

A DNA-Based Archival Storage System

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* University of Washington

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Facebook cold storage facility
1 exabyte (10^9 GB)
66,000 square feet



DNA molecules as storage



DNA molecules as storage

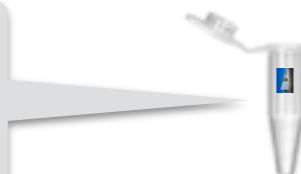
Extremely dense

Theory: 1 exabyte in 1 in³



DNA molecules as storage

Extremely dense
Theory: 1 exabyte in 1 in³



Extremely durable
Half life > 500 years

A DNA-based archival storage system



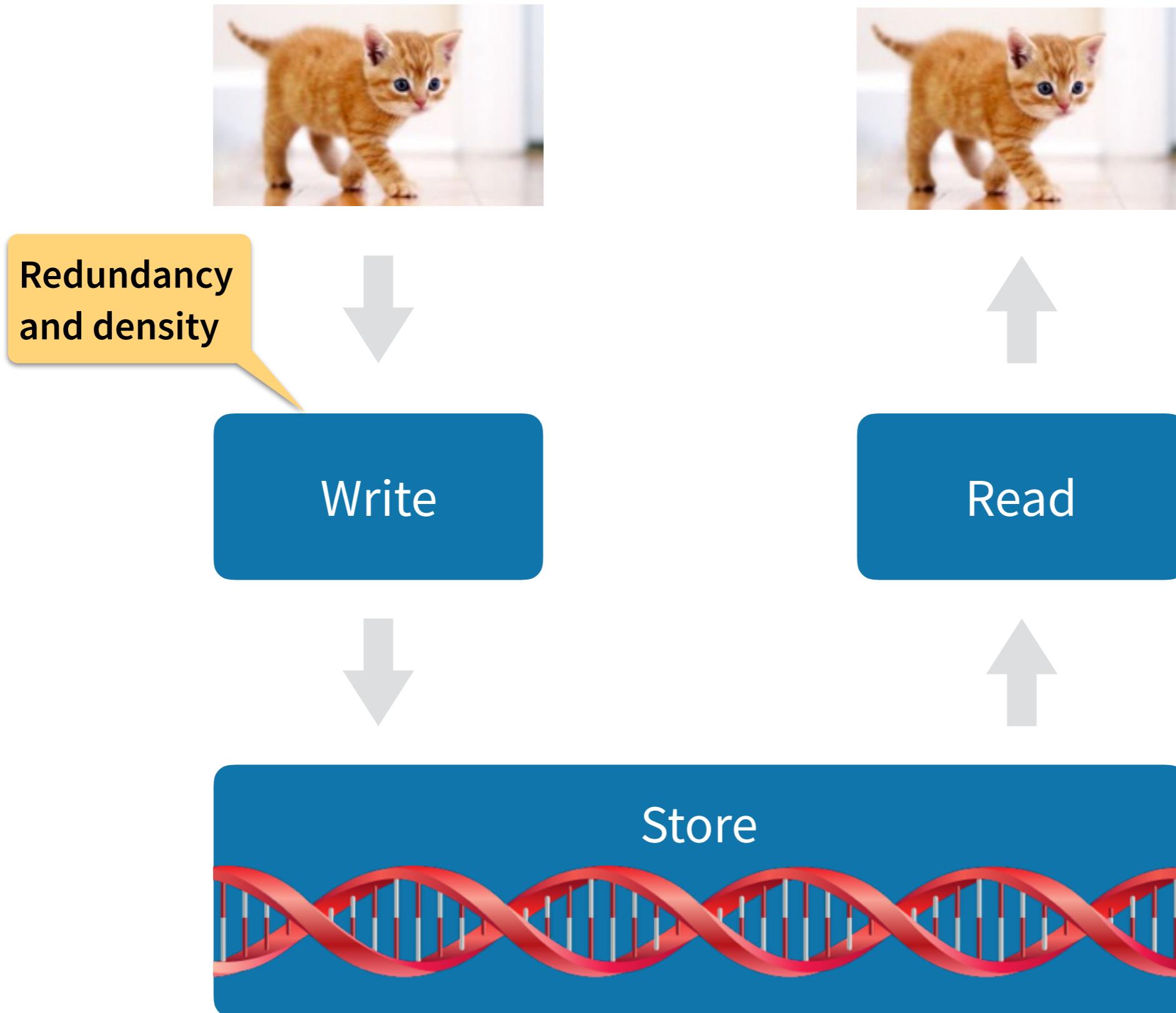
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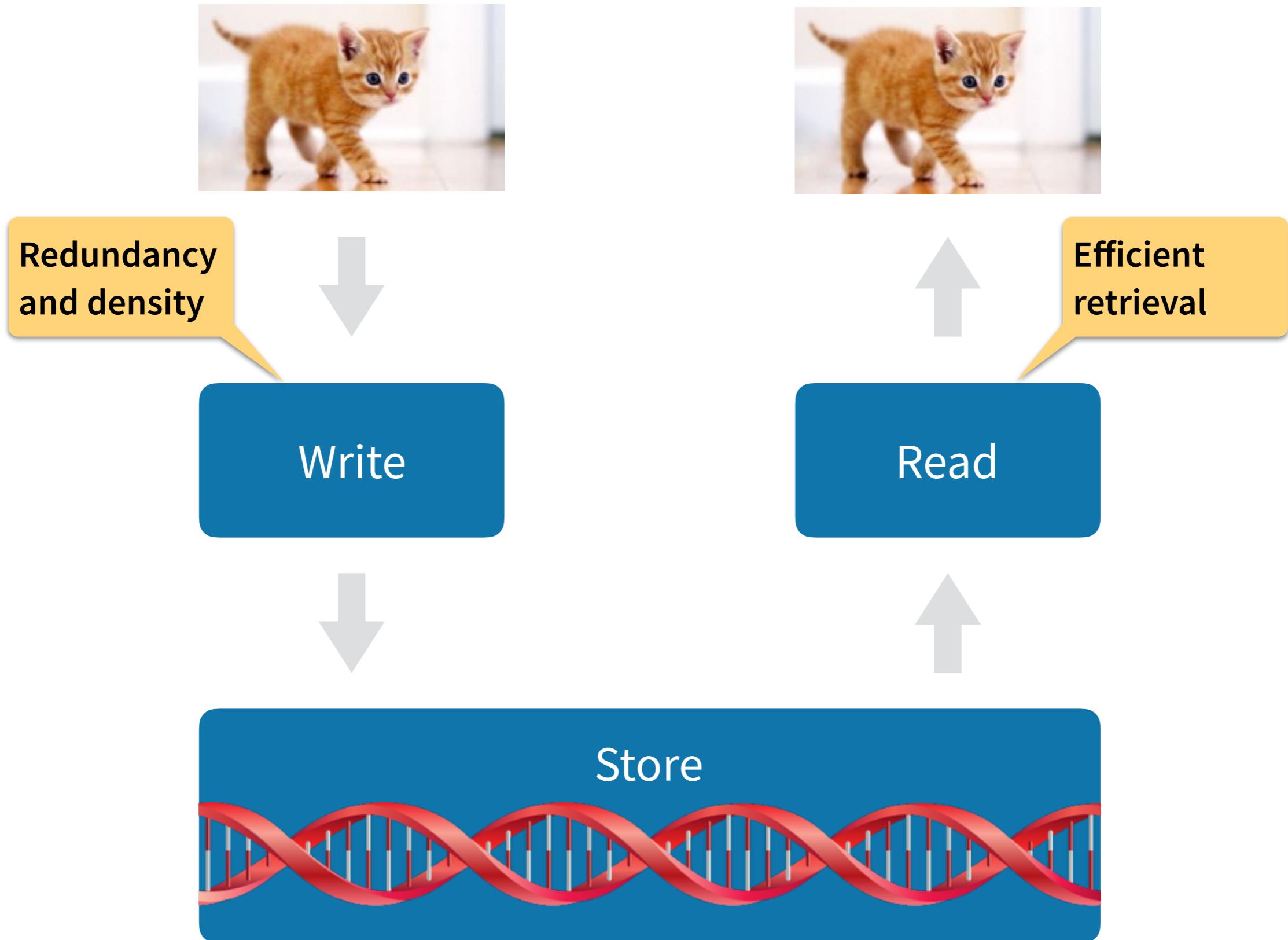
Read



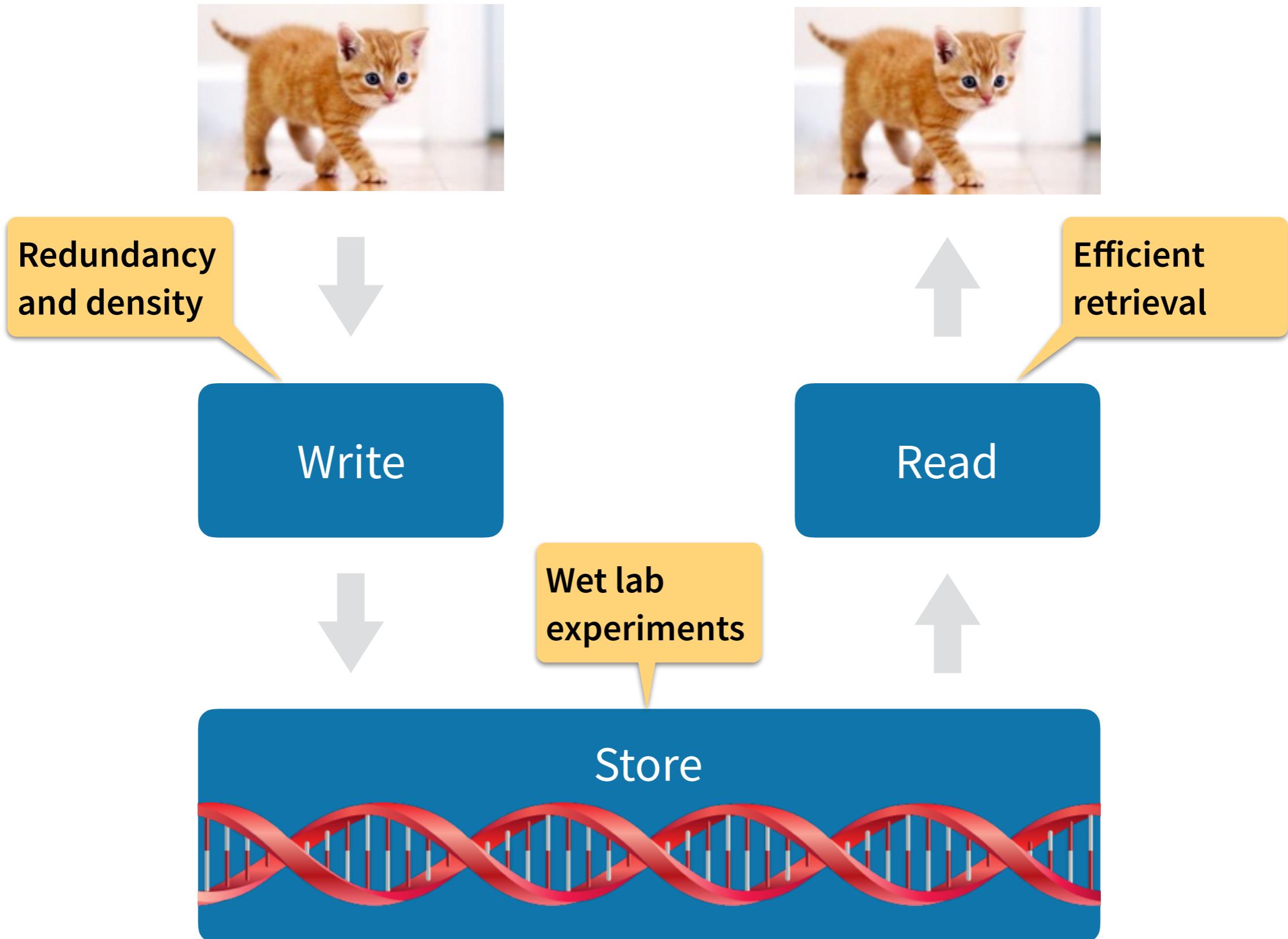
A DNA-based archival storage system



A DNA-based archival storage system



A DNA-based archival storage system



DNA manipulation



DNA molecules

Four nucleotides:

A Adenine

C Cytosine

G Guanine

T Thymine

DNA molecules

Four nucleotides:

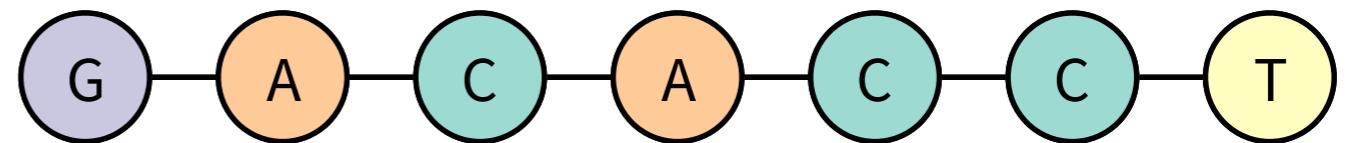
A Adenine

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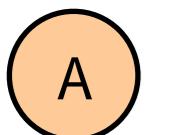
T Thymine

DNA strand (oligonucleotide) is a linear sequence of these nucleotides

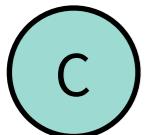


DNA molecules

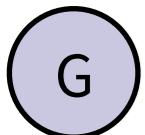
Four nucleotides:



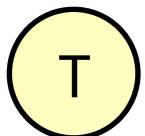
Adenine



Cytosine

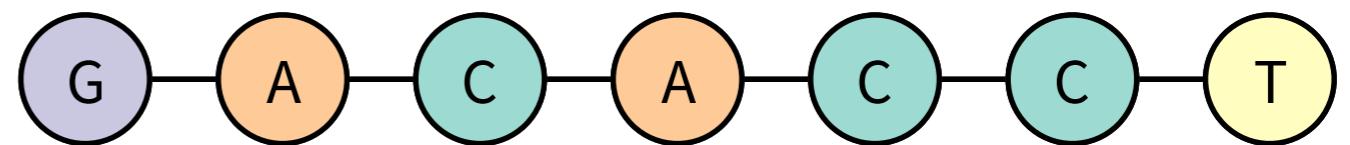


Guanine

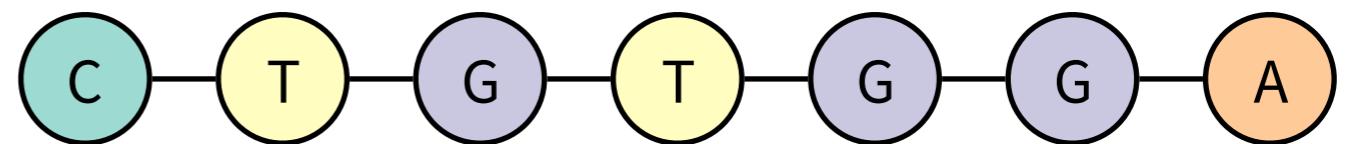


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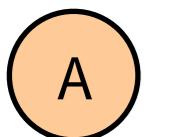


Two strands can bind to each other if they are complementary:

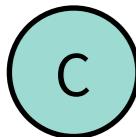


DNA molecules

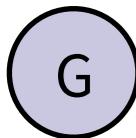
Four nucleotides:



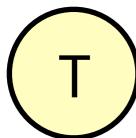
Adenine



Cytosine

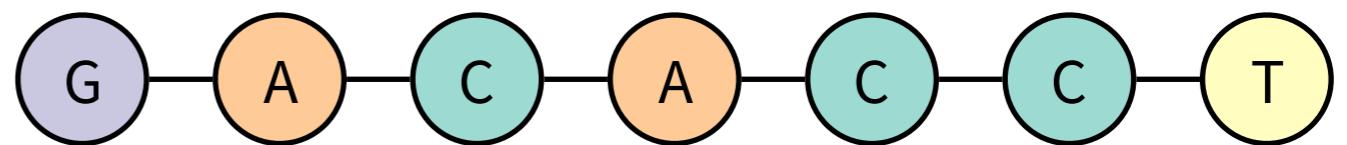


Guanine

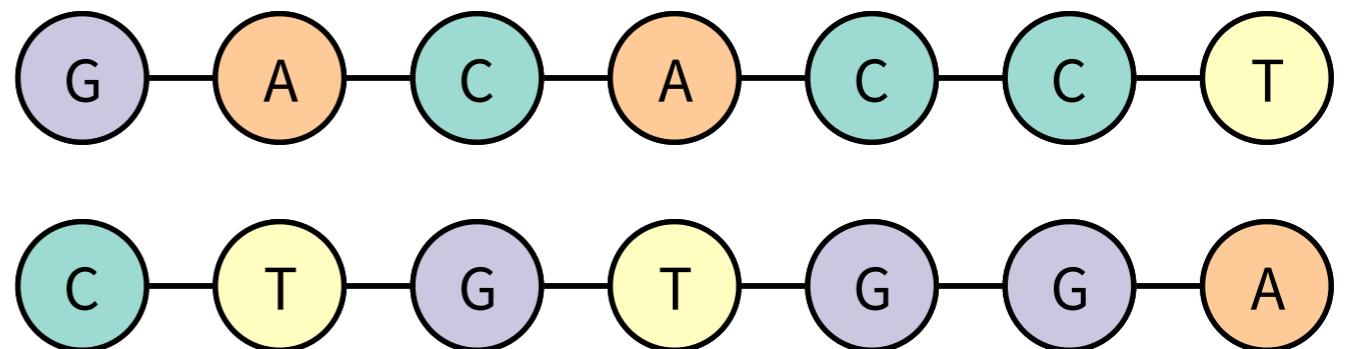


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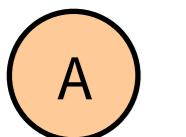


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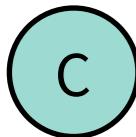


DNA molecules

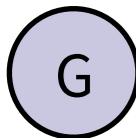
Four nucleotides:



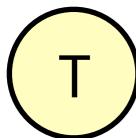
Adenine



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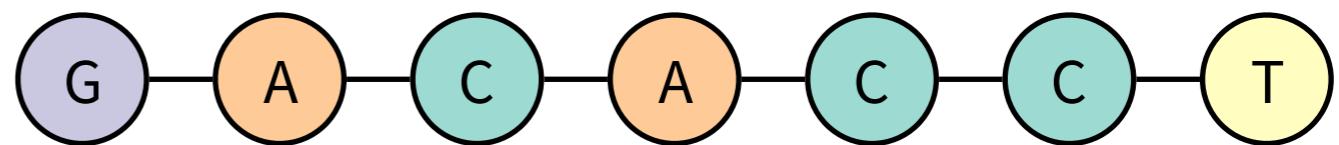


Guanine

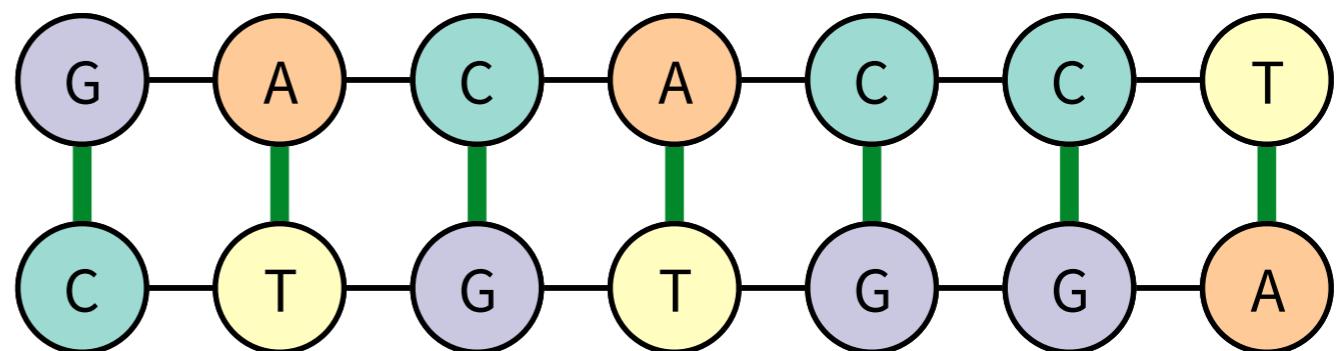


Thymine

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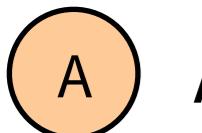


C, G are
complementary

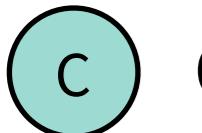
A, T are
complementary

DNA molecules

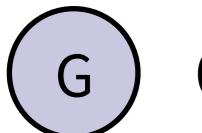
Four nucleotides:



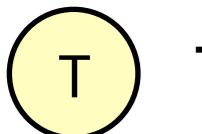
Adenine



Cytosine

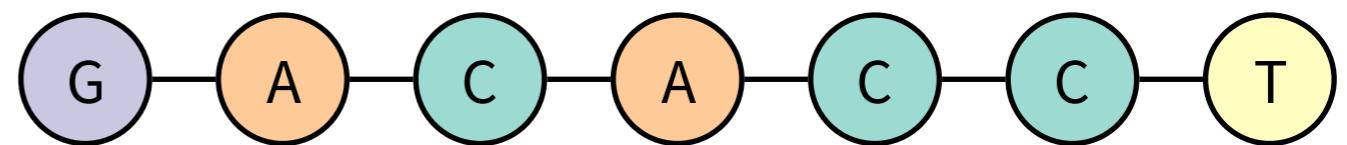


Guanine



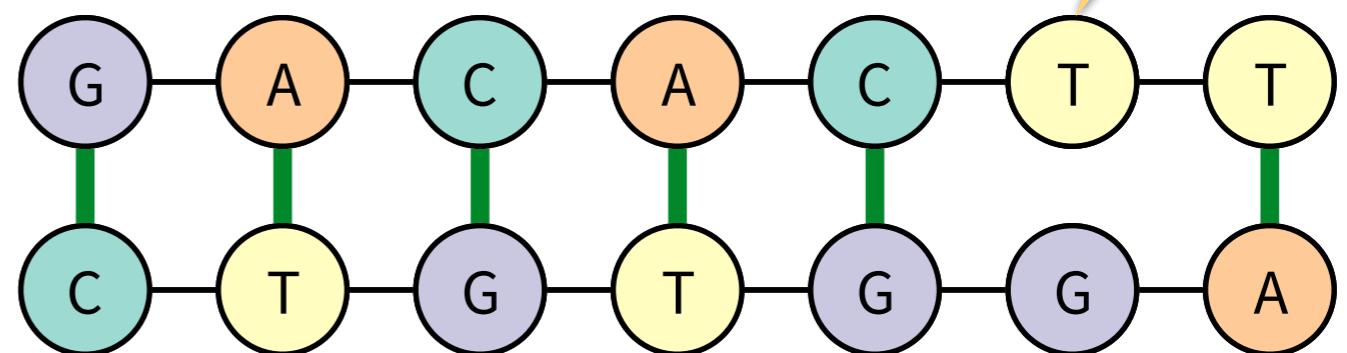
Thymine

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Two strands can bind to each other if they are complementary:

Partial errors allowed

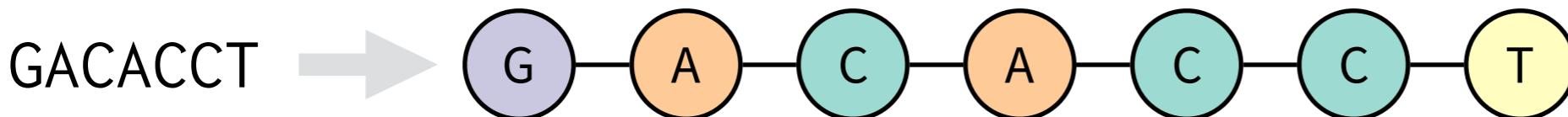


C, G are complementary

A, T are complementary

DNA manipulation

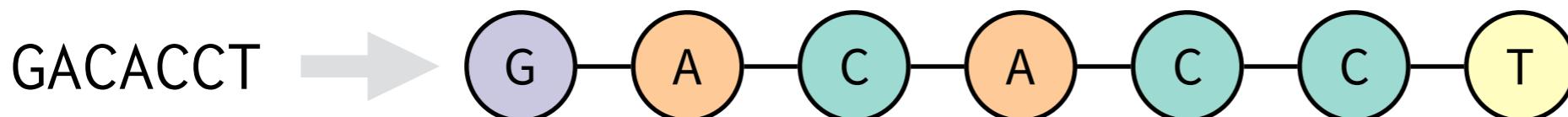
Synthesis: manufacturing DNA strands



- Chemical synthesis process appends one nucleotide at a time
- Maximum practical length ~200 nts
- Typically produces thousands of copies of the strand

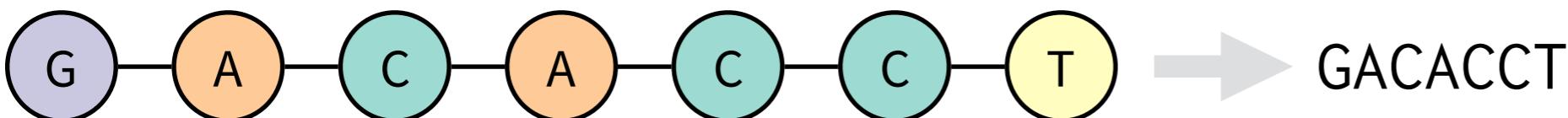
DNA manipulation

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- Maximum practical length ~200 nts
- Typically produces thousands of copies of the strand

Sequencing: reading DNA strands



- Produces *many* reads of a strand
- Much higher throughput than synthesis

An archival storage system

System overview

Archival storage system structured as a key-value store

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put(key, value)

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get(key)

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cat.jpg



↓ 01001...

put(key, value)

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Archival storage system structured as a key-value store

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Pool

get(key)

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cat.jpg



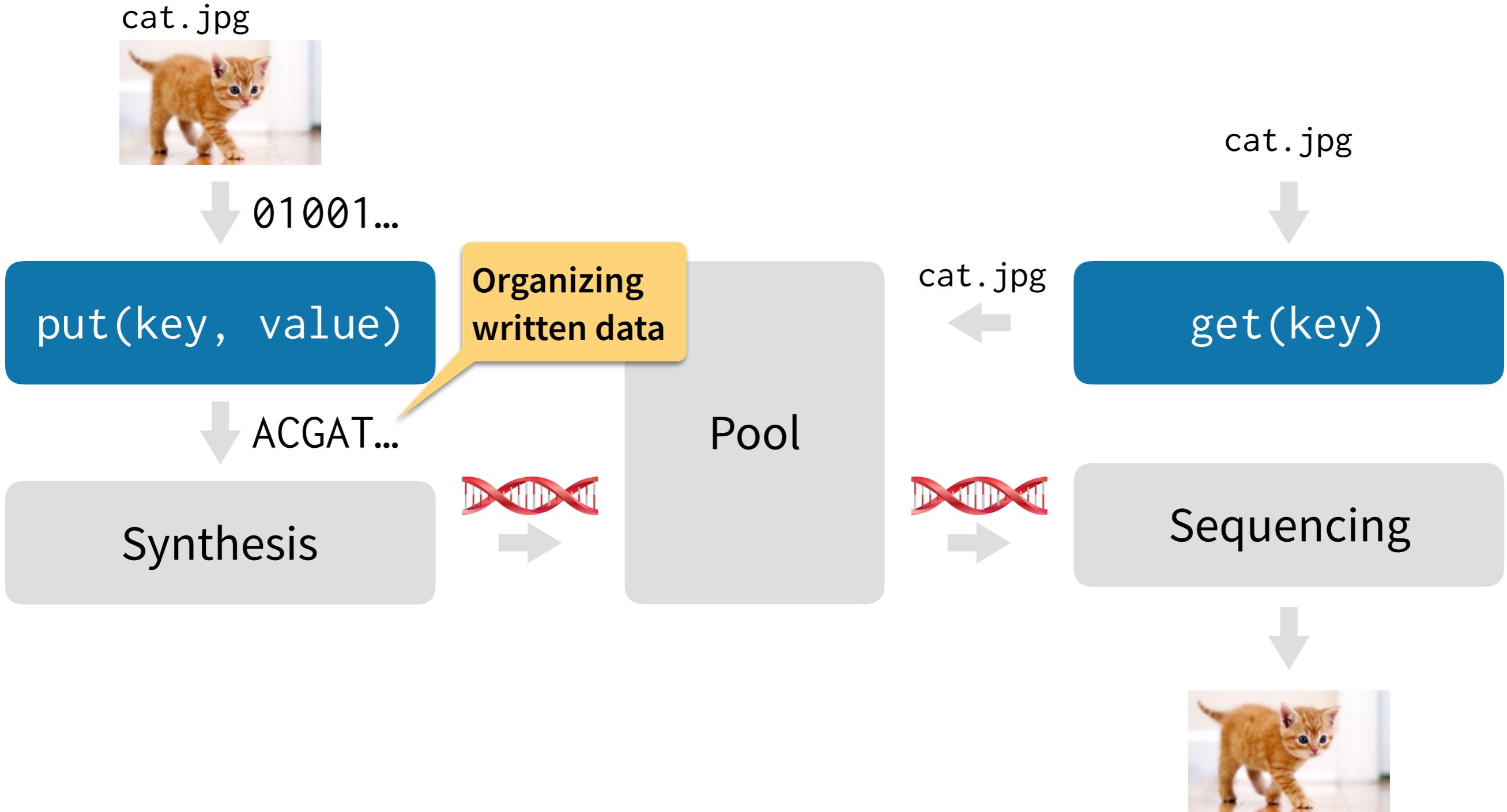
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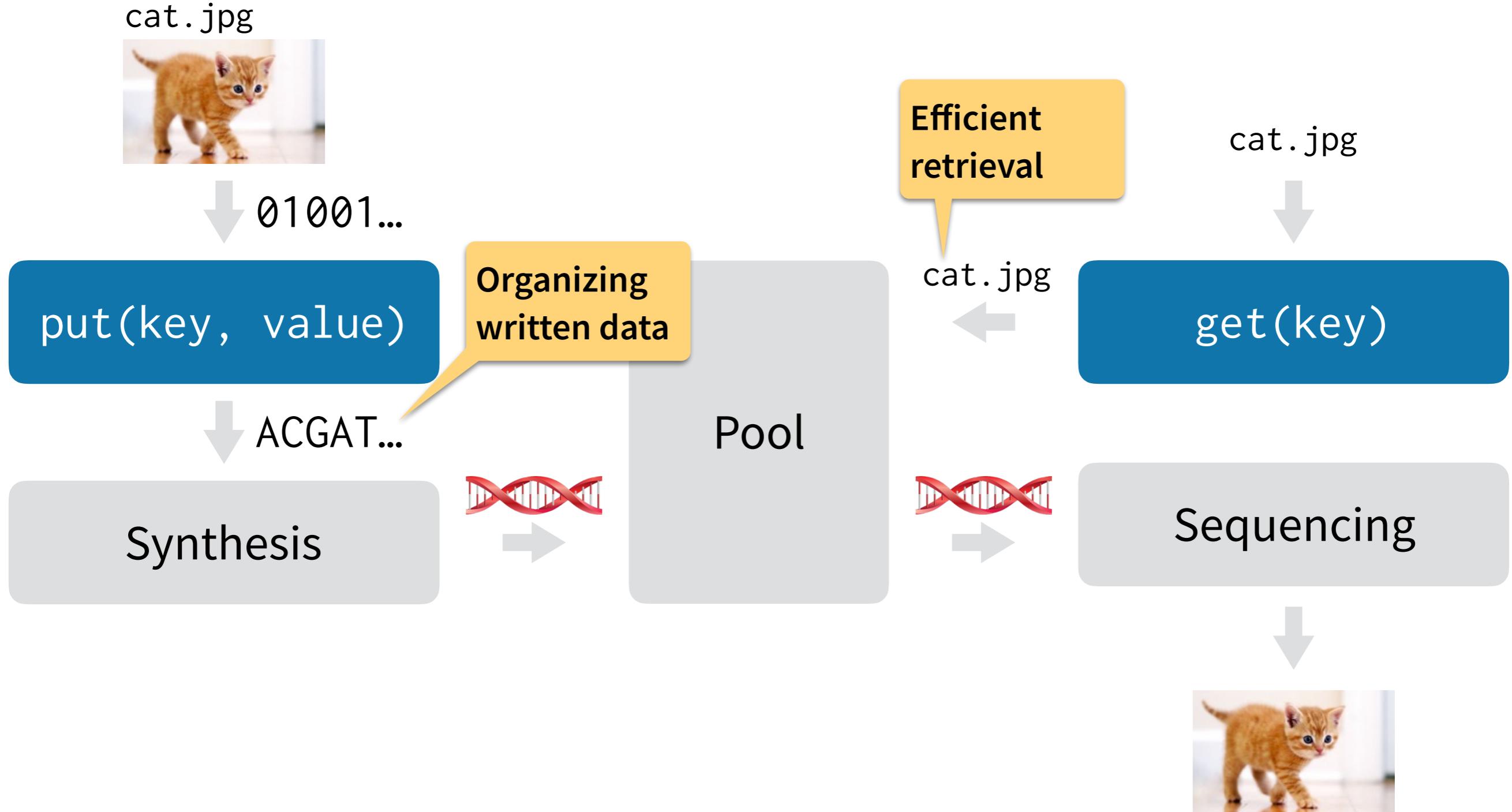
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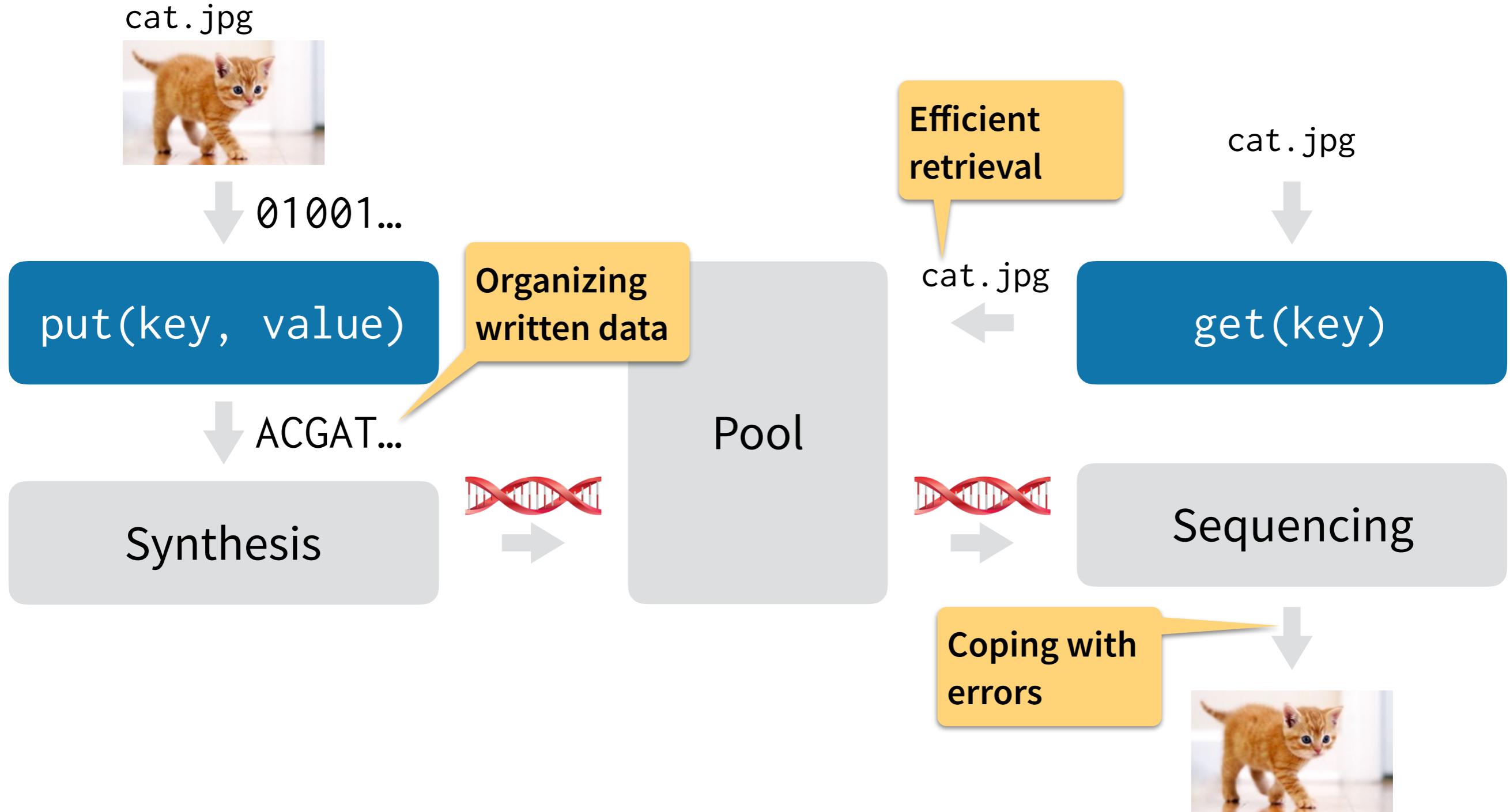
System overview

