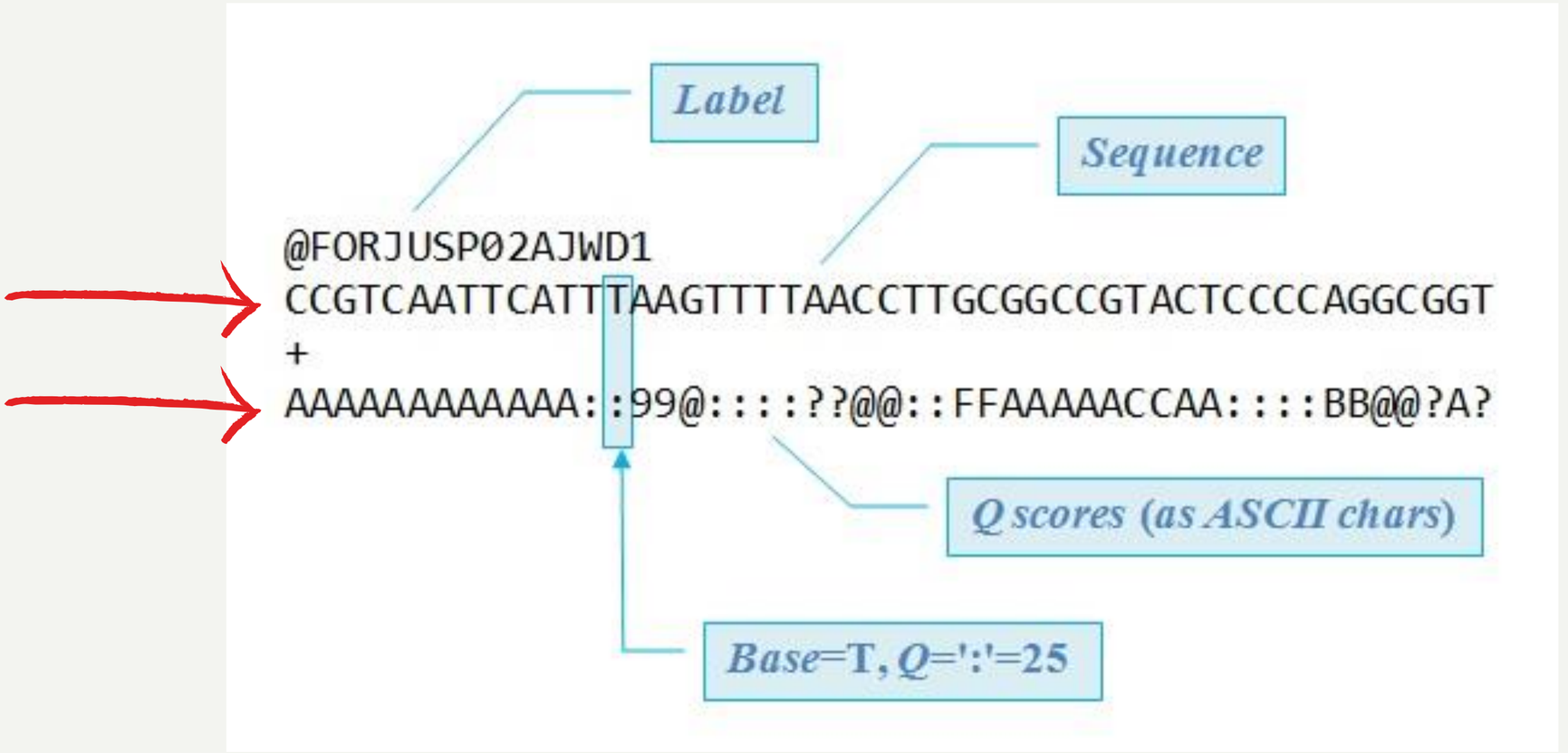
Fastq



DNA

~~Pasequence~~

quality



Challenges of processing NGS reads

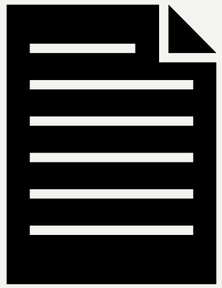
Analogy!

Encoding complexity

Fasta

Decoding complexity

Fastq



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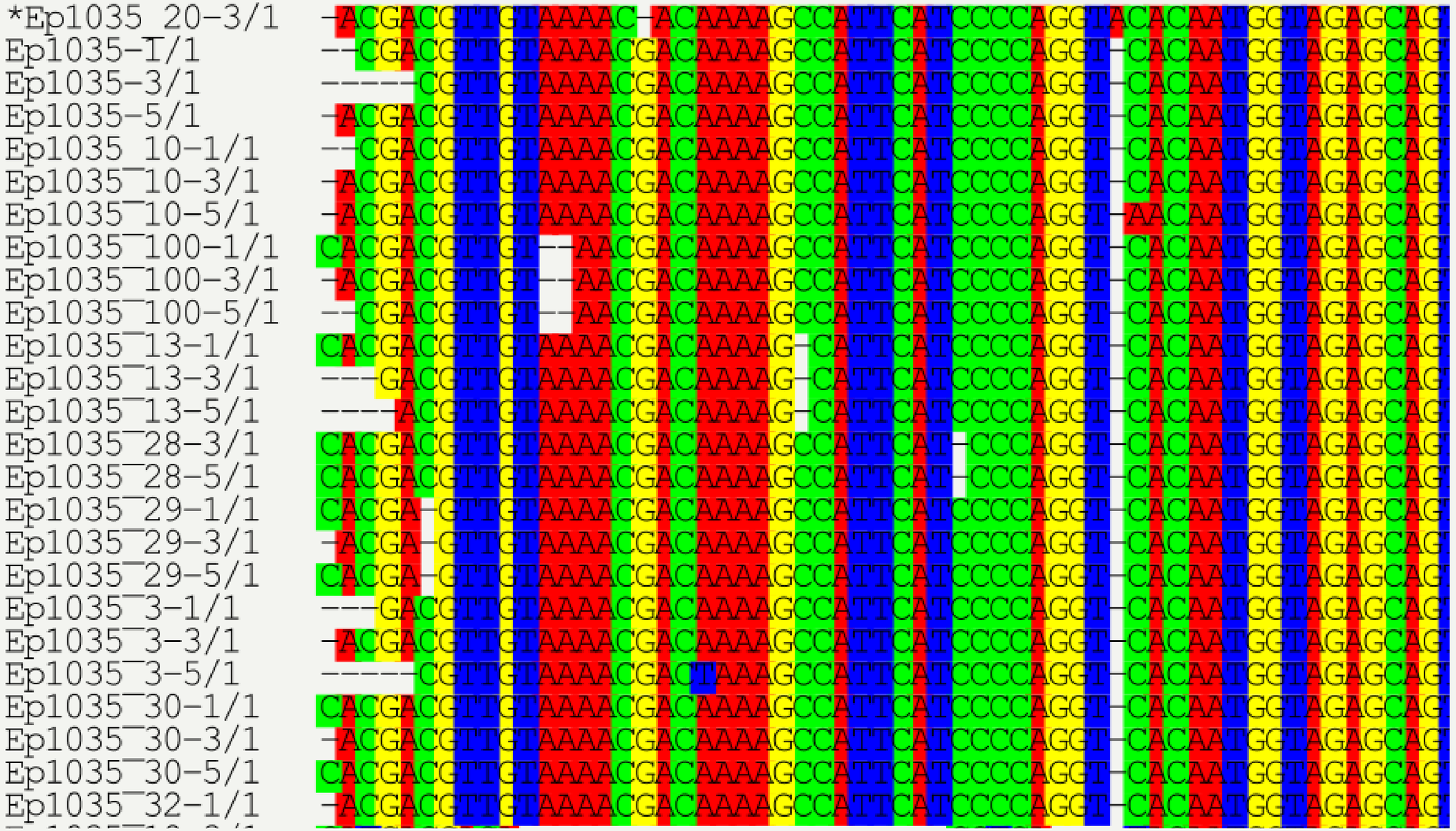
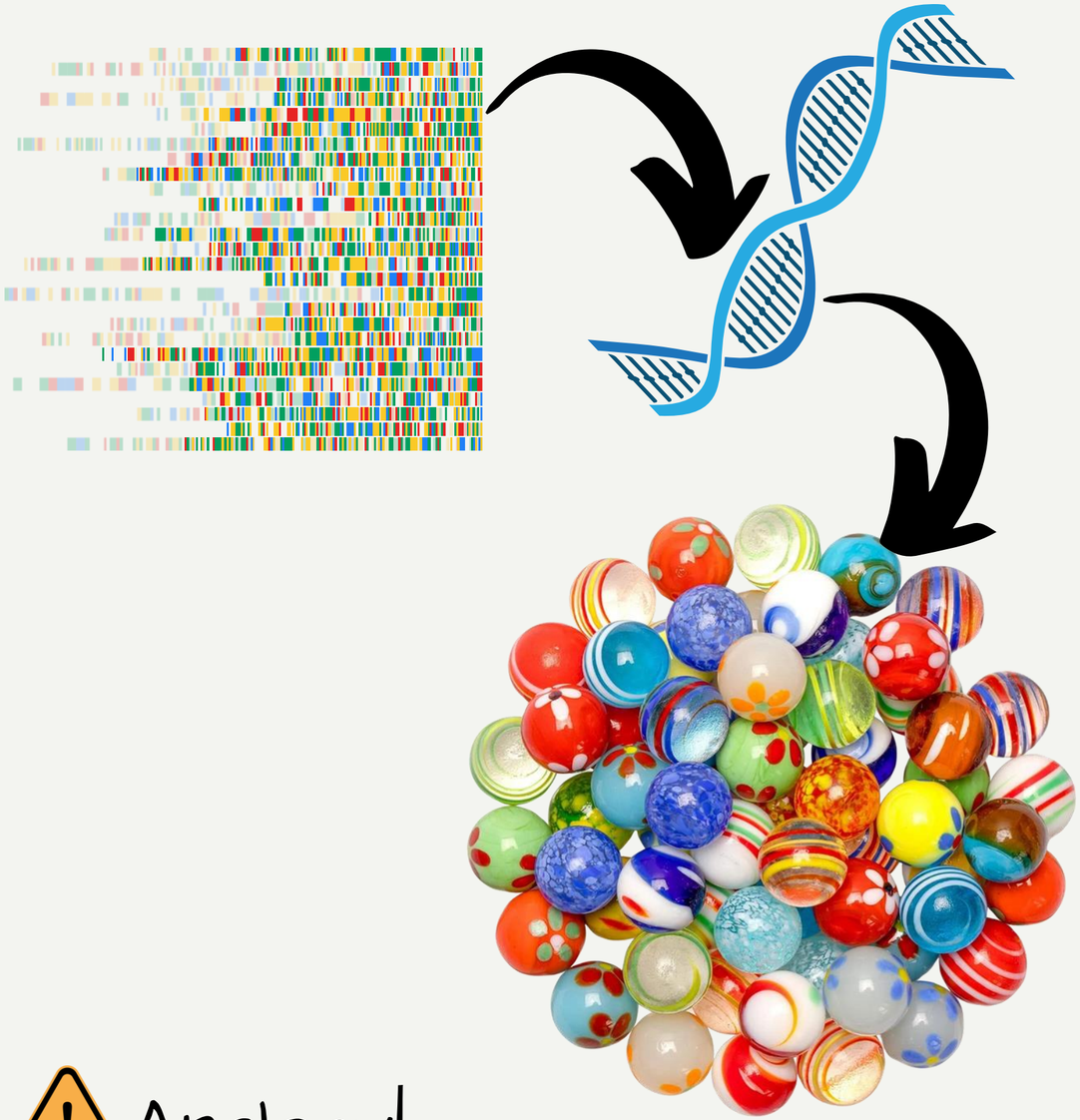
Challenges of processing NGS reads

