Can We Store the Whole World's Data in DNA Storage?

HotStorage'20

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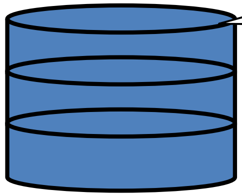
Outlines

- Motivation
- DNA background
- Contributions
  - Trade-offs in DNA storage
  - DNA storage modeling
  - How many tubes to store the whole world’s data?
- Indexing scheme
- Conclusion

Big Data Era



Data is doubled almost every **2 years**
44 Zettabytes in 2020
175 Zettabytes in 2025

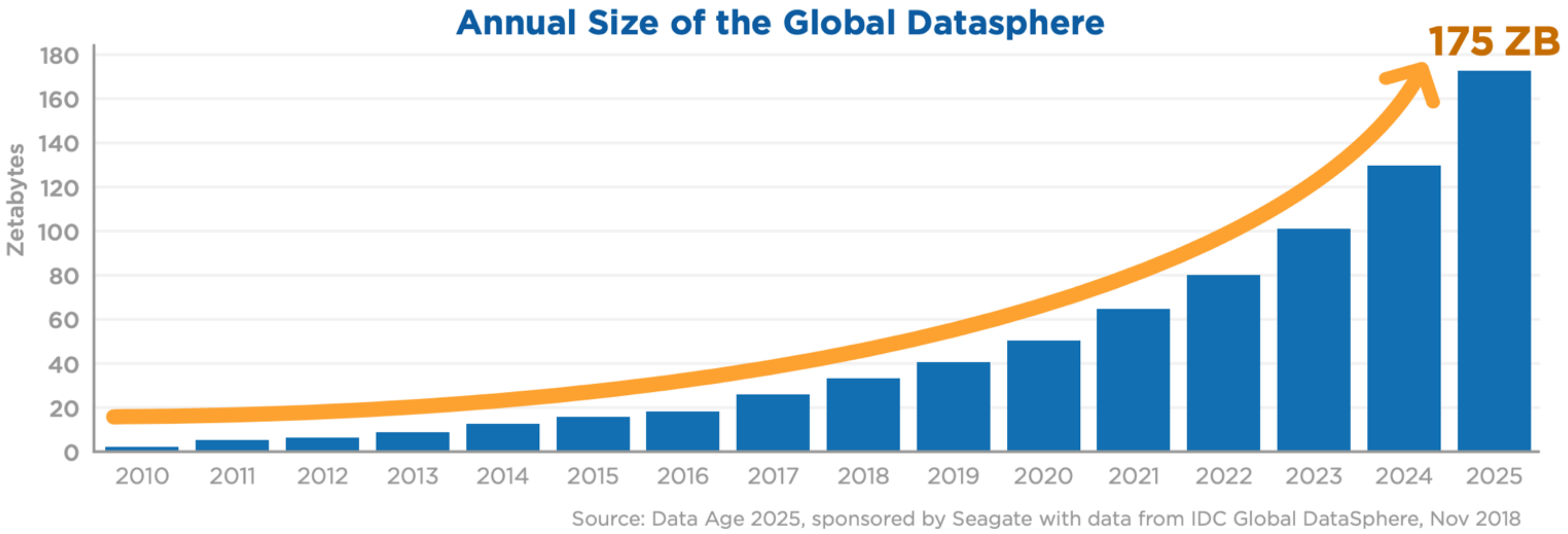
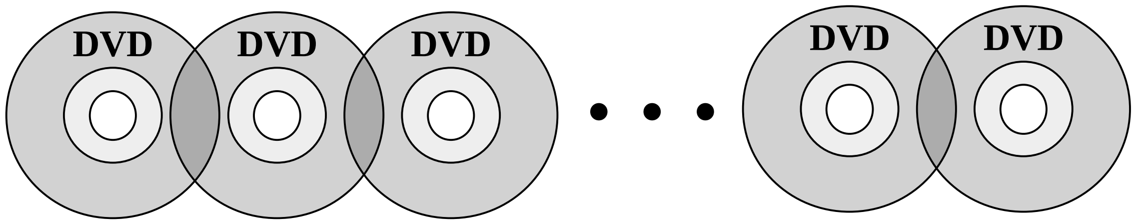


Image from: https://www.seagate.com/files/www-content/our-story/trends/files/idc-seagate-dataage-whitepaper.pdf

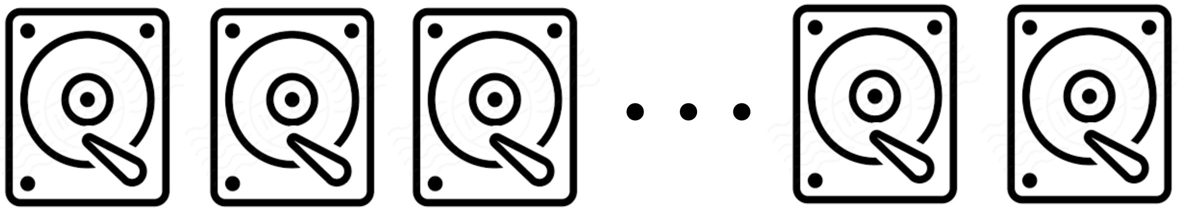
How to Store these Data?