Archival storage system structured as a key-value store



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Archival storage system structured as a key-value store



Writing data to DNA

The easy way: convert base 2 to base 4

10100011 10010001 11100111 11000101 10010100 10111101

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2 2 0 3 2 1 0 1 3 2 1 3 3 0 1 1 2 1 1 0 2 3 3 1

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But this approach isn't feasible for more than a few bytes

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G

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The easy way: convert base 2 to base 4

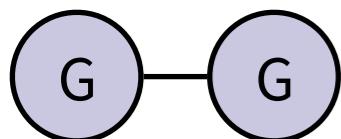
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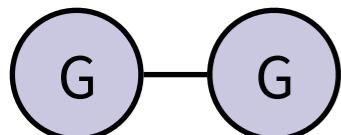
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$$P[\text{Attach}] = 99\%$$



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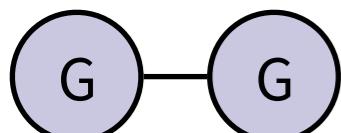
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99%

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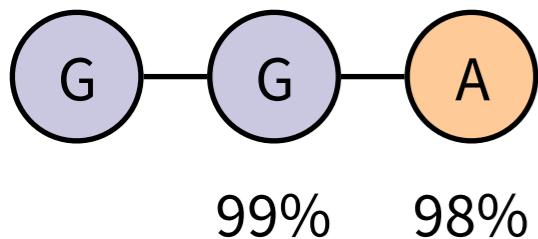
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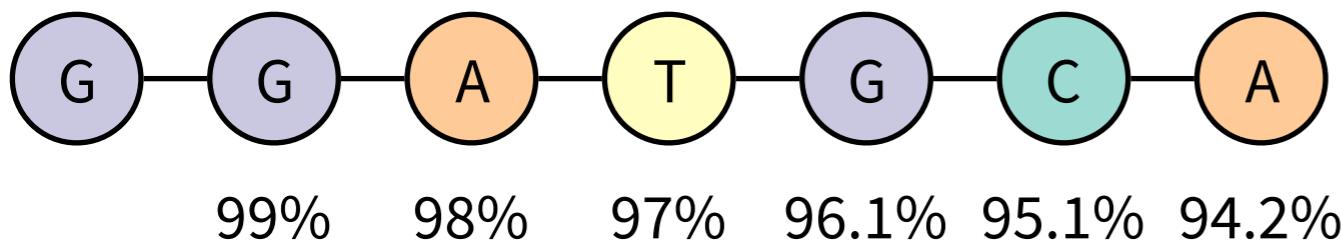
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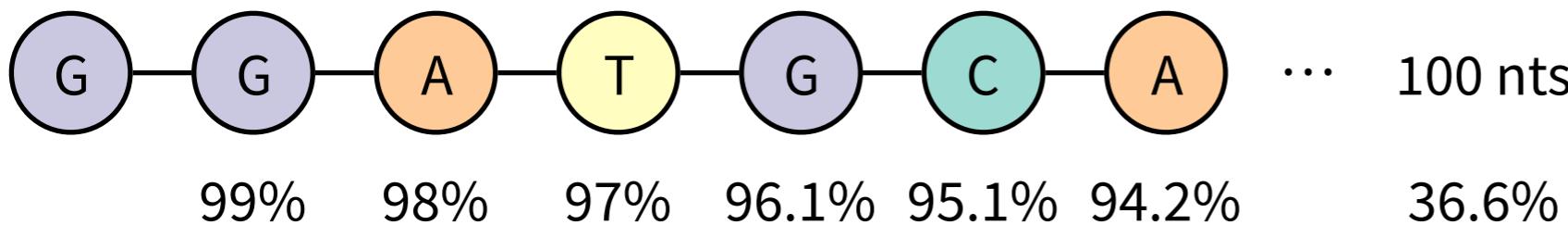
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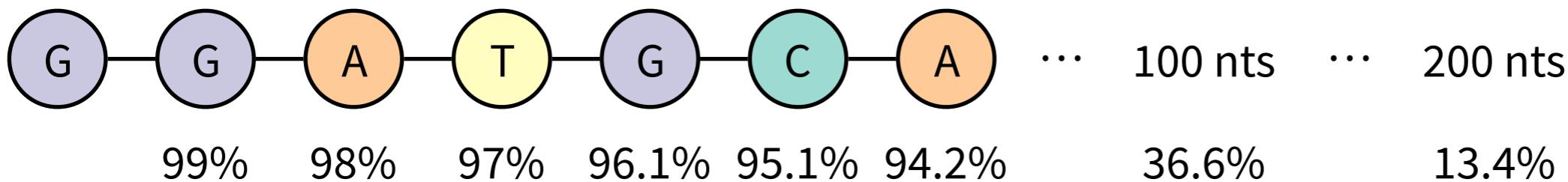
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Chunking data

Break binary data into chunks stored in separate strands

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T G C T T A C C

G C C A G T T C

Chunking data

Break binary data into chunks stored in separate strands

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2 2 0 3 2 1 0 1 3 2 1 3 3 0 1 1 2 1 1 0 2 3 3 1



G G A T G C A C A A A A
T G C T T A C C C A A A C
G C C A G T T C A A A G

Addresses
within the value

Chunking data

Break binary data into chunks stored in separate strands

10100011 10010001 11100111 11000101 10010100 10111101

2 2 0 3 2 1 0 1 3 2 1 3 3 0 1 1 2 1 1 0 2 3 3 1



A T G T T	G G A T G C A C A A A A	C A T C C
A T G T T	T G C T T A C C A A A C	C A T C C
A T G T T	G C C A G T T C A A A G	C A T C C

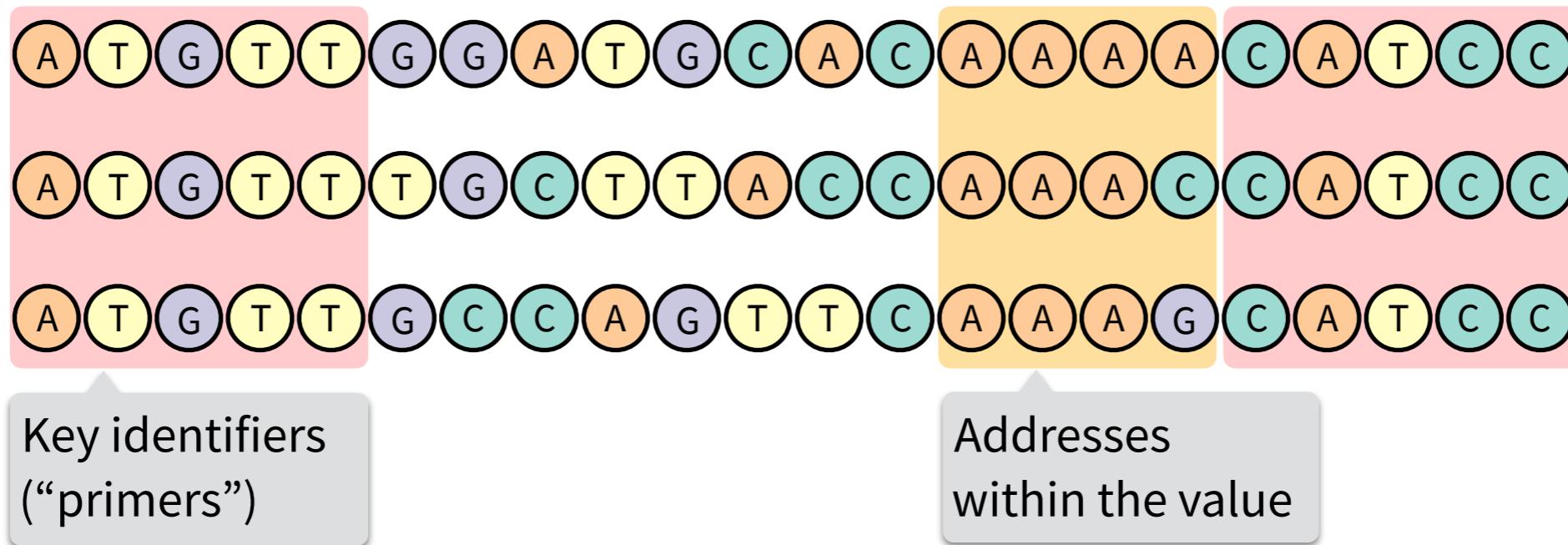
Key identifiers
("primers")

Addresses
within the value

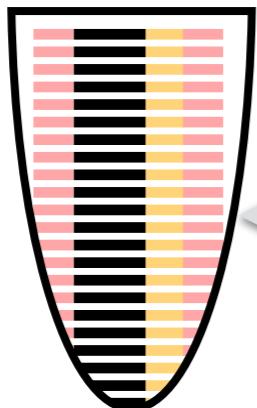
Efficient reads



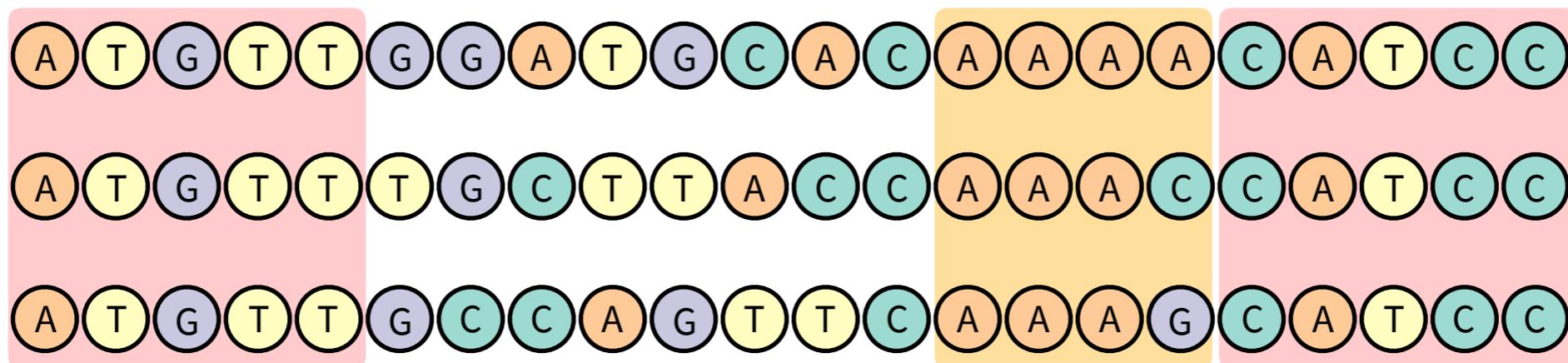
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Efficient reads



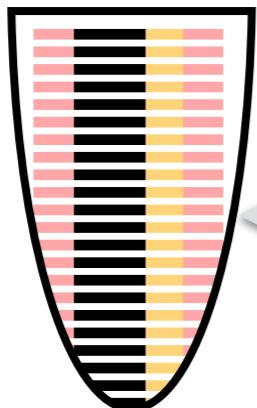
Pool containing
stored strands for
all keys & values!