Analogy!

Challenges of processing NGS reads

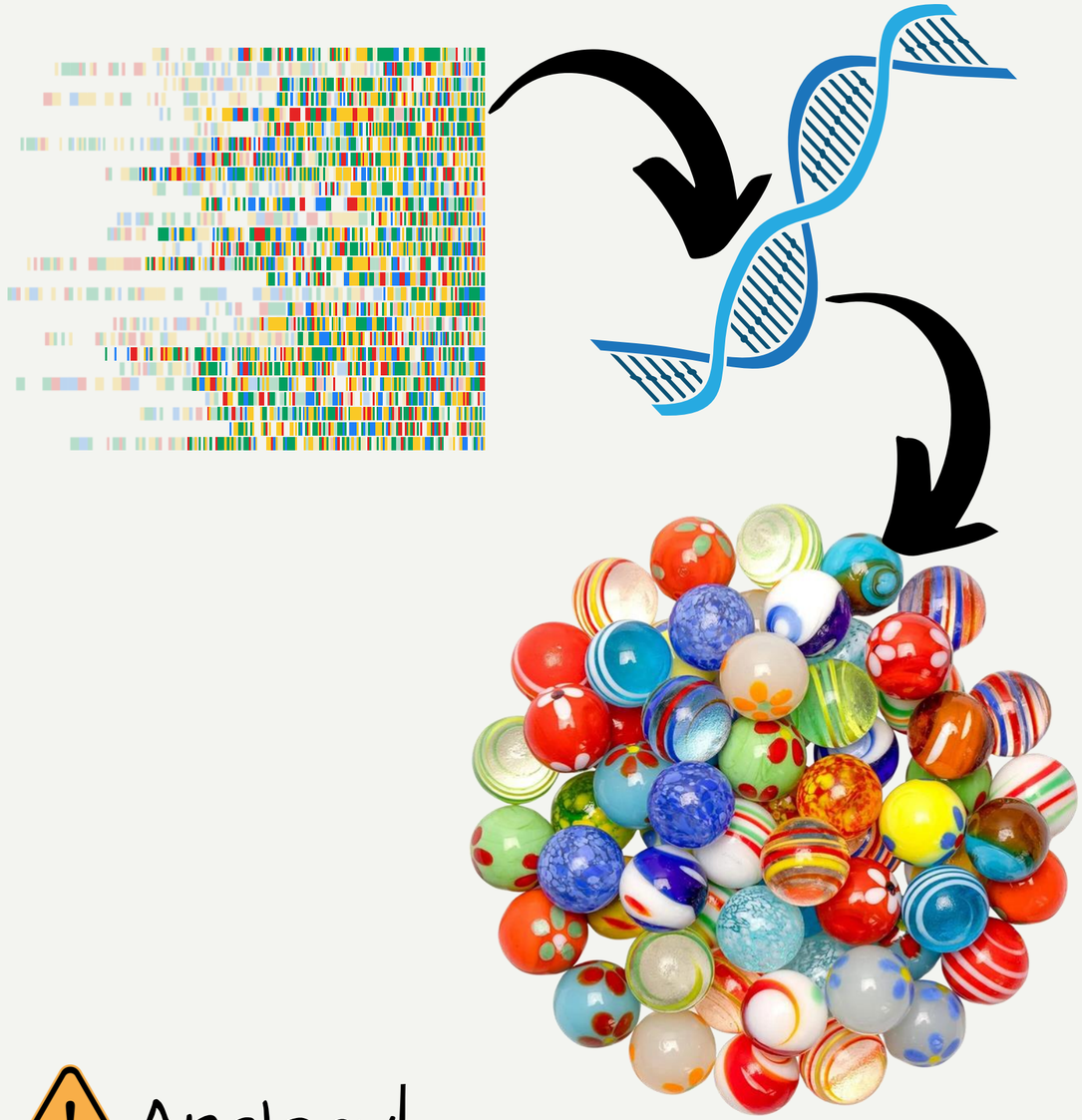


Challenges of decoding

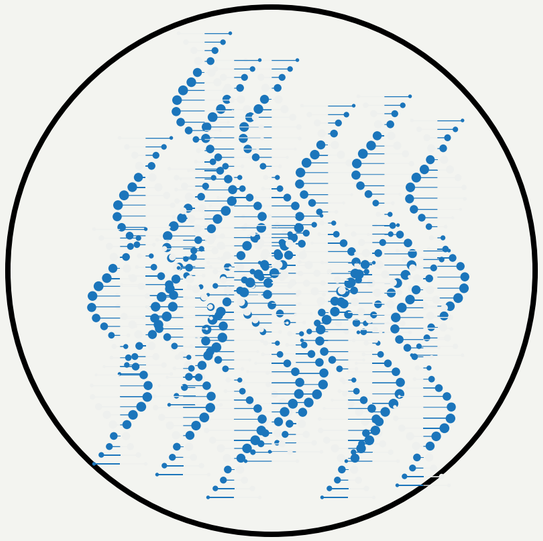


Analogy!

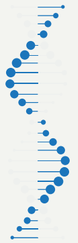
Challenges of decoding



Each DNA synthesis site



10^n copies of same ssDNA



PCR amplification

dsDNA

Analogy!

Challenges of decoding

Analogy!

Challenges of decoding

Library preparation for NGS

Illumina Nextseq 2000

Analogy!

Challenges of decoding

Expectations... :)

Challenges of decoding

Reality... :(

Developed tools

PROMETHEUS

apollo

artemis

chiron

hermes

hephaestus

gaia

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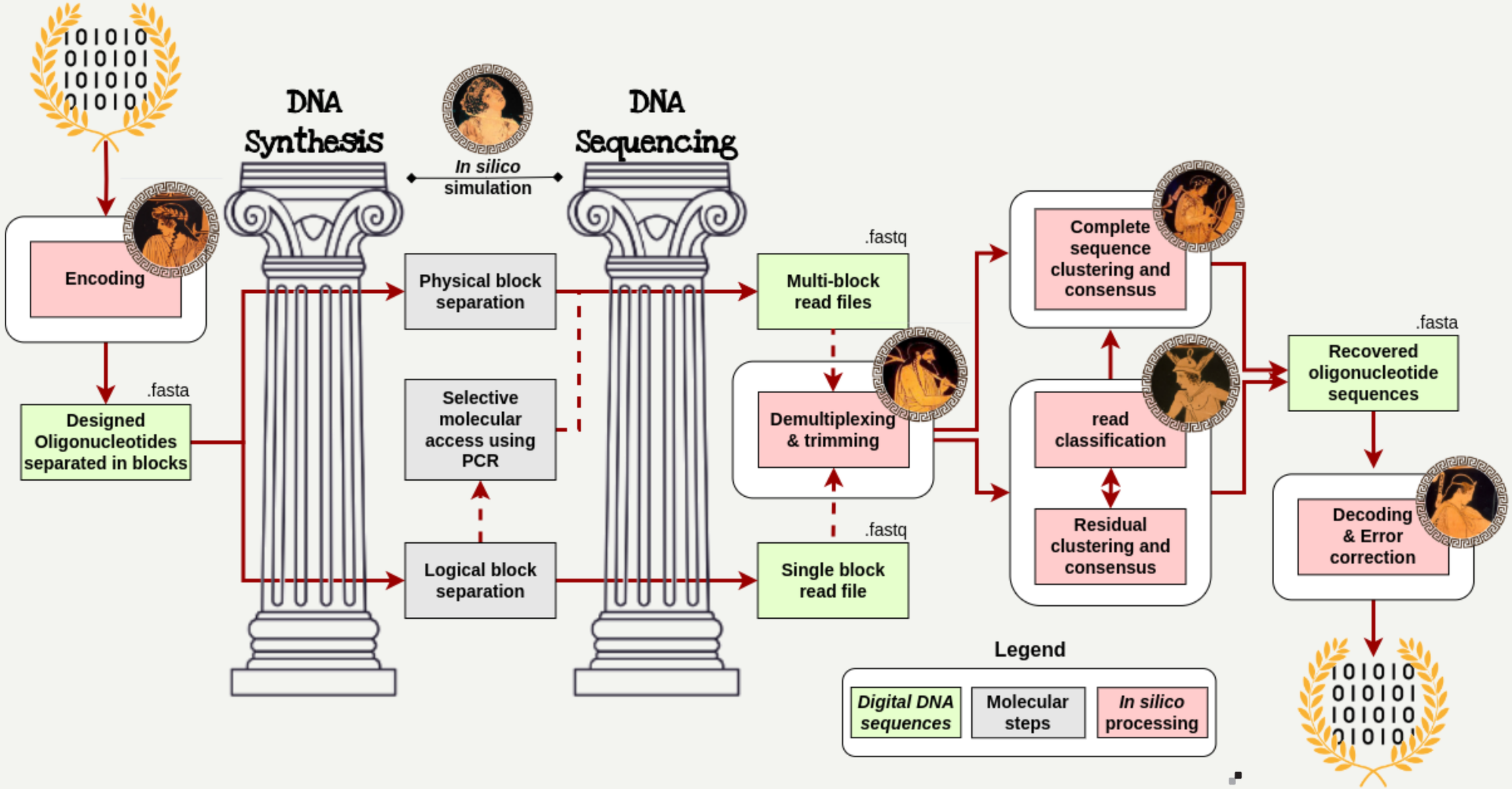
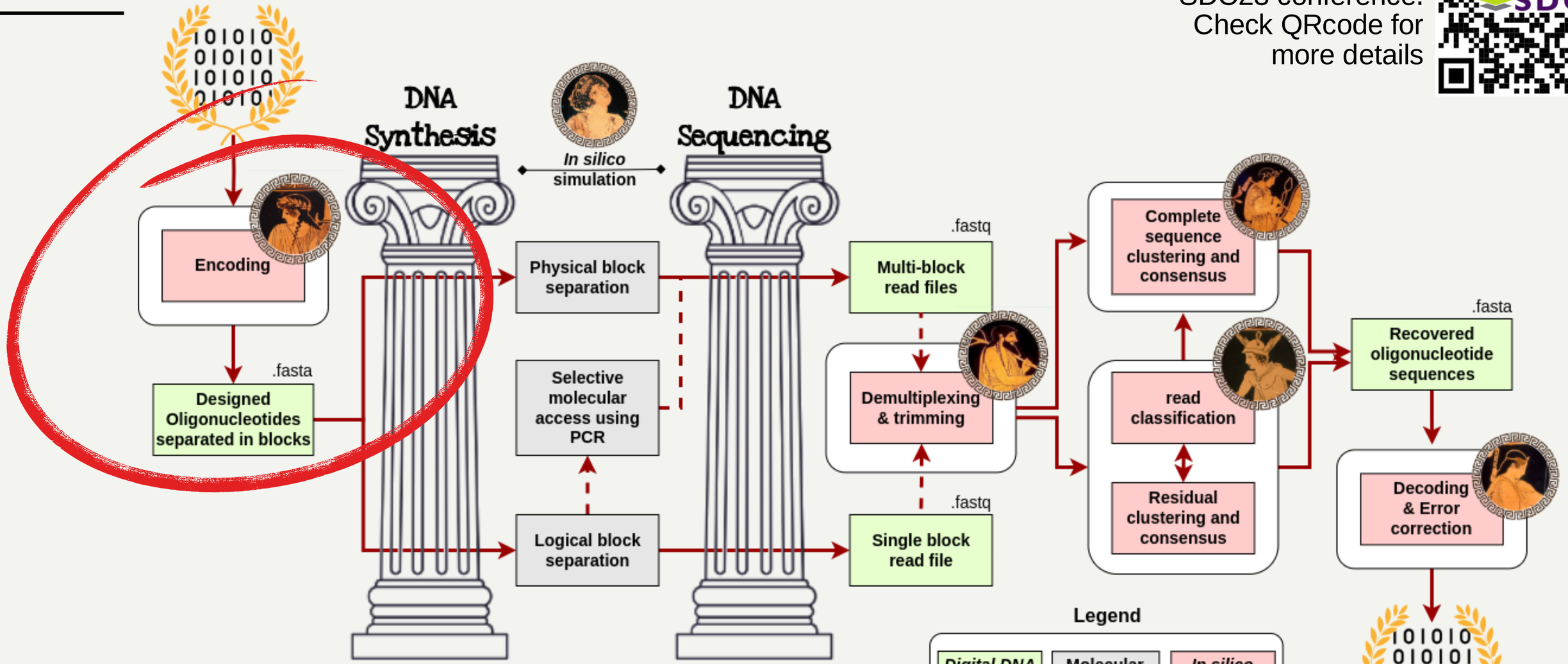
Lenovo™