Key identifiers
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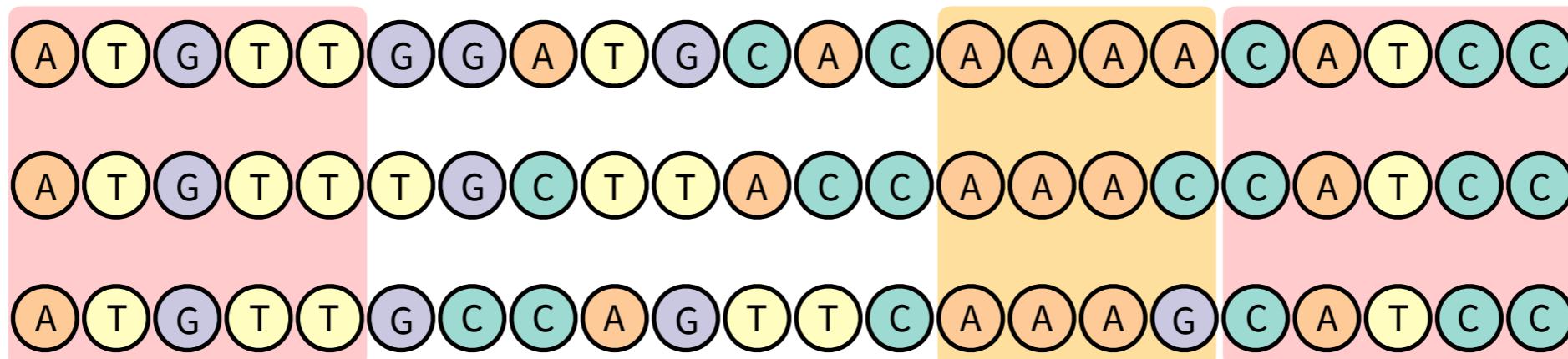
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cat.jpg

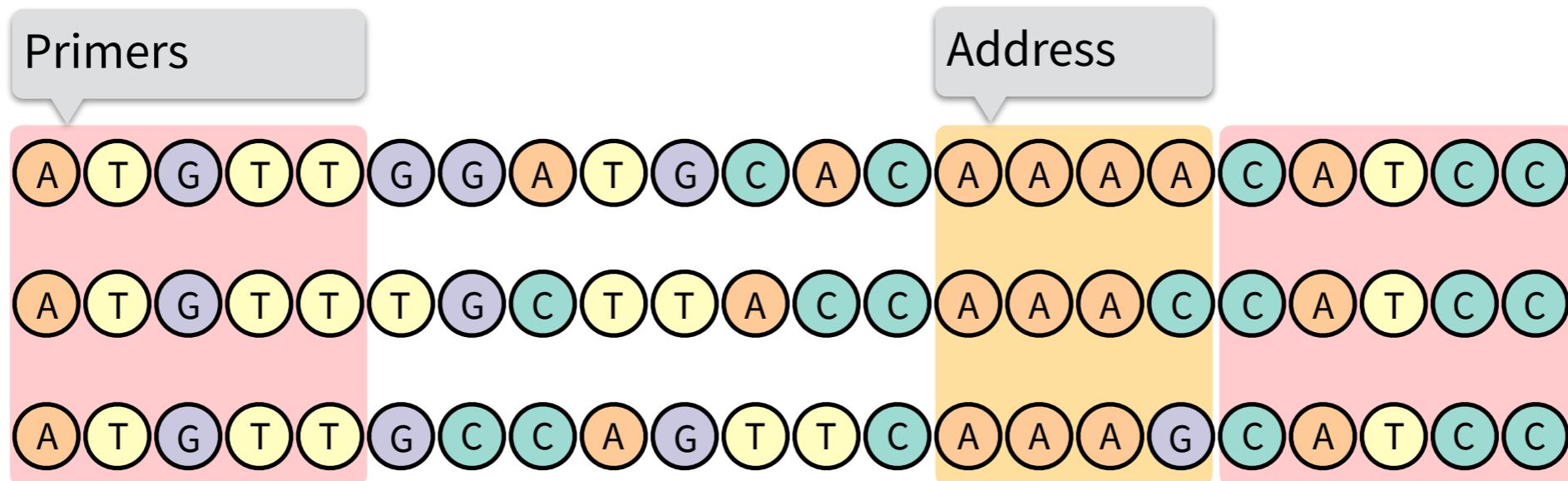
get(key)



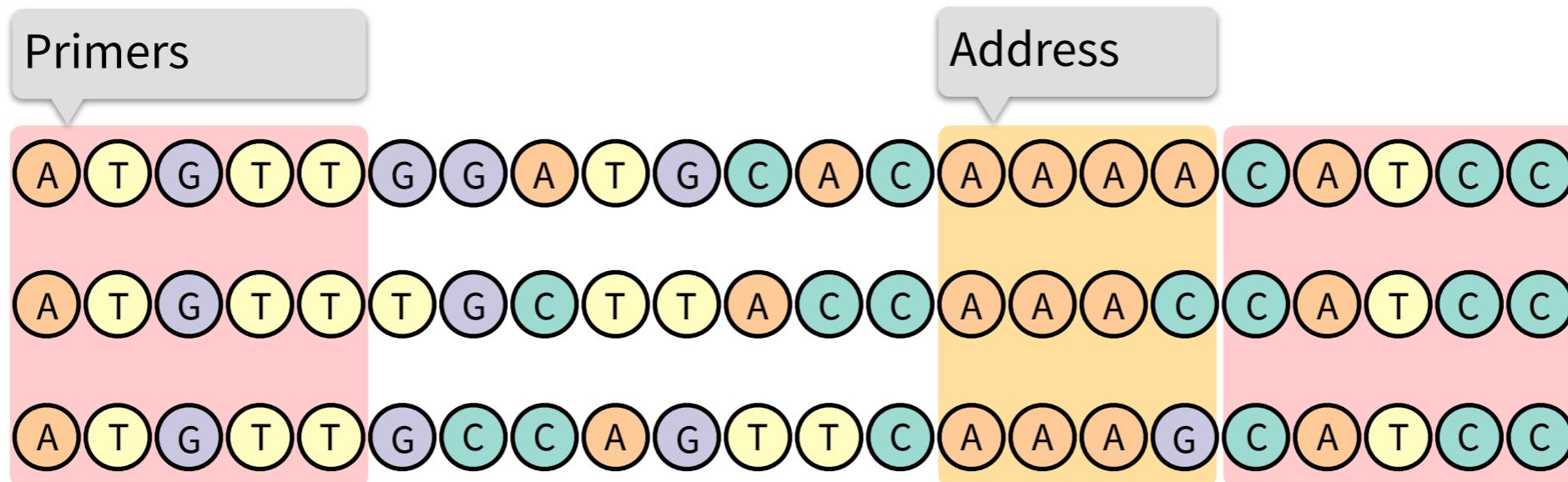
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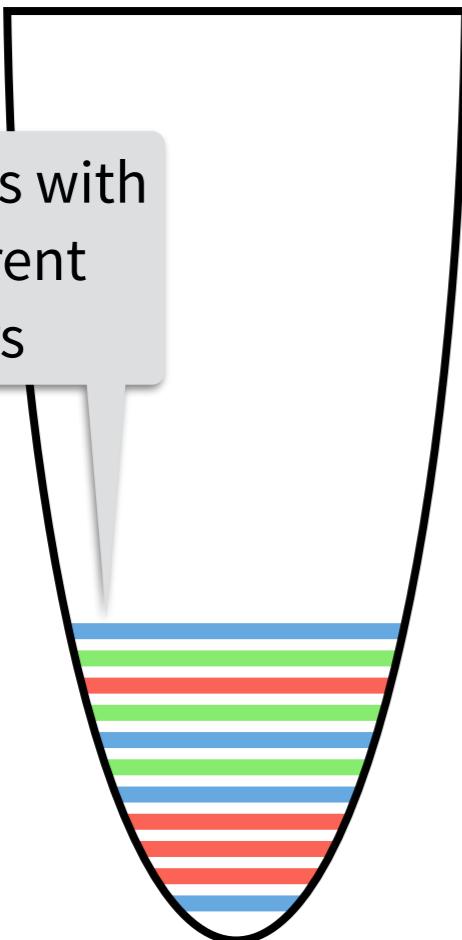
Random access



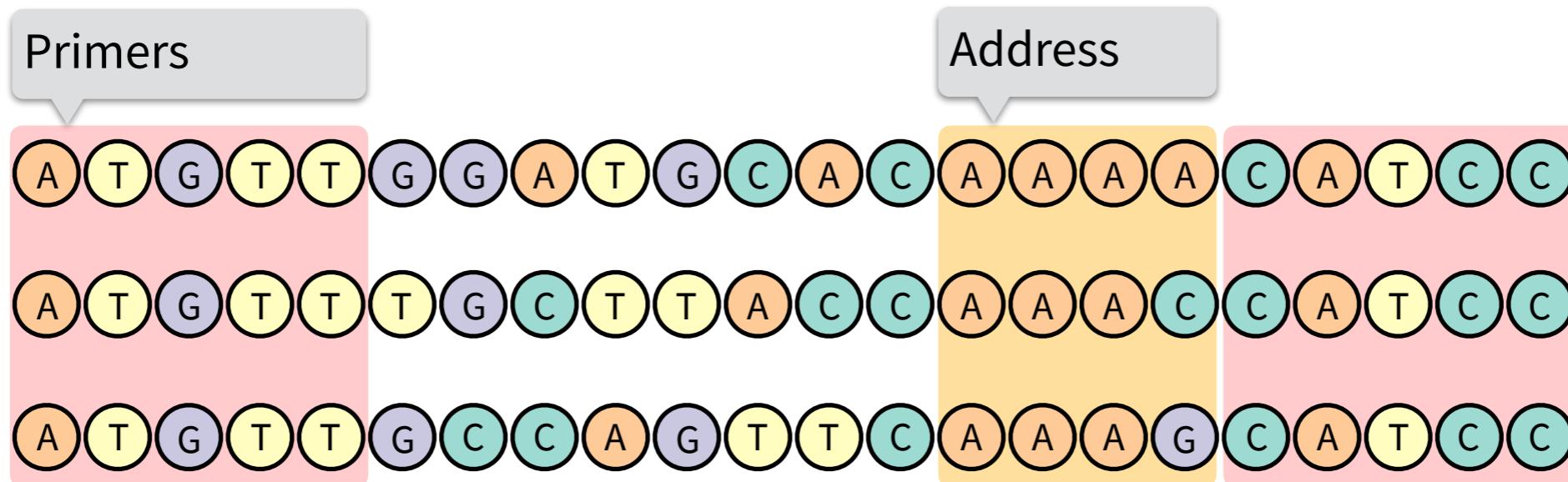
Random access



Strands with
3 different
primers



Random access

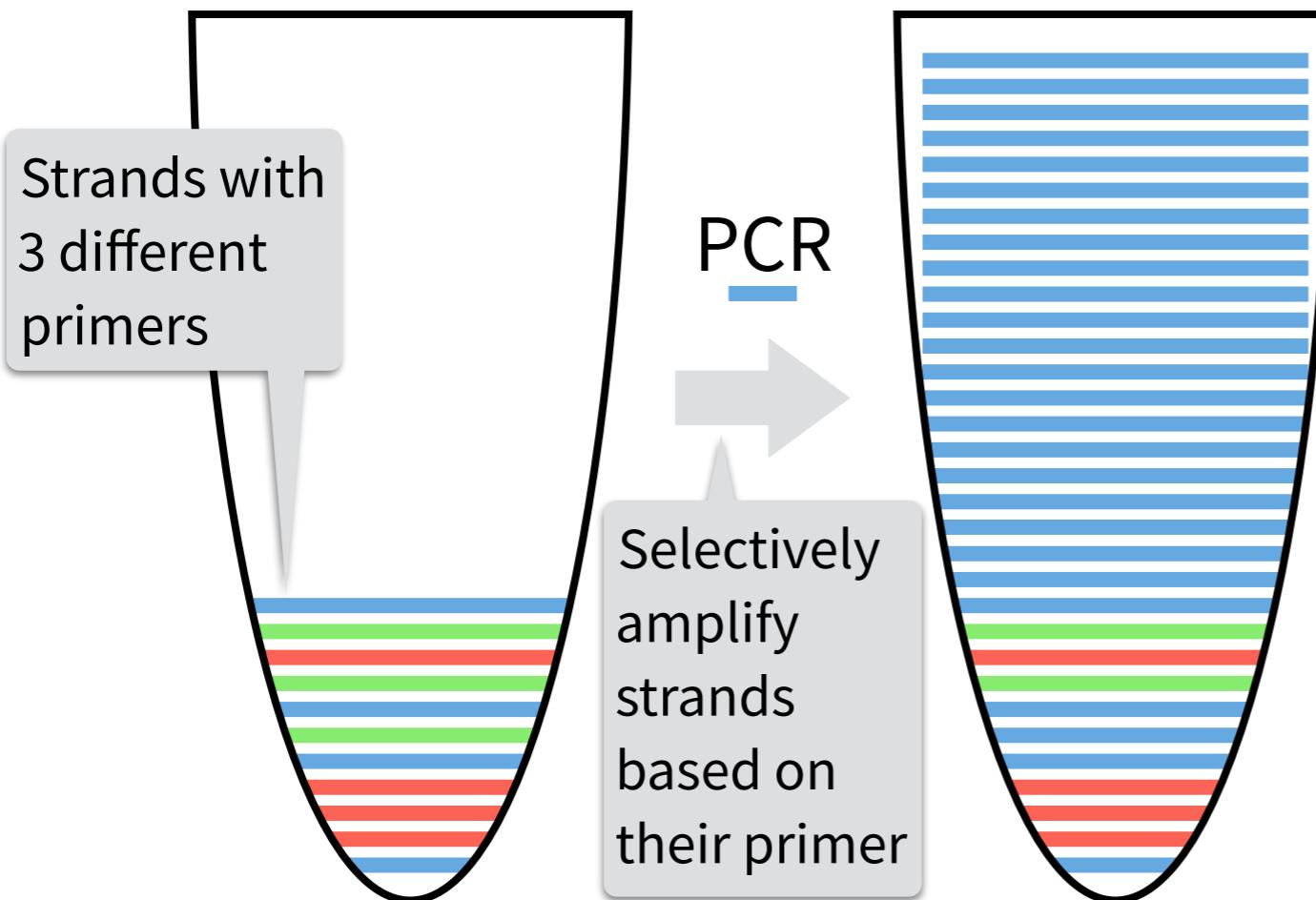
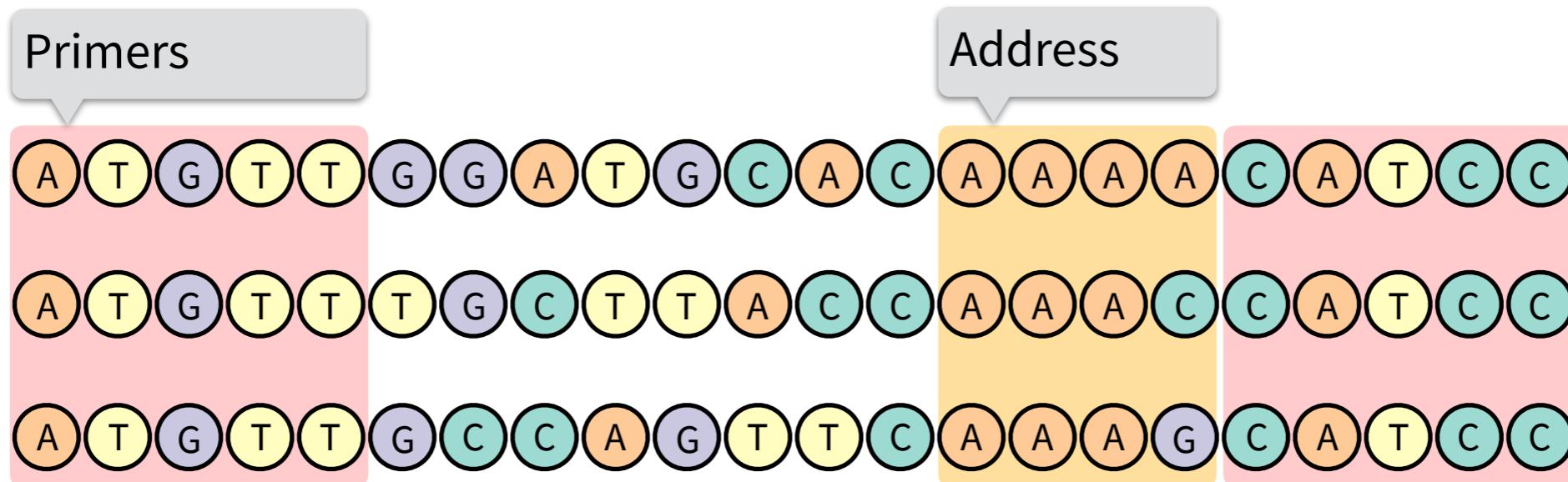