DDS Workflow



DDS Workflow

We have presented all Pantheon DNA Gods at SDC23 conference. Check QRcode for more details



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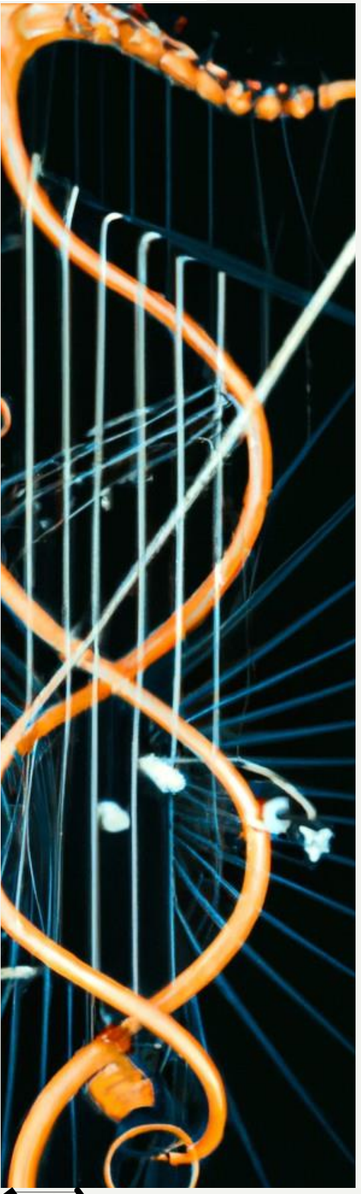
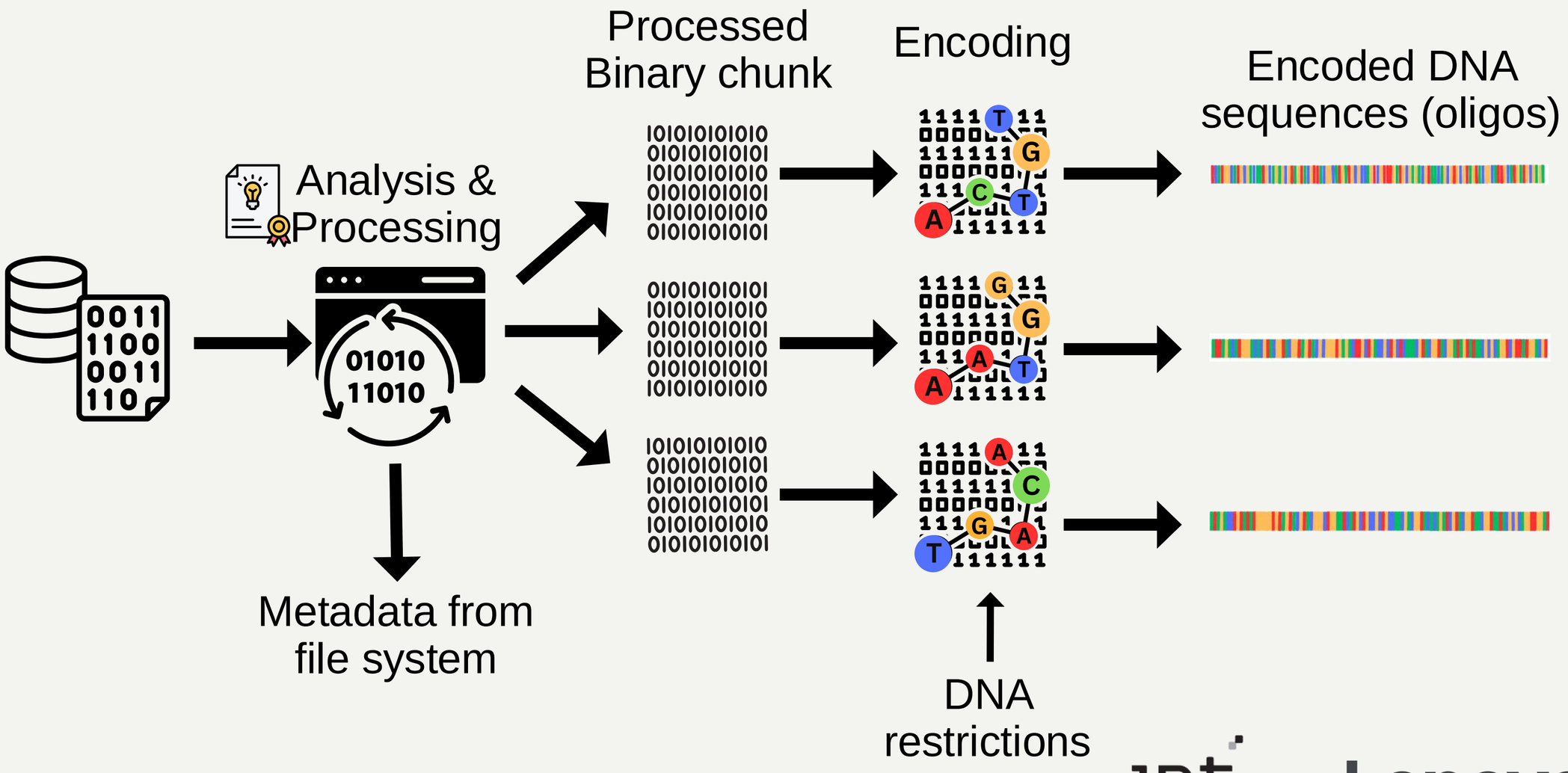
How data is organized into DNA?





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Oligonucleotide data structure

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Cytosine
Guanine
Adenine
Thymine

Analogy!

Floppy disk

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Data Block structure

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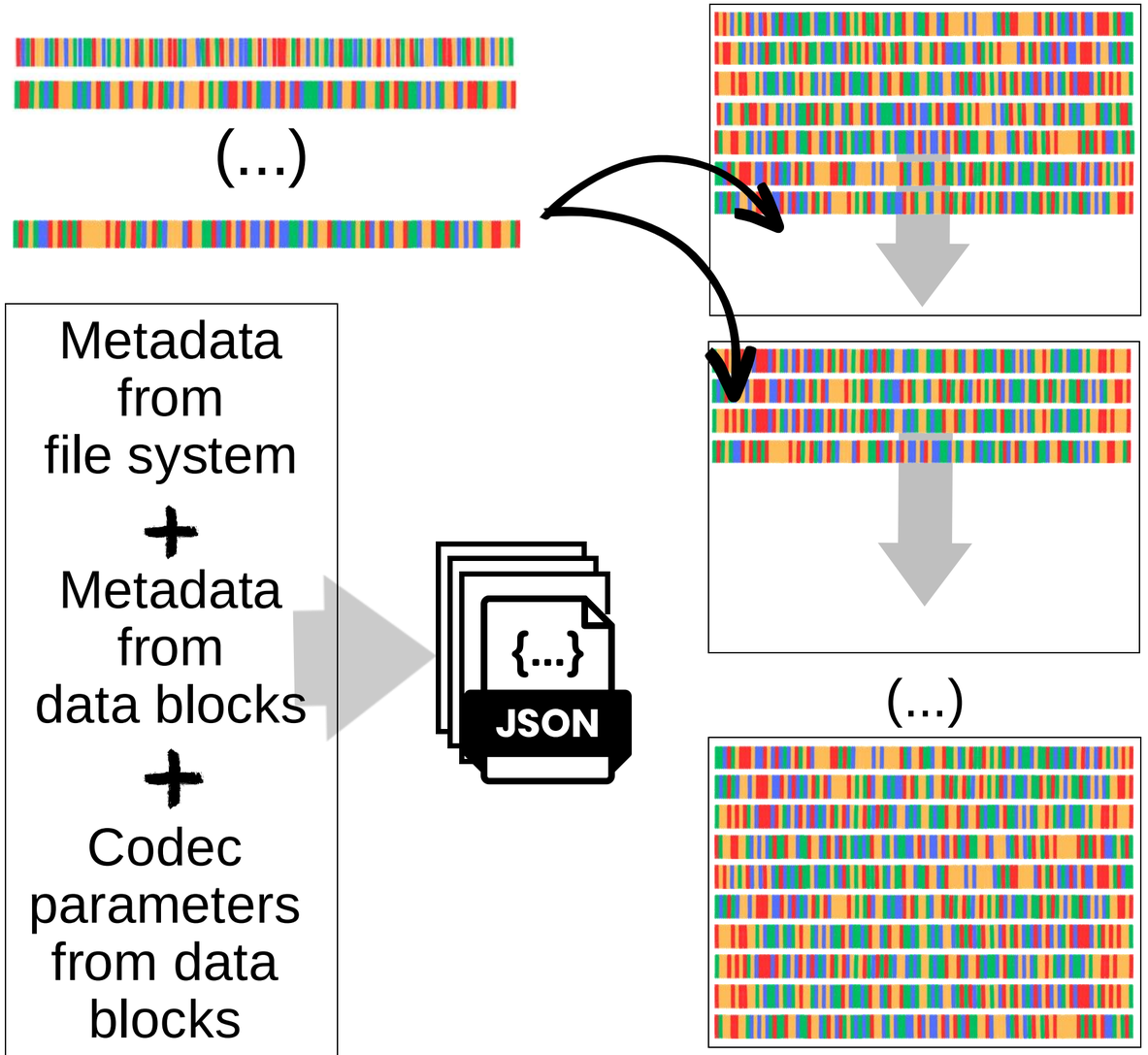