Strands with
3 different
primers

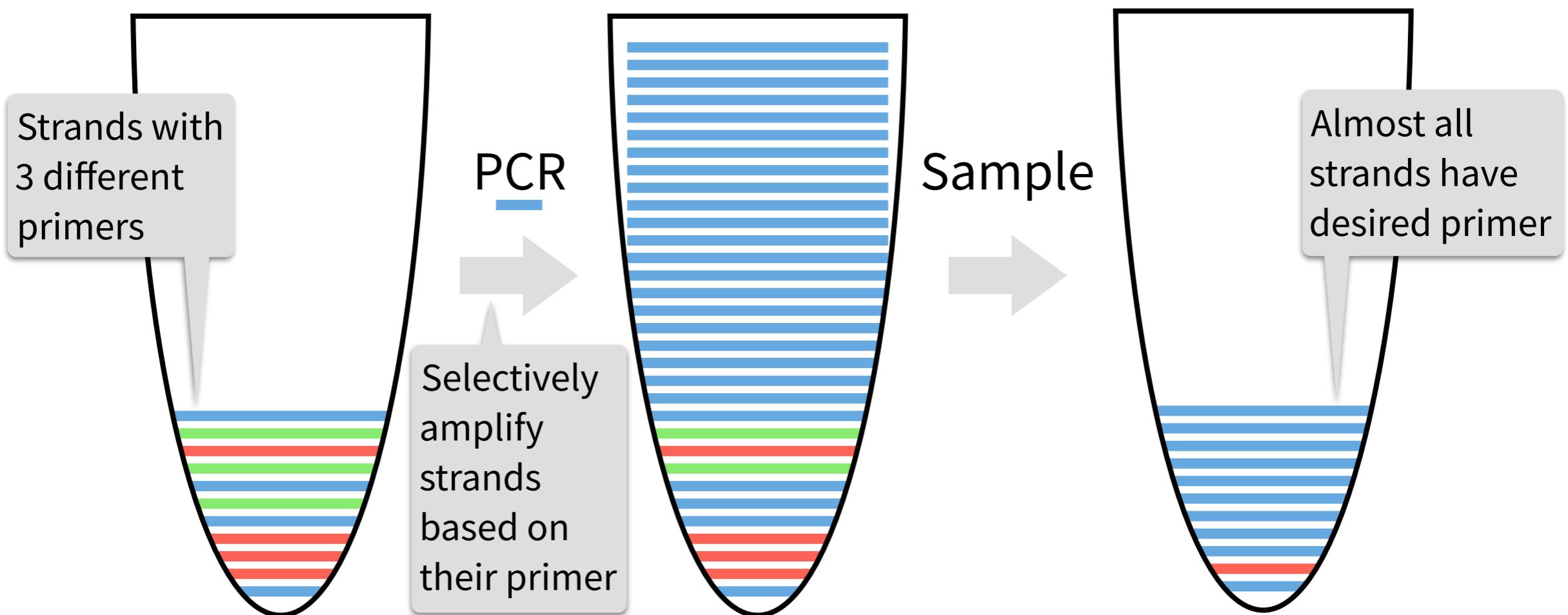
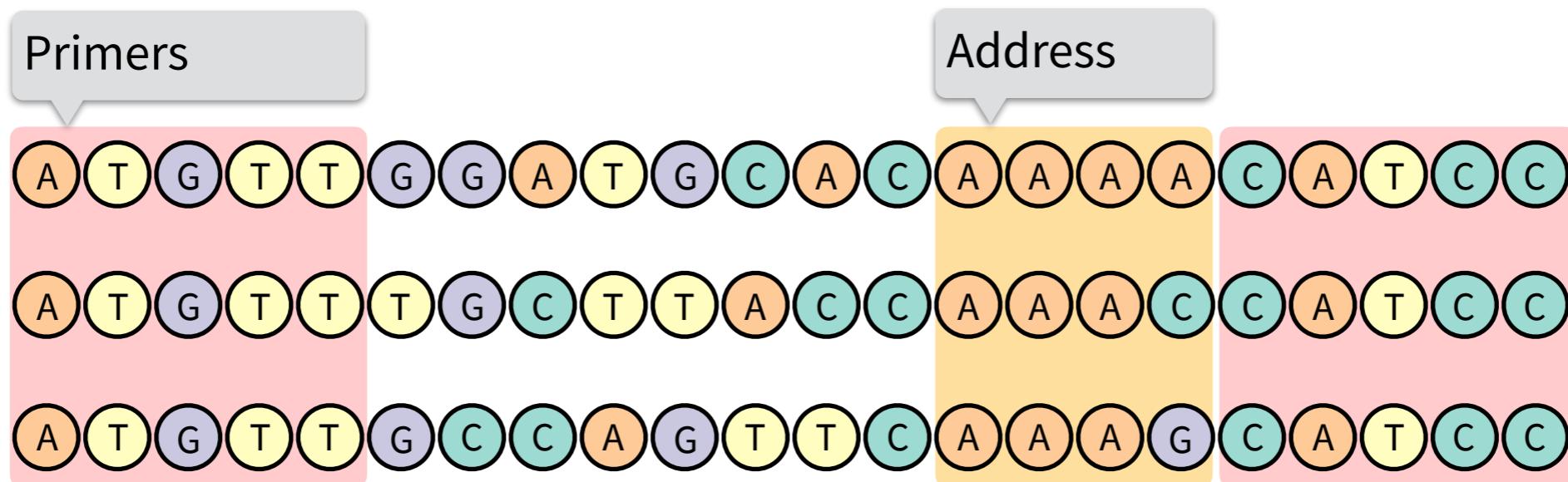
PCR

Selectively
amplify
strands
based on
their primer

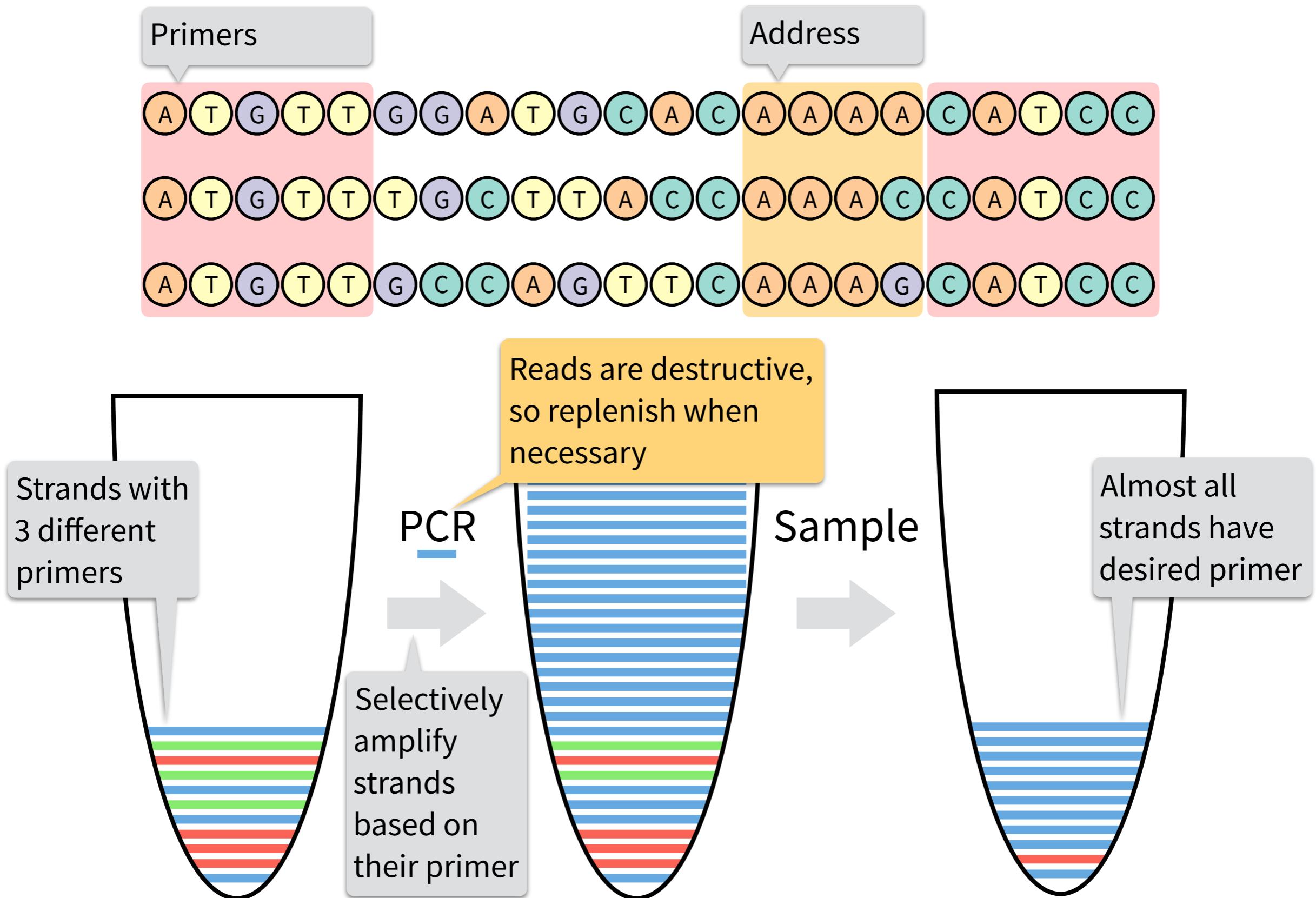
Random access



Random access

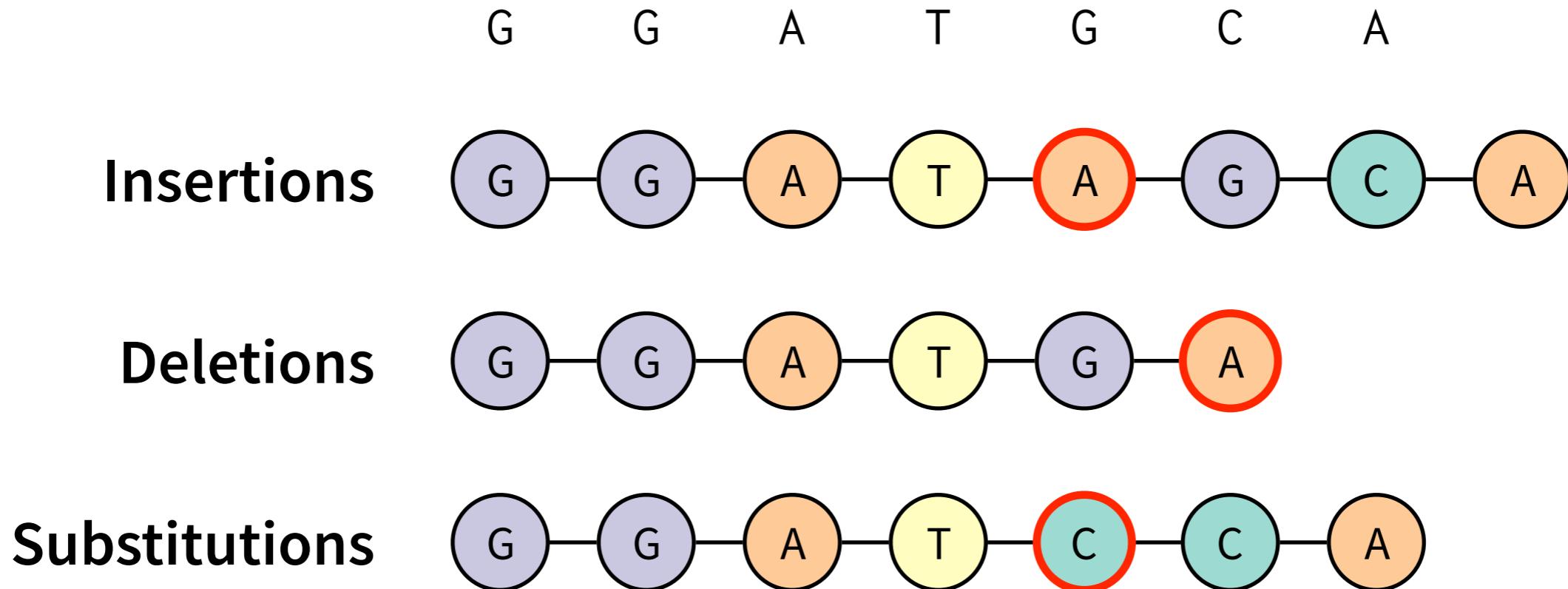


Random access



Error correction

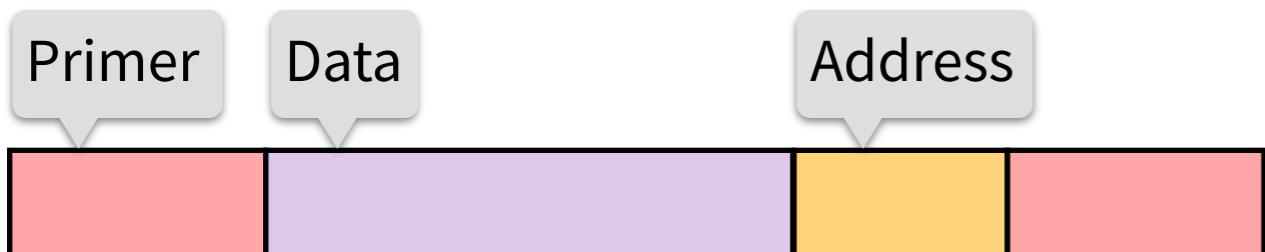
Both synthesis and sequencing are error prone:



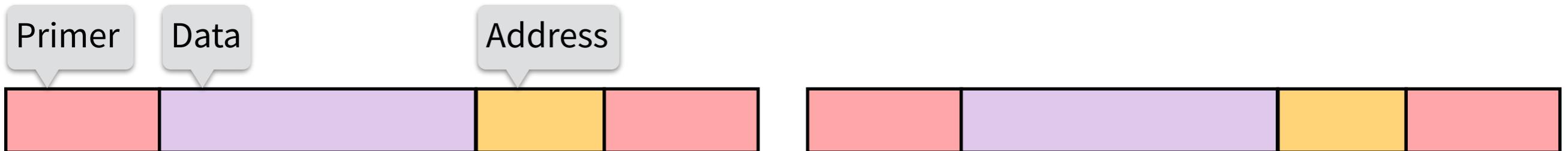
Error rates ~1%
per nucleotide!