Apollo

Cytosine
Guanine
Adenine
Thymine

“Disk sectors“

Analogy!

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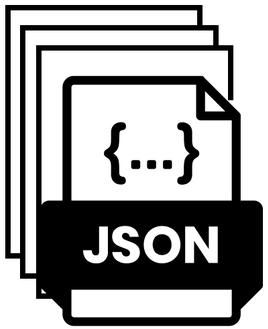
Data Block structure



Archive Metadata Block (AMB)

(...)

Data blocks

Outer ECC

Outer ECC

Outer ECC

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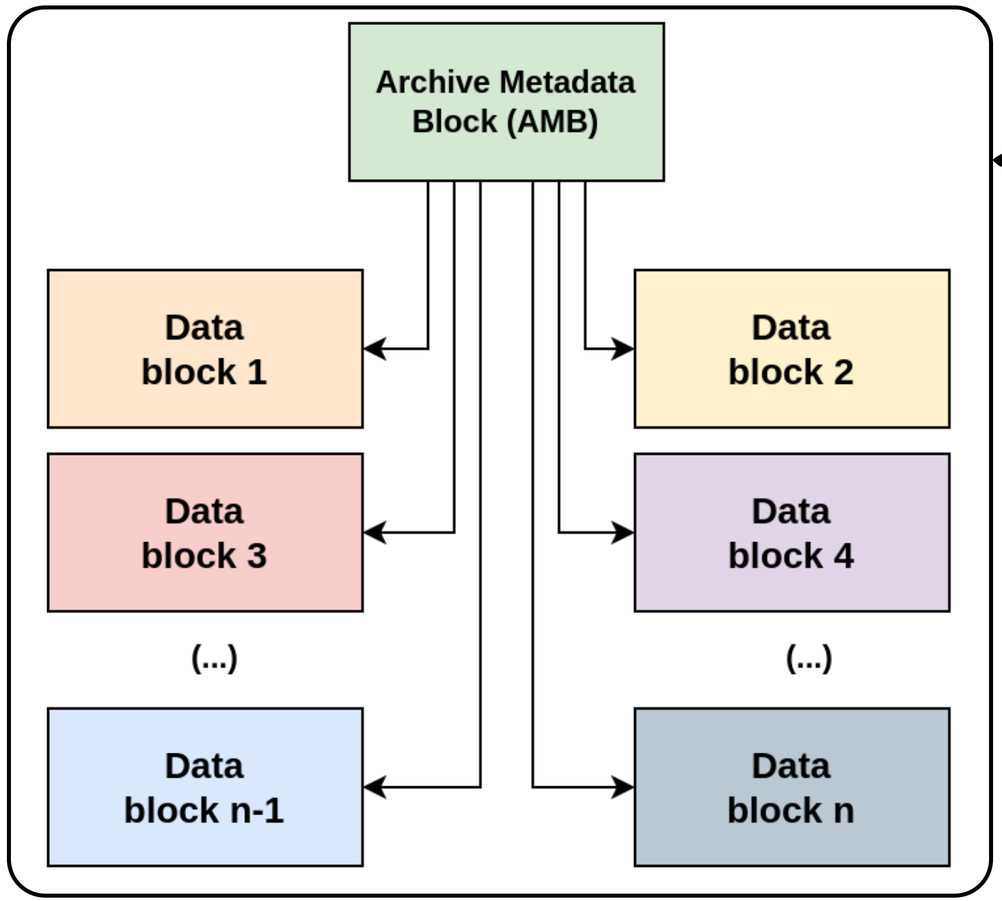
How data are organized into DNA?



Codec parameters.json
Directory tree.json
Files checksum.json
(...)

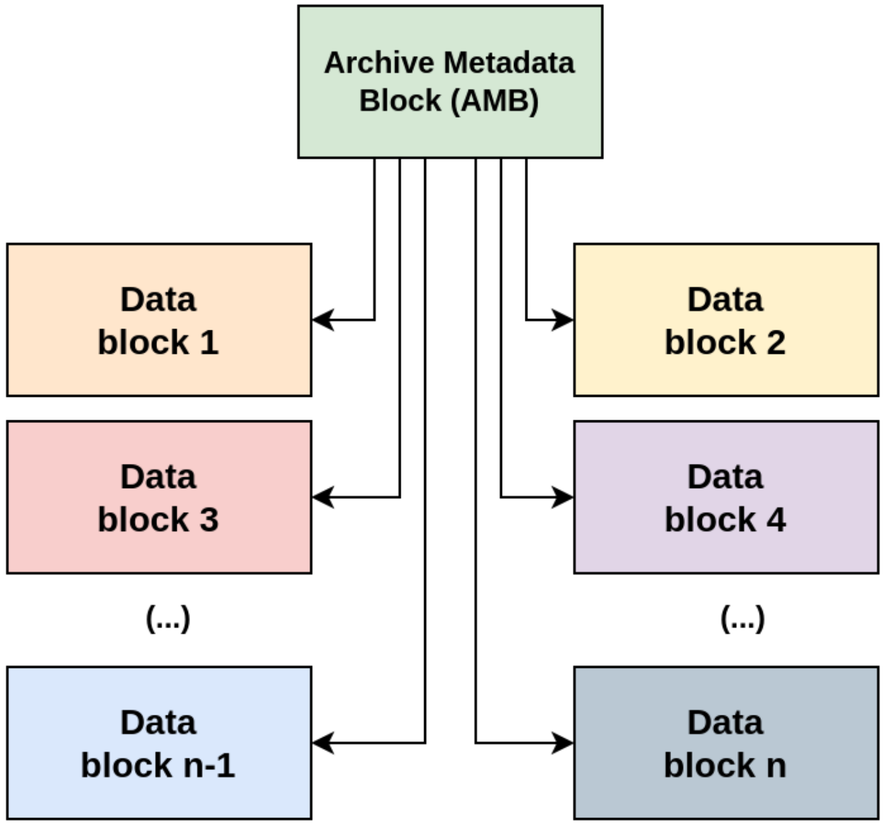
File 1 (...)
File 16 File n
File 3 File n-1

File 12
File 15

File 8 File 8

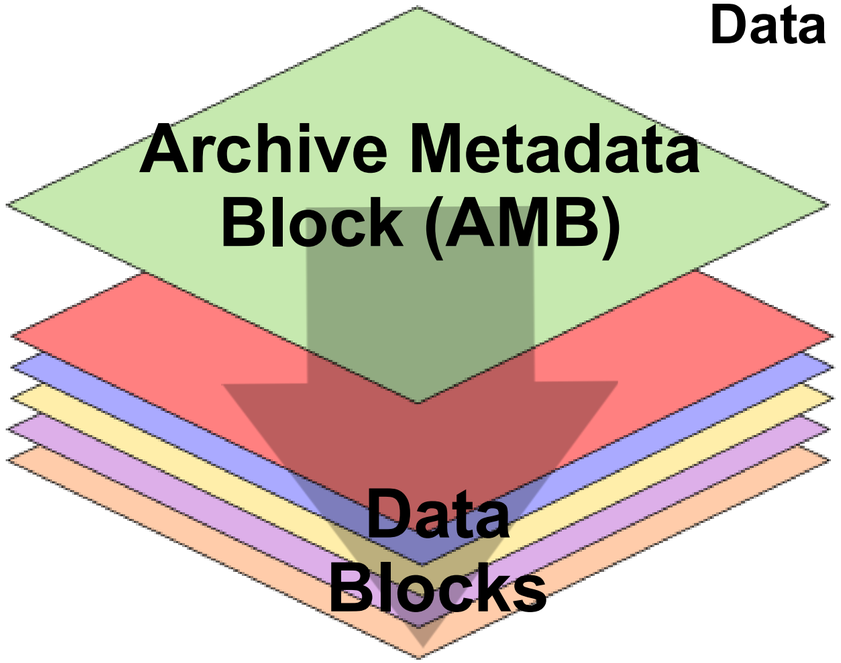
Filling the block is like a Tetris game...

How to read it back?



Chiron

Demultiplexing Data Blocks



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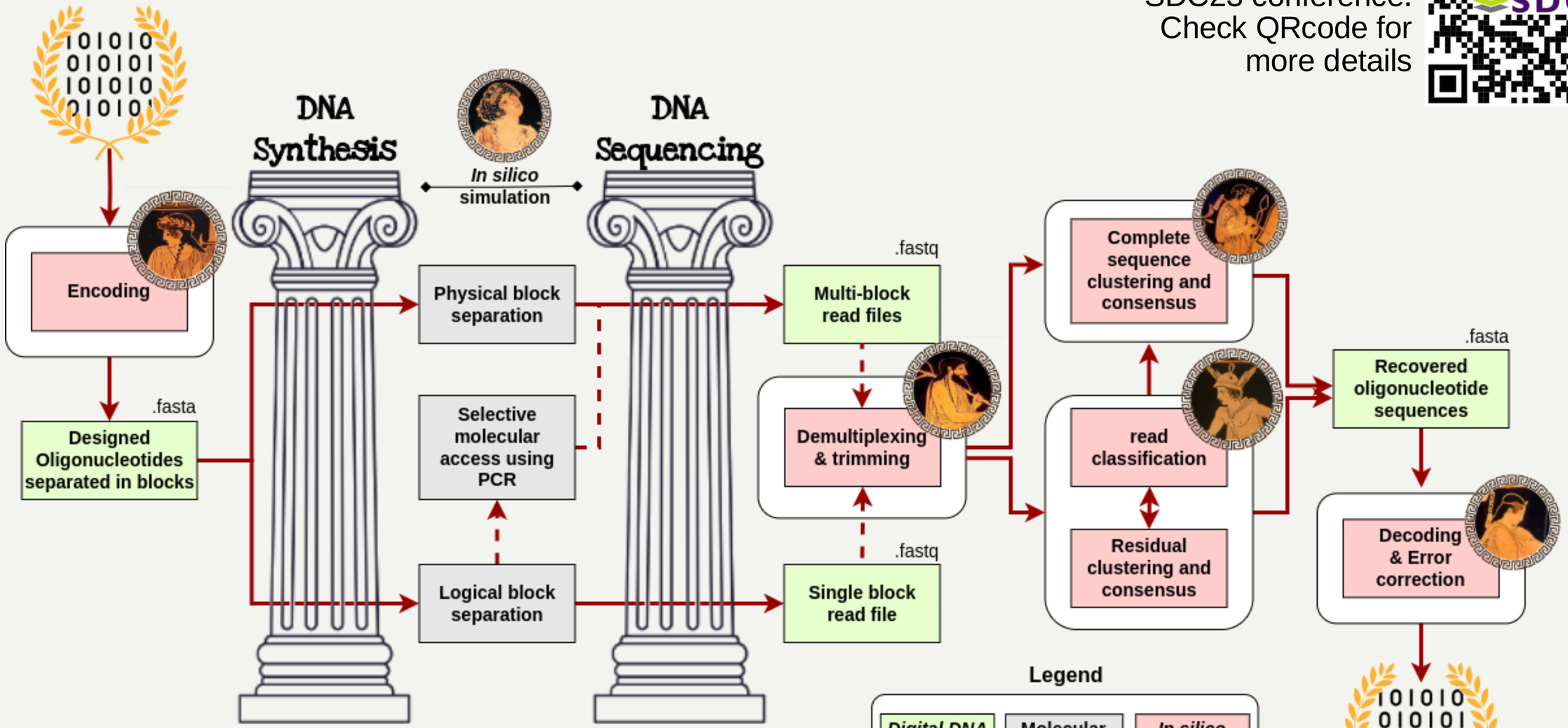

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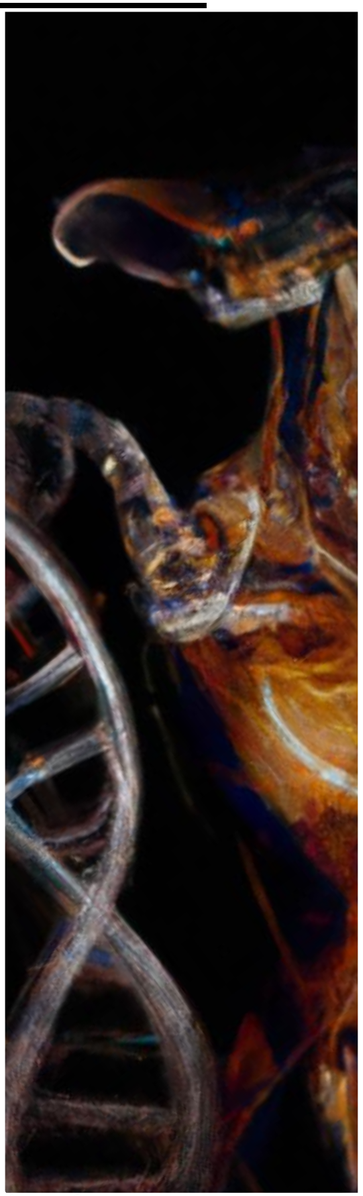
Pre-processing NGS reads



Pre-processing steps:

- Adapters/Primer trimming
- Demultiplexing coding blocks
- Merge read pair (paired-end strategy)
- Reorient DNA sequences
- Discard low-quality reads and contaminants