Logical redundancy

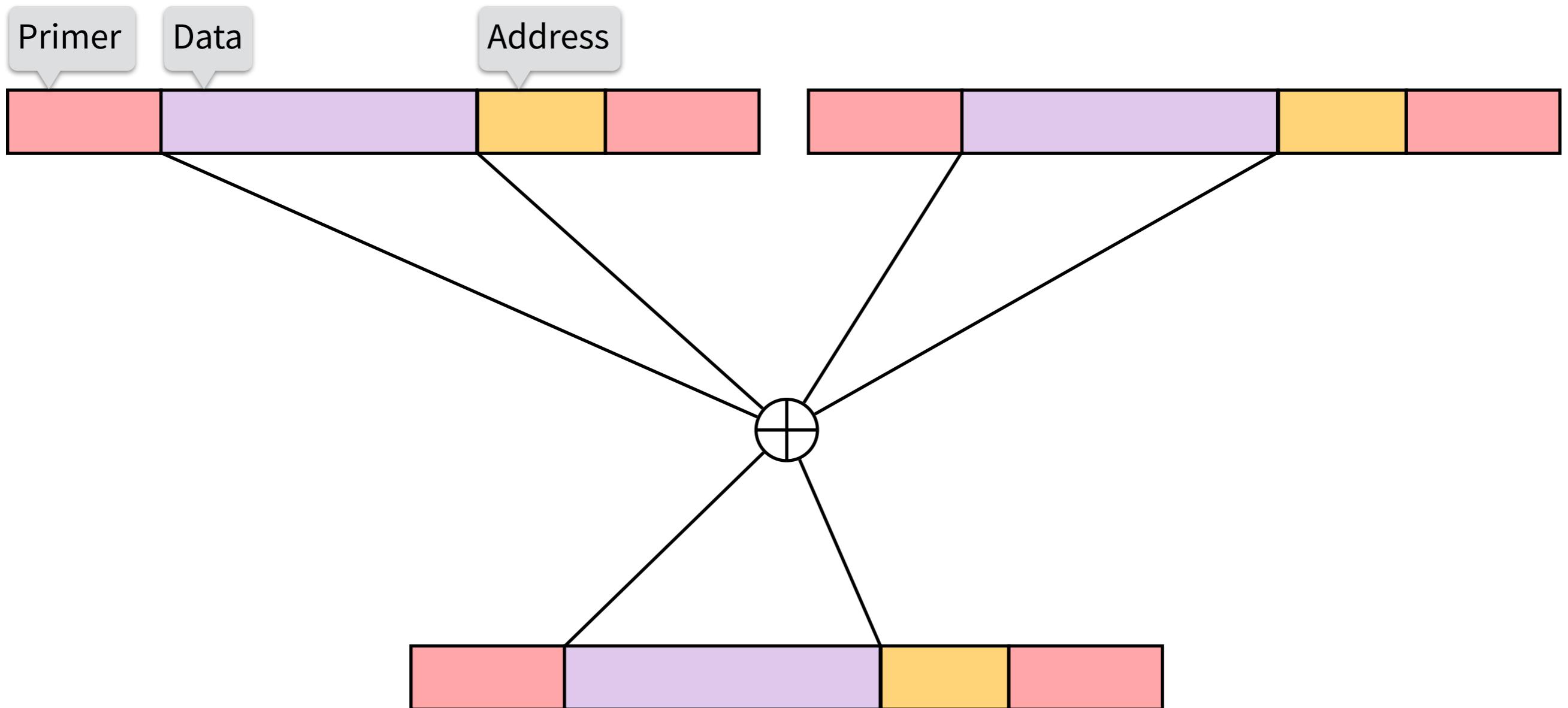
Logical redundancy



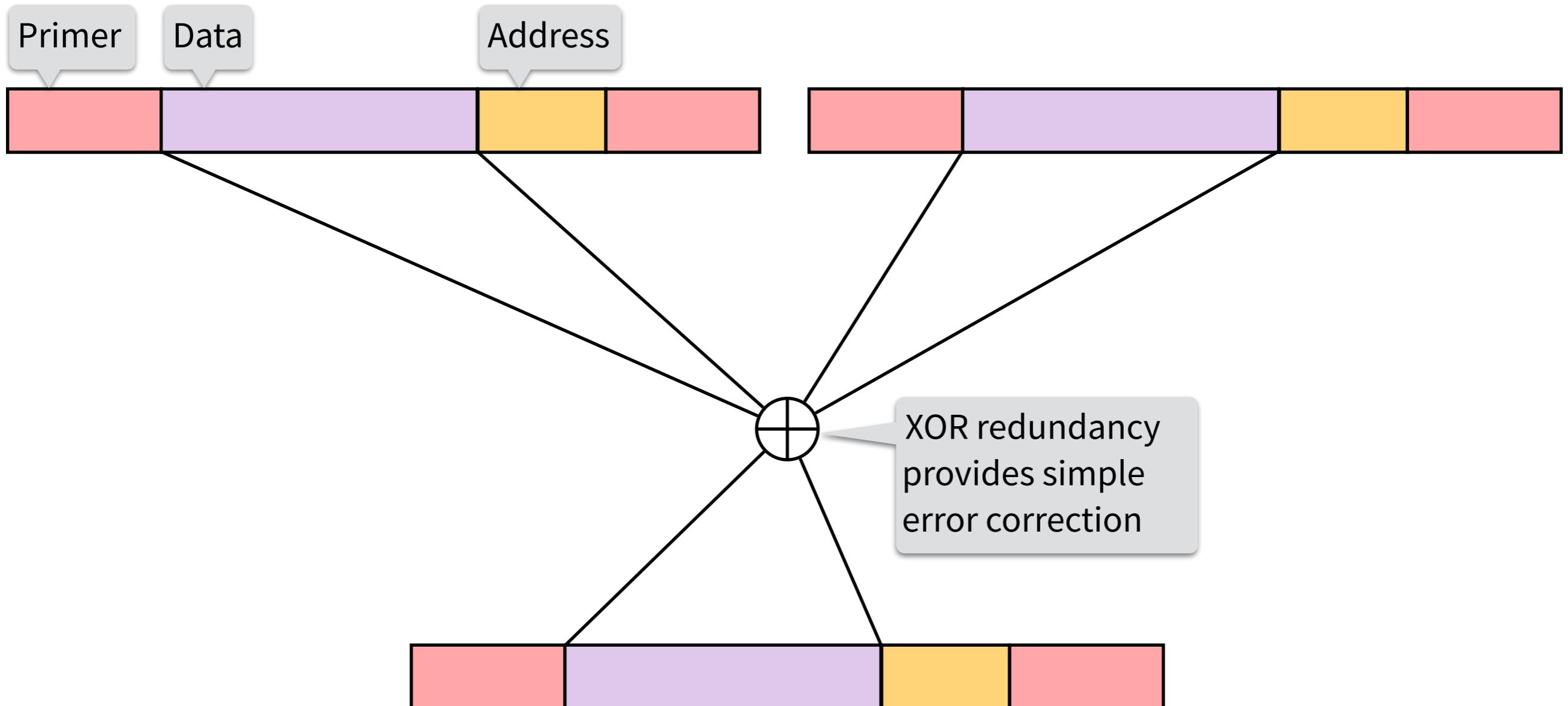
Logical redundancy



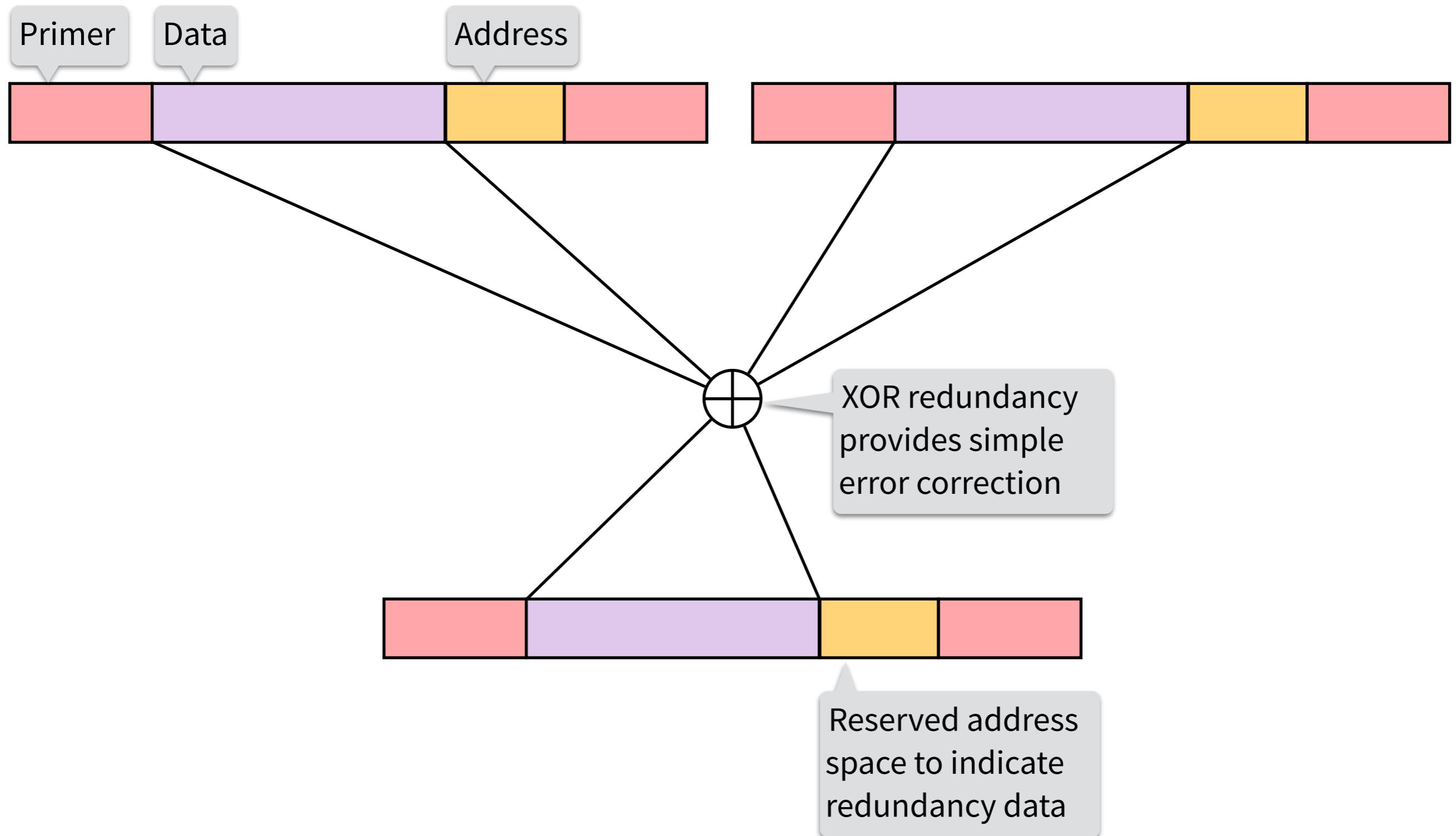
Logical redundancy



Logical redundancy



Logical redundancy



Wet lab results

The process

The process



The process



The process

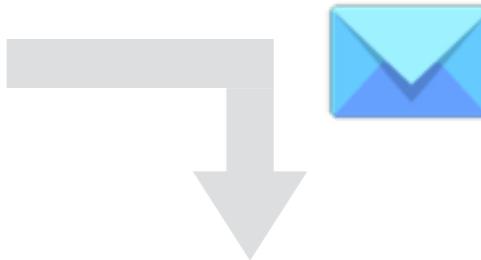


catcatgg

The process



catcatgg



The process



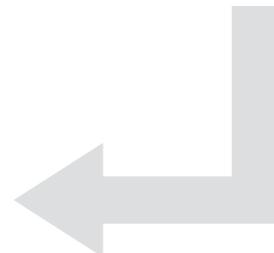
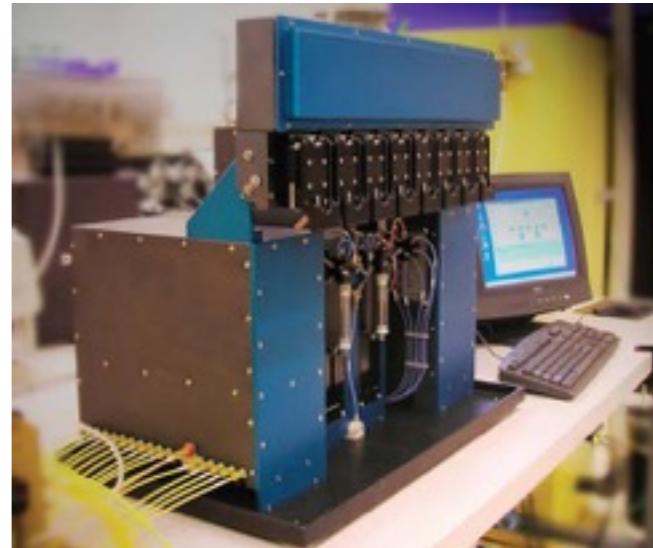
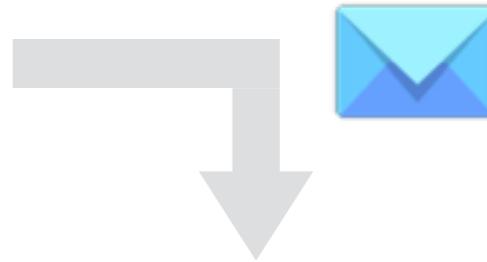
catcatgg



The process



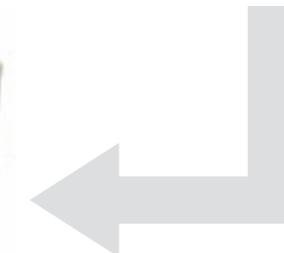
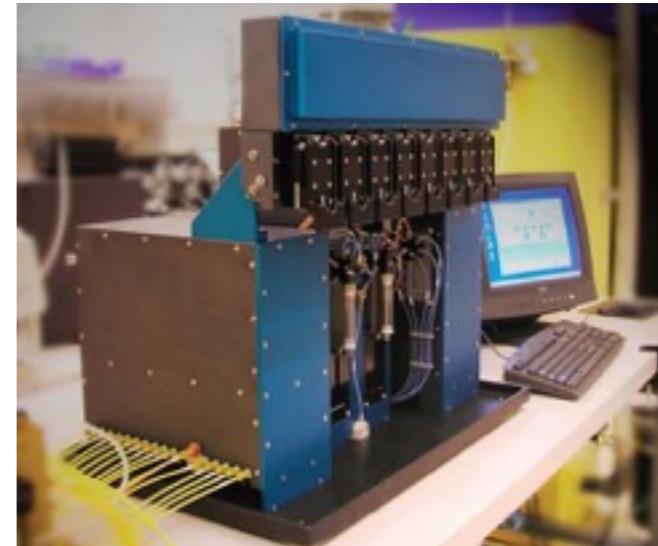
catcatgg



The process



catcatgg



FedEx

The process



catcatgg



catcatg**c**

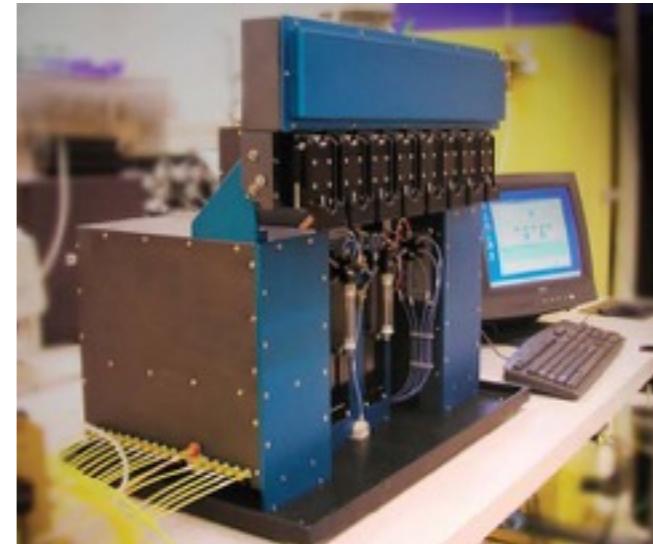


FedEx

The process



catcatgg



catcatg**c**

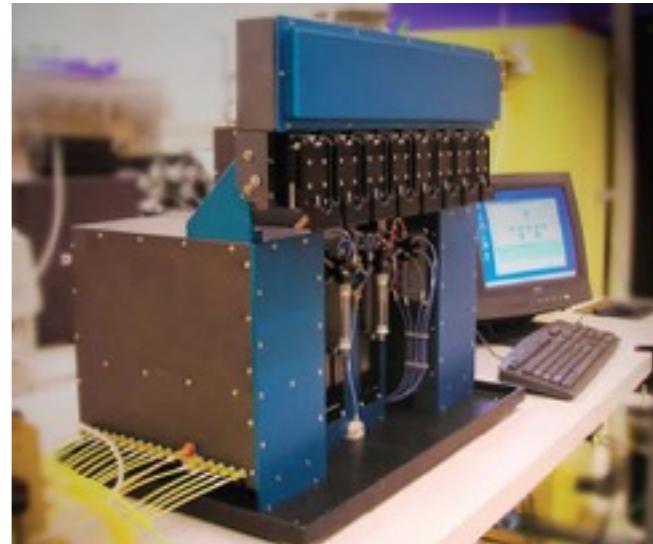
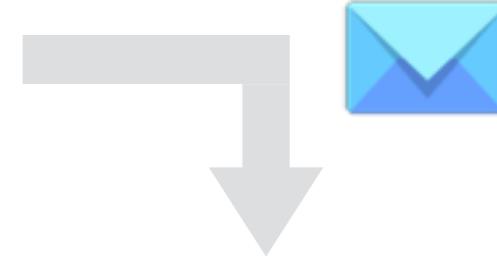


FedEx

The process



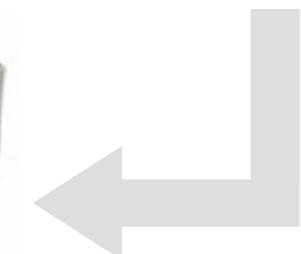
catcatgg



catcatg**c**



Throughput
MBs/week



FedEx



Decoding

Encoded and synthesized 3 files (151 kB):





Photo: Tara Brown / UW

Decoding

Encoded and synthesized 3 files (151 kB):



Decoding

Encoded and synthesized 3 files (151 kB):



Selected and PCRed one file for random access (42 kB):



Decoding

Encoded and synthesized 3 files (151 kB):



Selected and PCRed one file for random access (42 kB):



Sequenced and decoded the resulting amplified pool:

Decoding

Encoded and synthesized 3 files (151 kB):



Selected and PCRed one file for random access (42 kB):

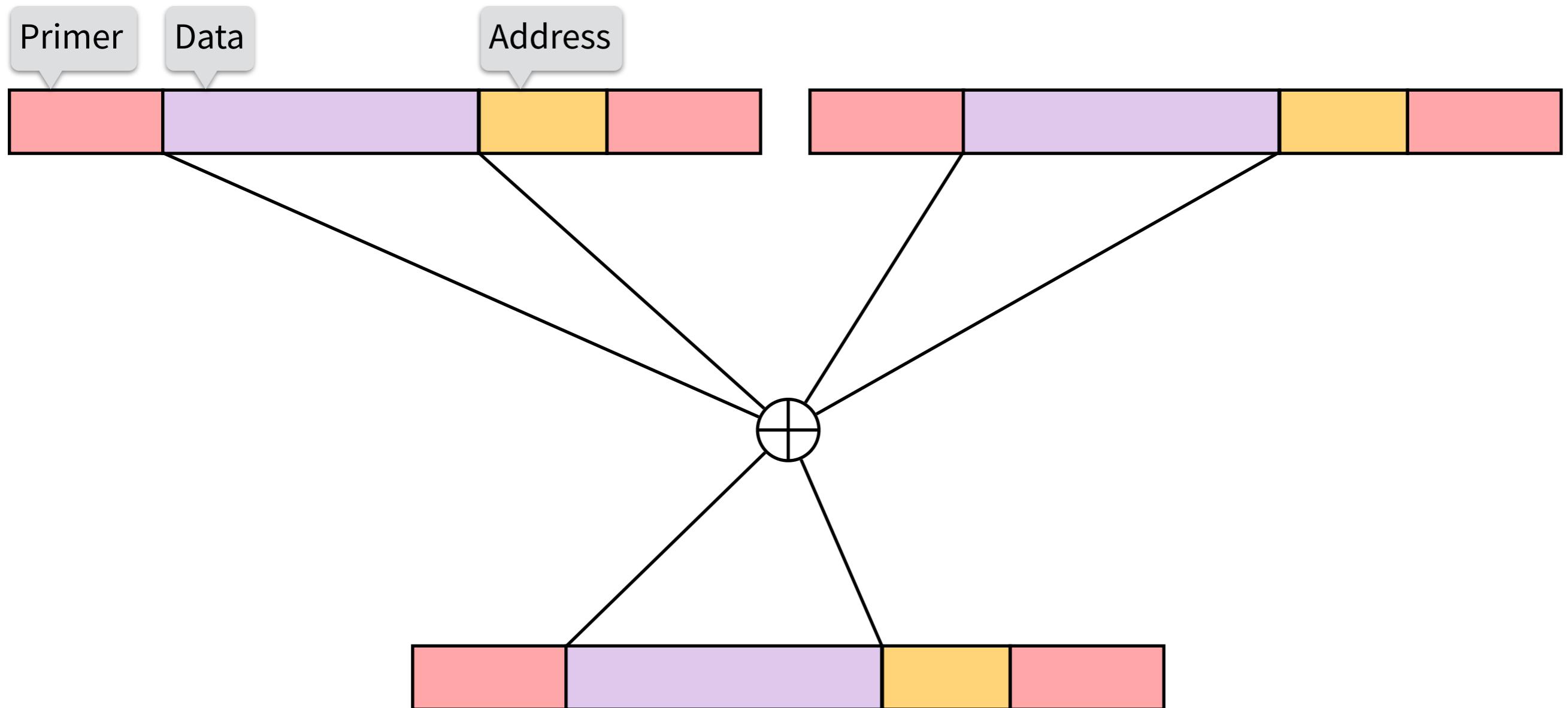


Sequenced and decoded the resulting amplified pool:

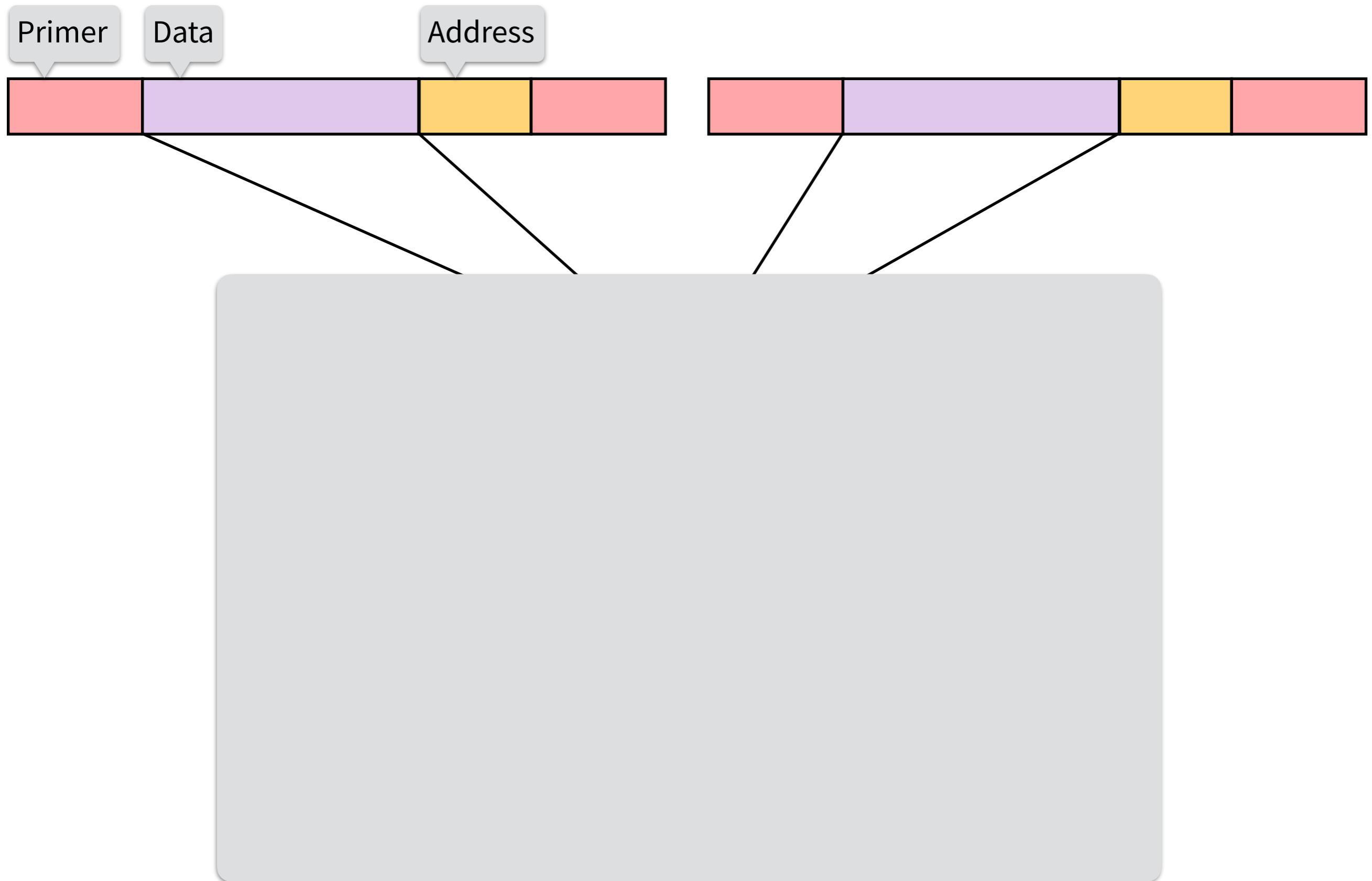


Recovered every *bit*
despite errors in
synthesis and
sequencing

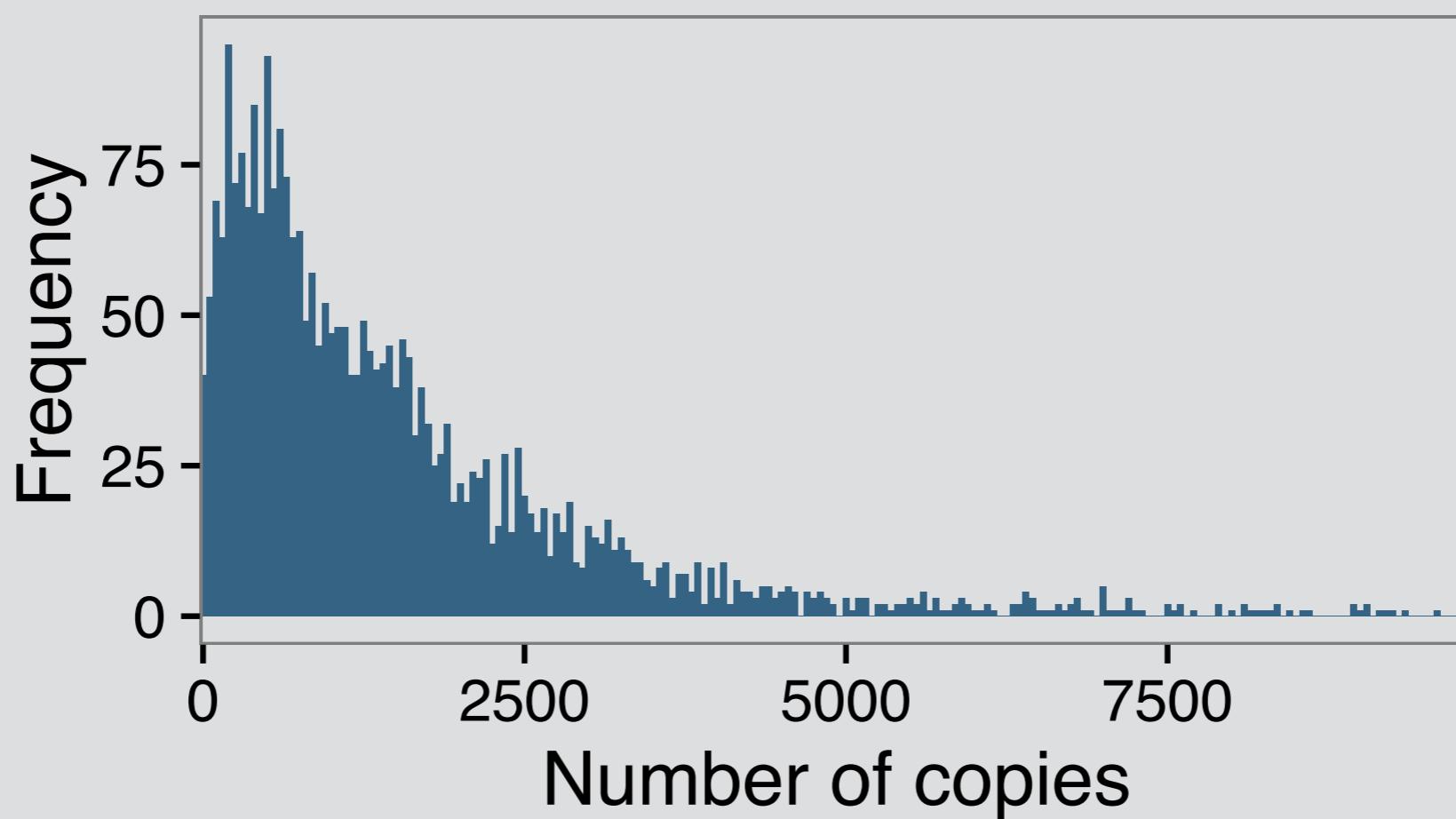
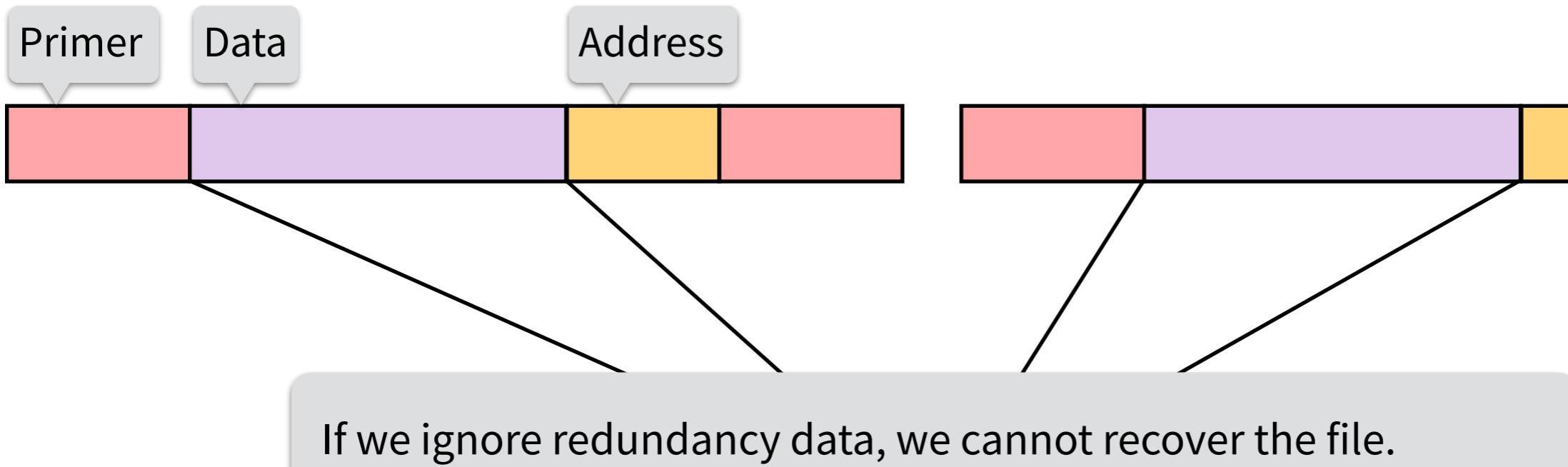
The importance of redundancy