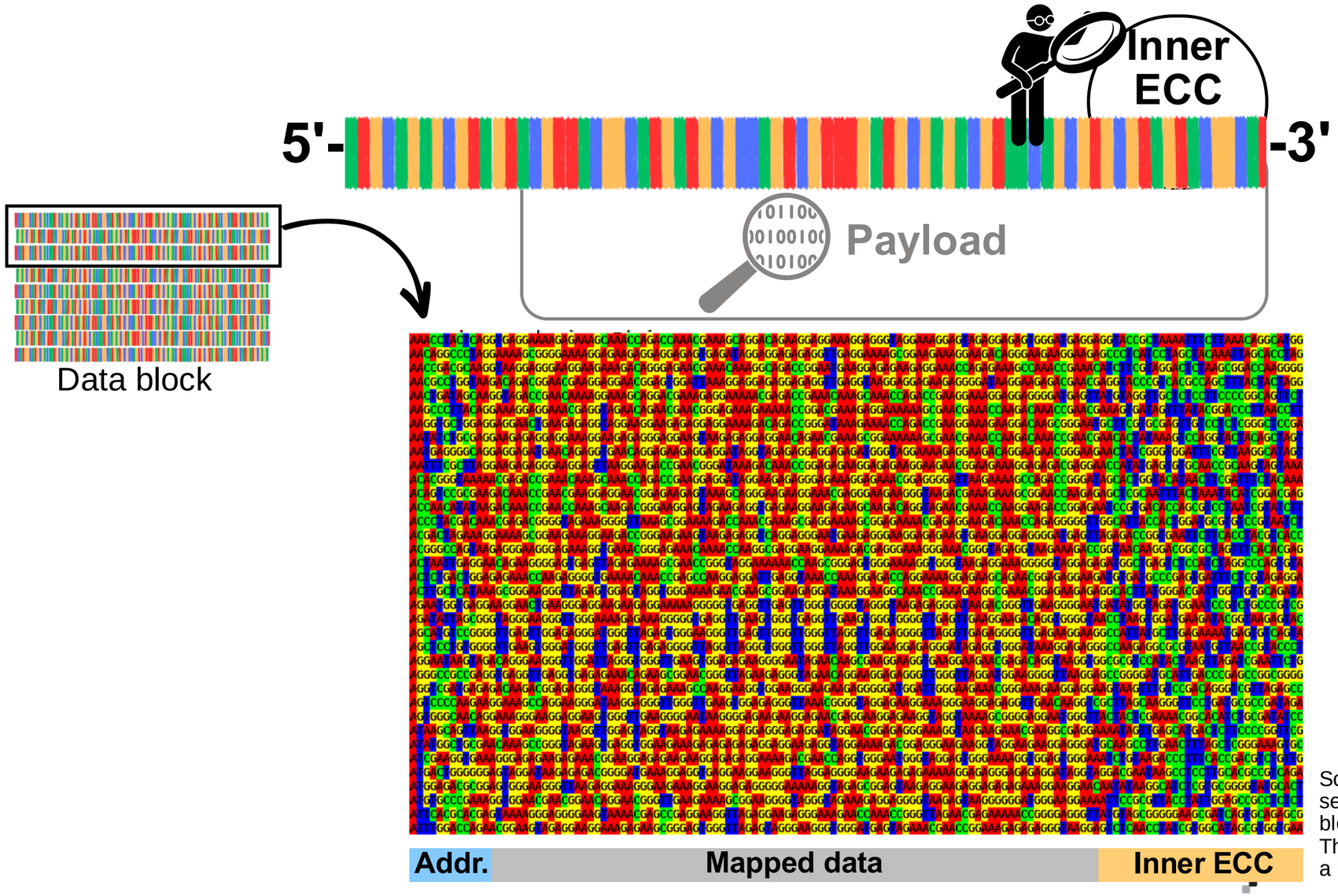
Block specific prime pairs

Planned data blocks

Sequenced DNA reads

Sequenced & Demultiplexed into data blocks

Pre-processing NGS reads



Cytosine
Guanine
Adenine
Thymine

Screenshot of the first 35 DNA sequences from a planned data block in a multi-fasta format. The payload was encoded using a G&A rich scheme.

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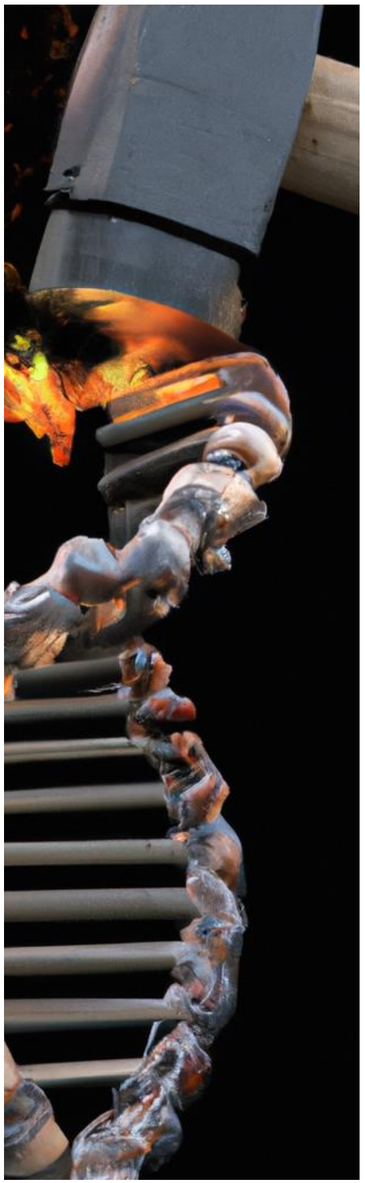
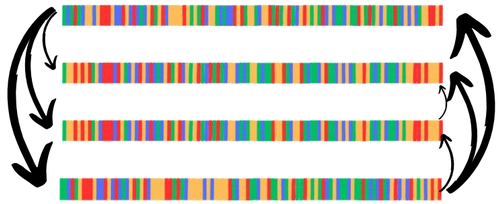
Pre-processing NGS reads



Demultiplexed block.fastq



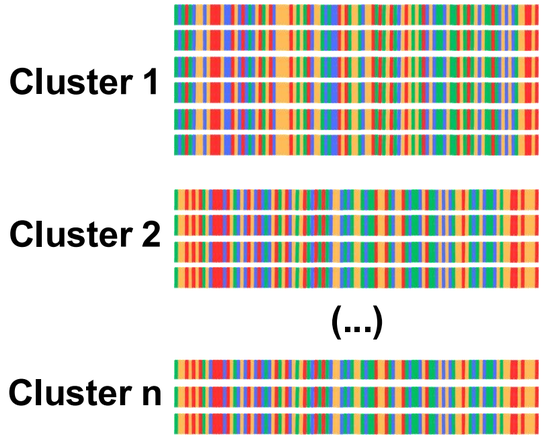
Demultiplexing speeds up clustering

5'-ATCGGCAT-3'