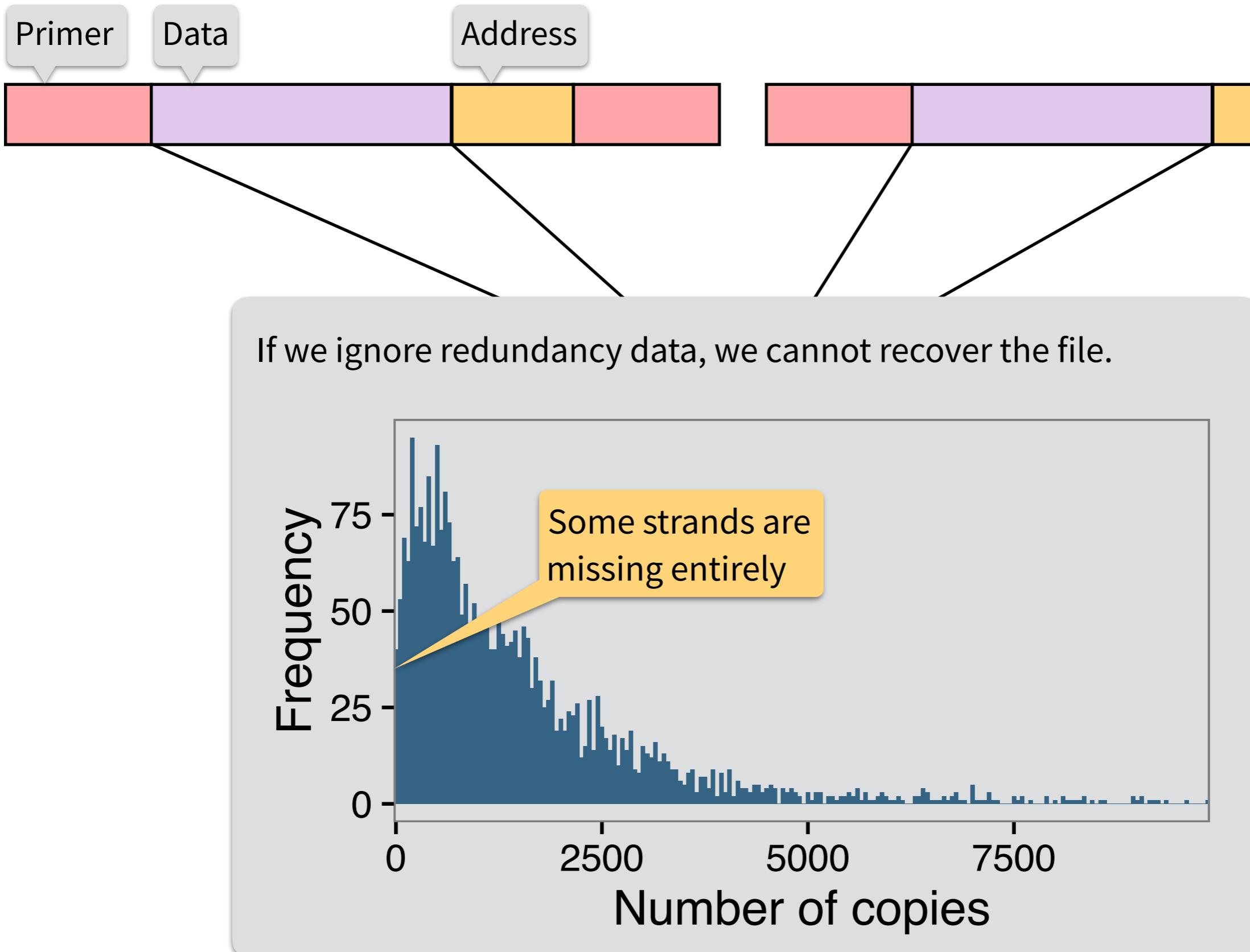
The importance of redundancy



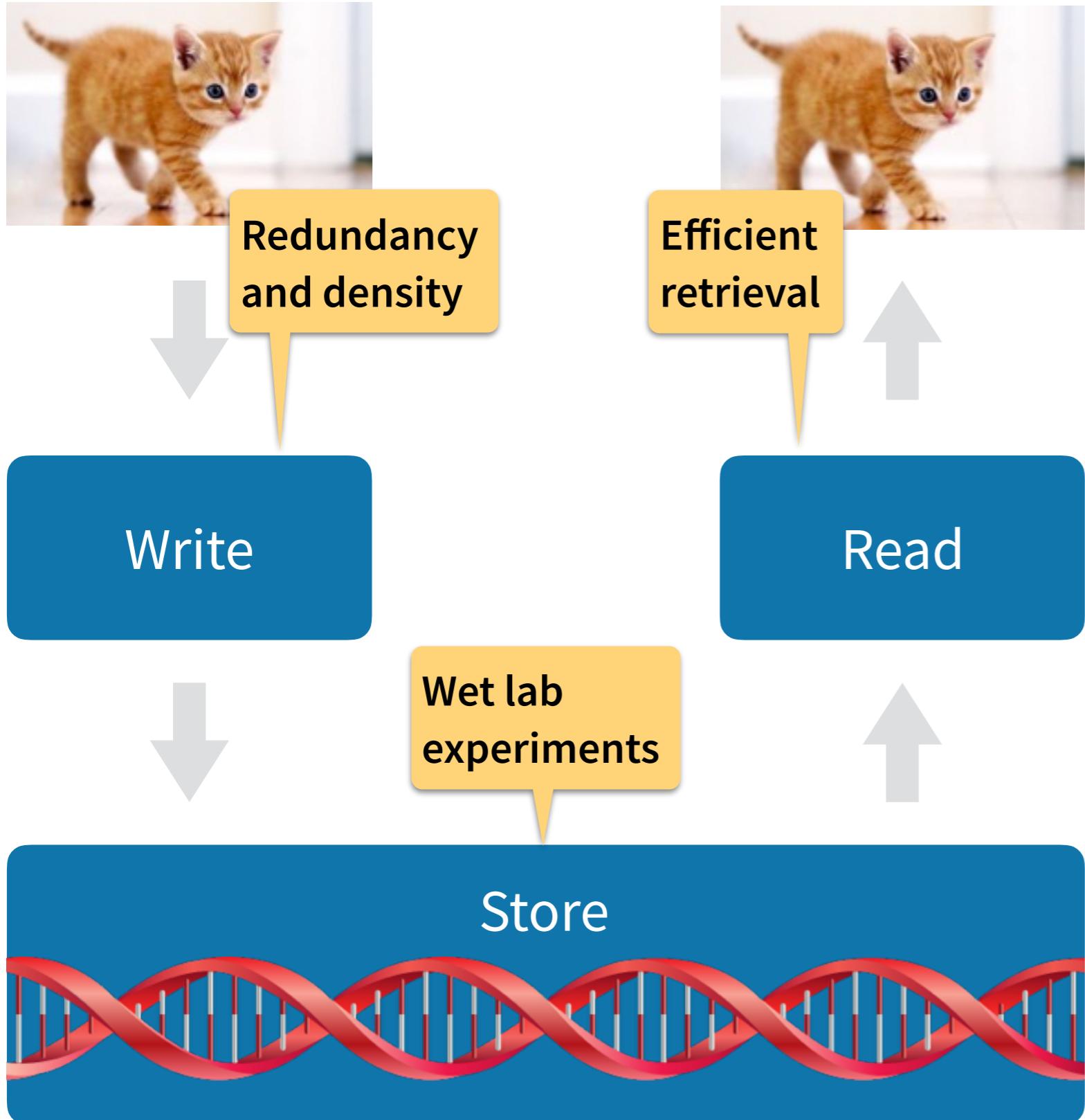
The importance of redundancy



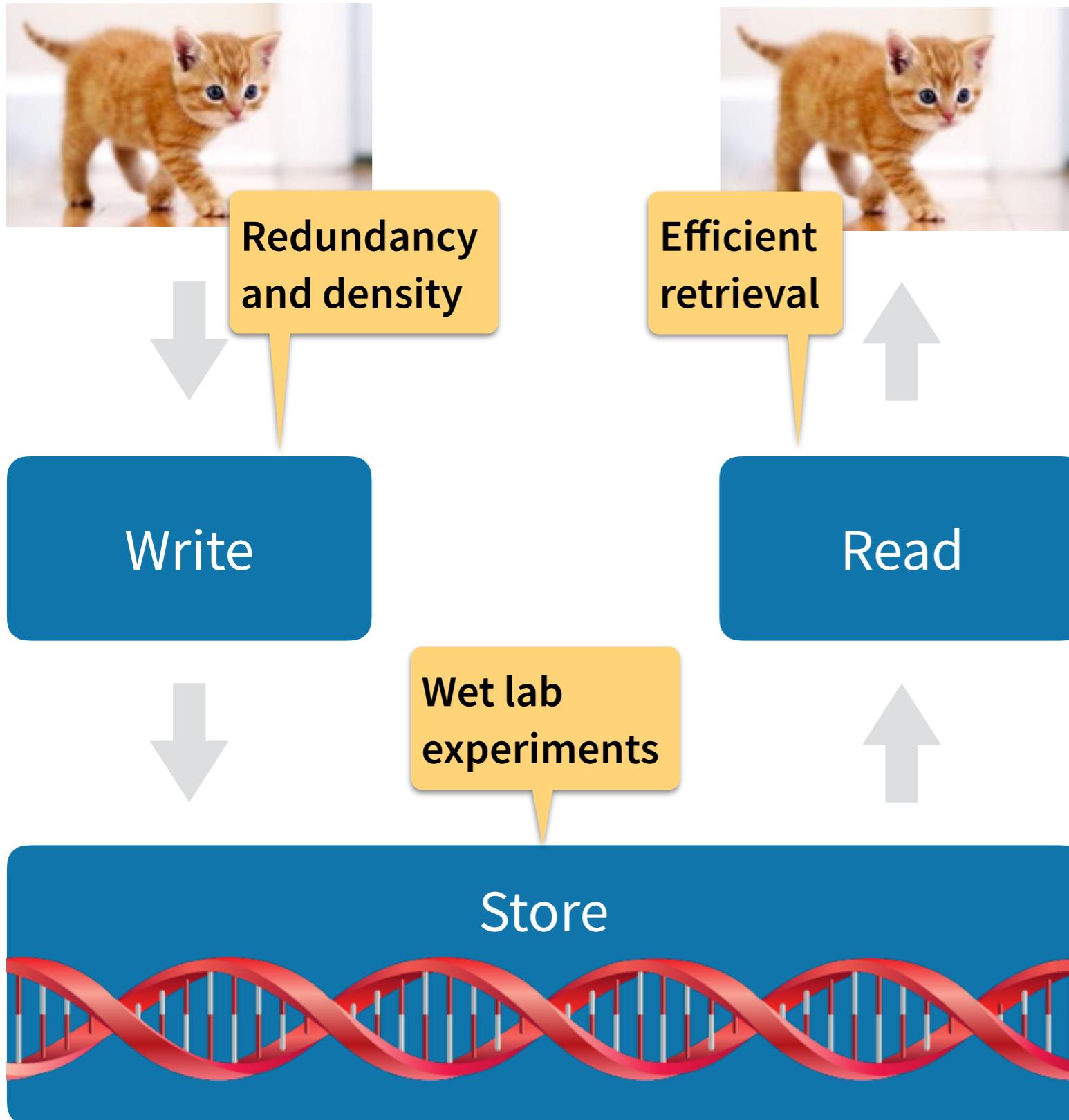
The importance of redundancy



A DNA-based archival storage system



A DNA-based archival storage system

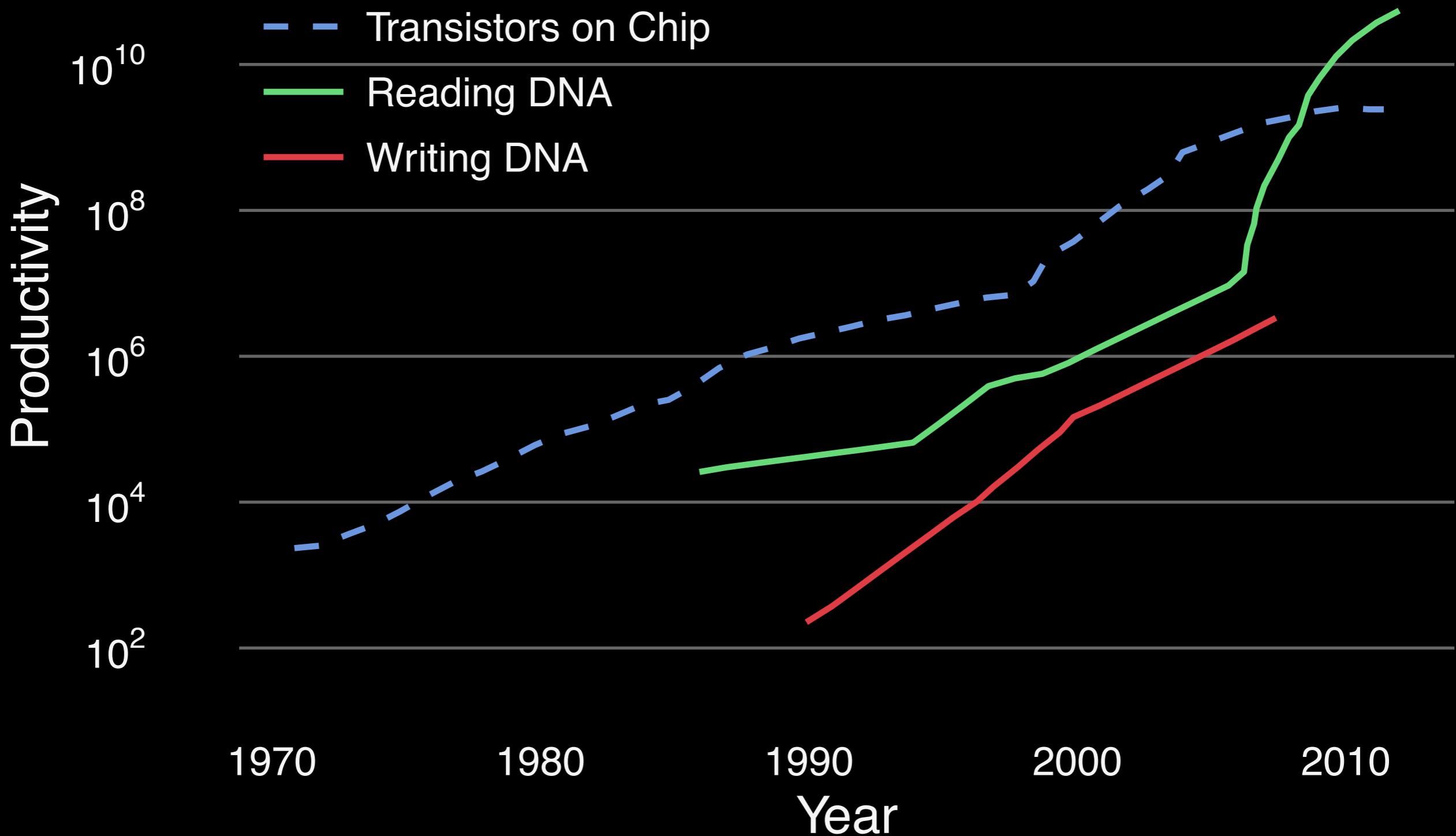


Also in the paper:

- Reliability-density trade-off
- Simulation of decay over time
- Error analysis
- Model of truncated strands

MBs/week → GBs/second

DNA productivity is growing

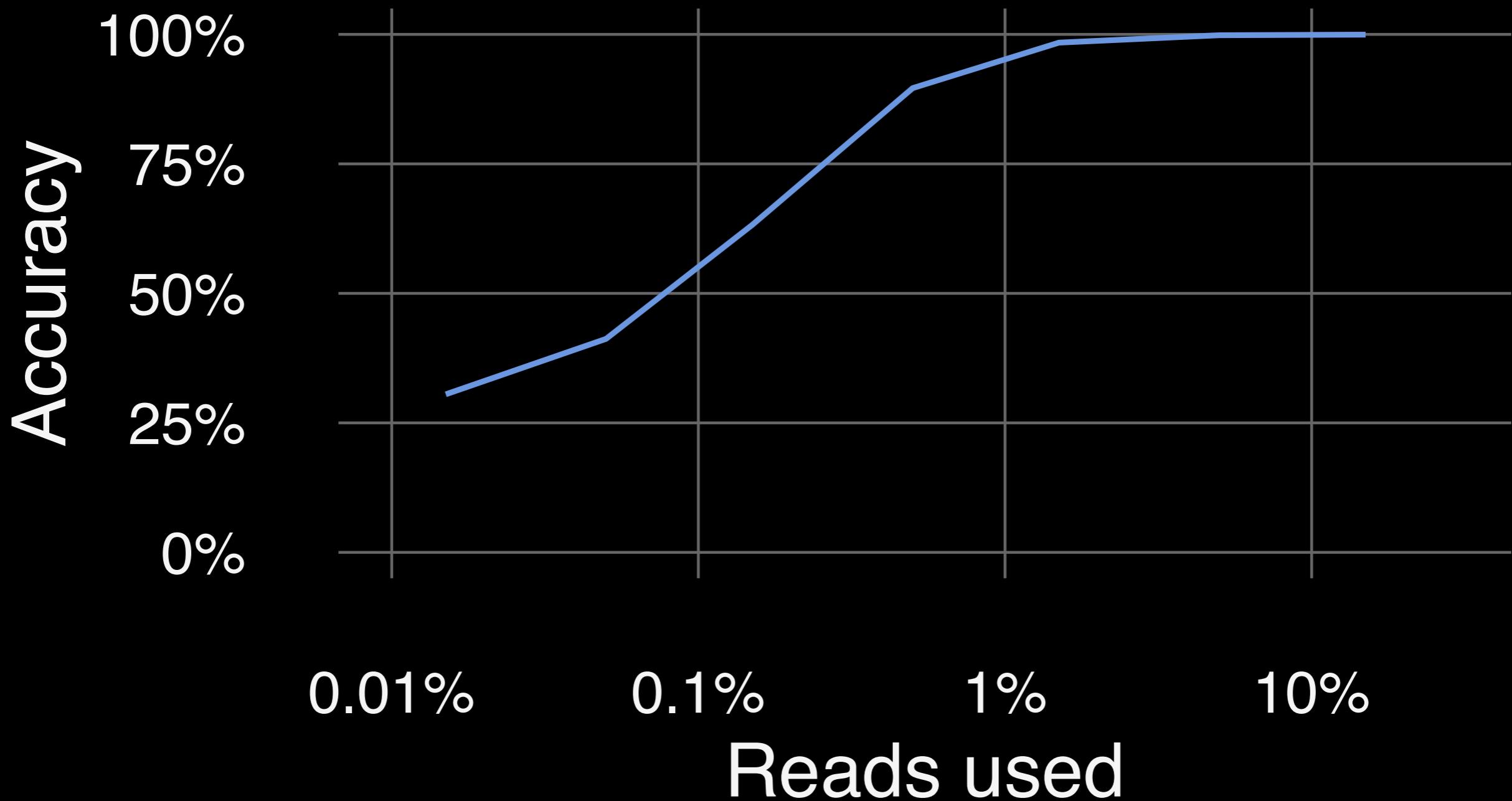


Source: Robert Carlson

DNA technology is miniaturizing



We've just barely scratched the surface



Our community has seen these challenges before

Simulation

Cache locality

Latency-hiding
optimizations

Scheduling

Error correction

Spatial addressing

Circuit design

Programming
with errors



Photo: Tara Brown / UW