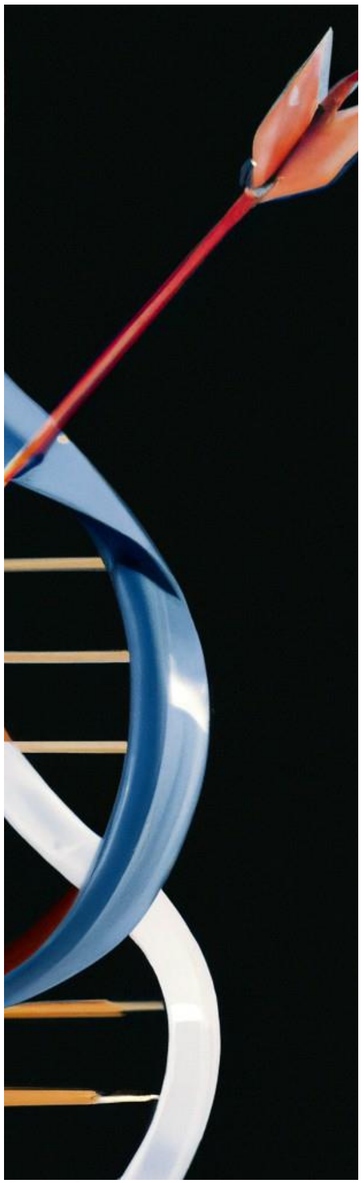
ATCG
TCGG
CGGC
GGCA
GCAT

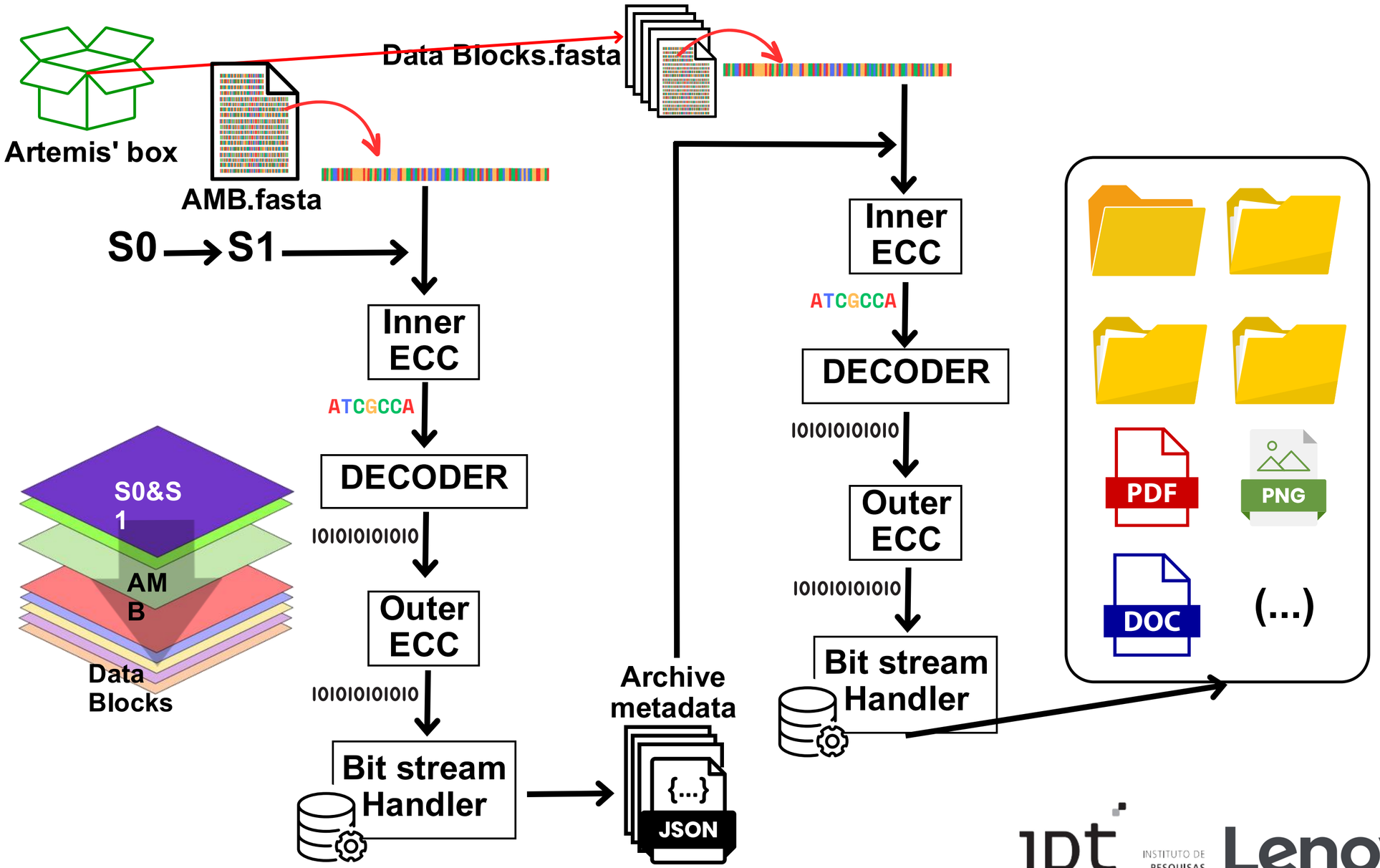
k=4

Shared K-mer strategy to quickly identify and align first highly similar DNA sequences



Decoding





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artemis

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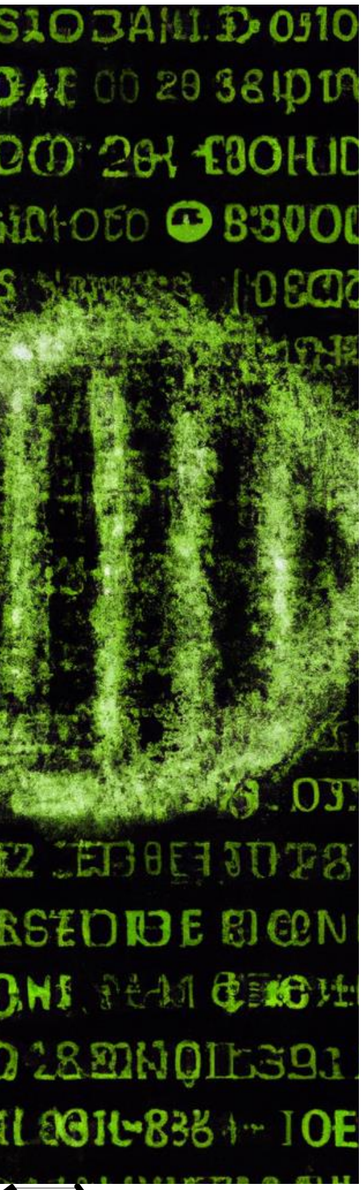
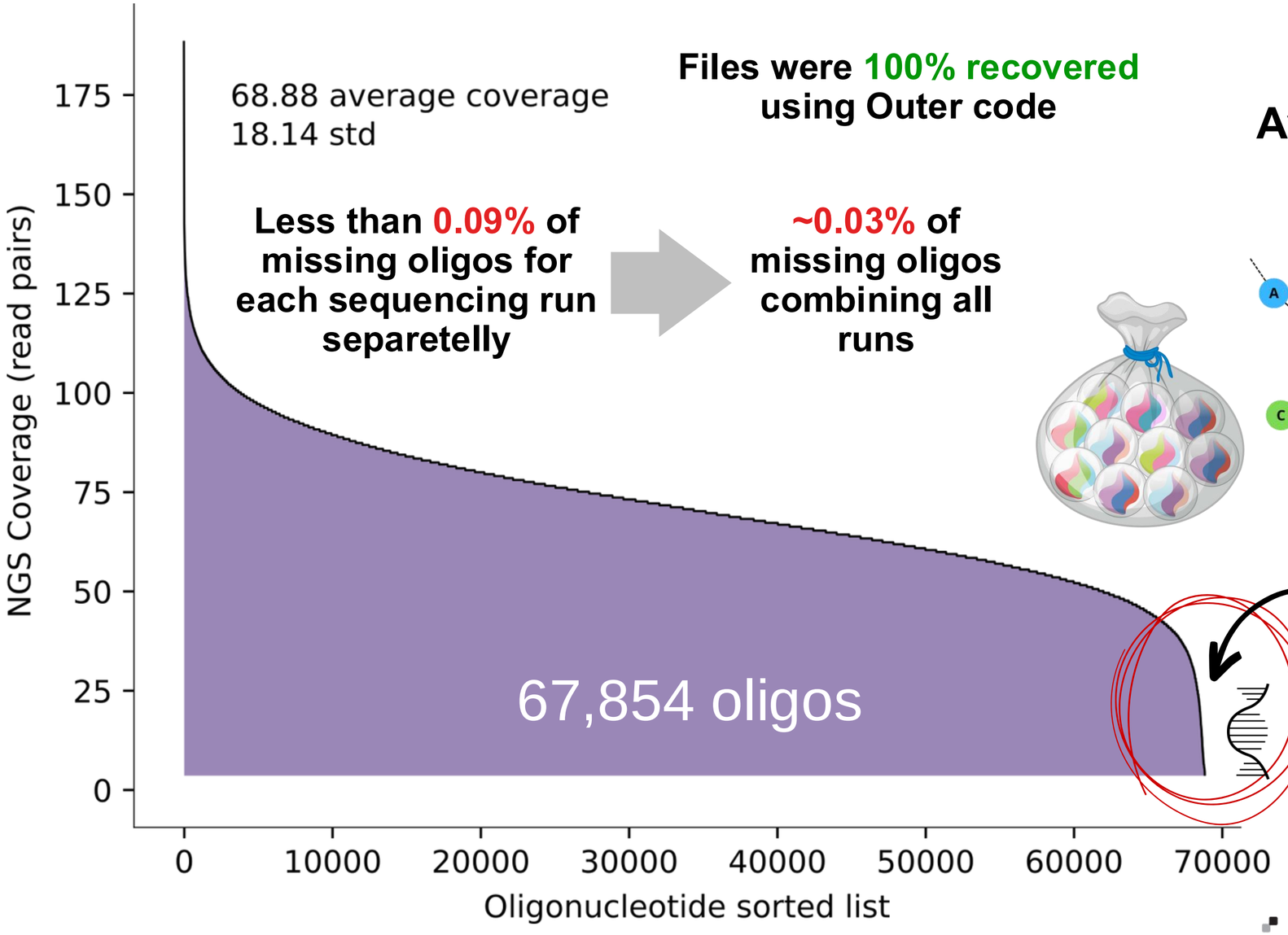
Simulation tool

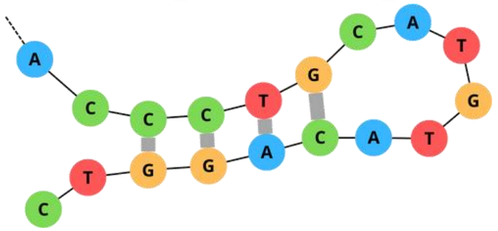
- What Gaia does:
  - Simulate different sequencing strategies
    - Single or Paired-ends
    - Library preparation
    - Coverage variation
    - Sequencing platforms
  - Simulate different synthesis strategies and biases
    - Pandora's box of bias models

Testing CODEC with real data





Avoiding unwanted DNA patterns in designed oligos



"The pit of Tartarus for DNA data storage"

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Thank you!

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