44 ZB

50 trillion DVD movies



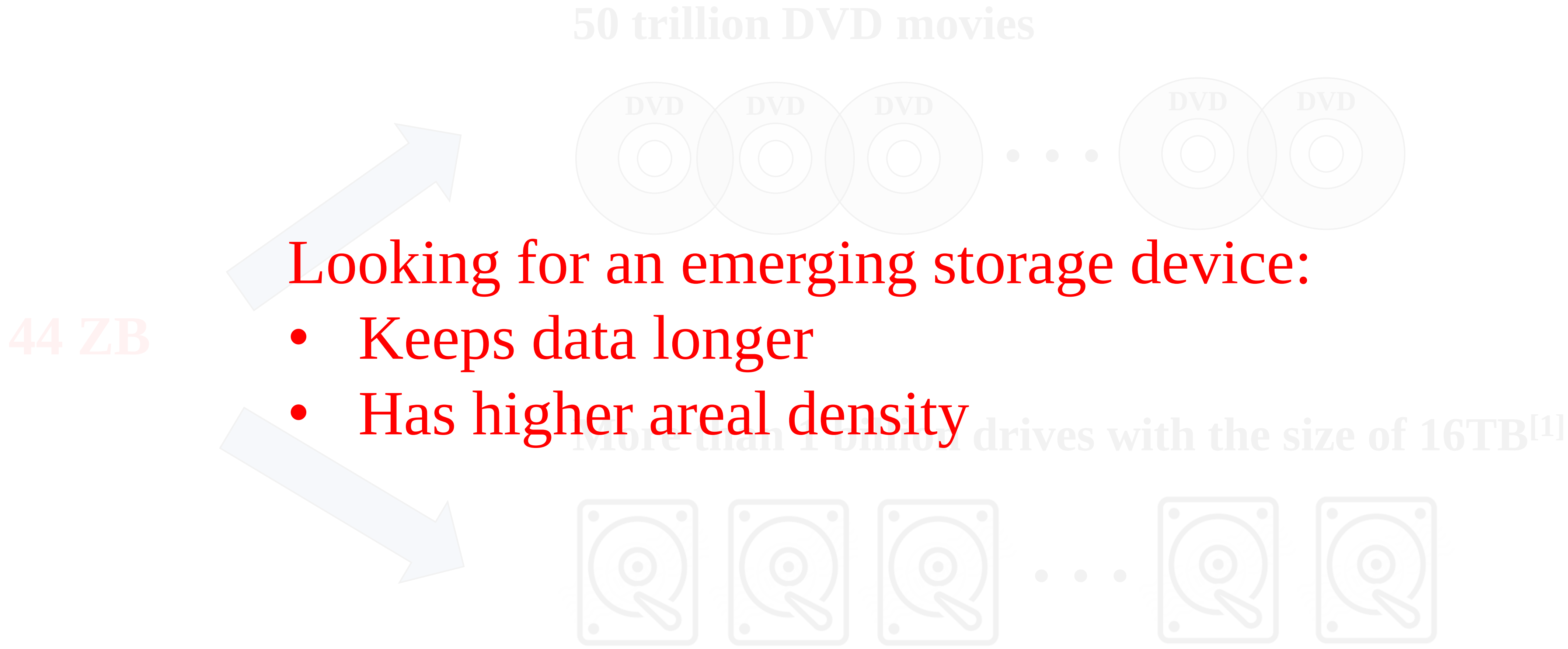
More than 1 billion drives with the size of 16TB[1]



5 years or 10 years warranty

[1] https://www.seagate.com/enterprise-storage/

How to Store these Data?



Looking for an emerging storage device:

- Keeps data longer
- Has higher areal density

[1] *https://www.seagate.com/enterprise-storage/*

DNA Storage

- High spatial density
  - A theoretical density of 455 EB/g [1]

- Long persistency
  - Several centuries [2][3]

[1] Raja Appuswamy, Kevin Le Brigand, Pascal Barbry, Marc Antonini, Olivier Madderson, Paul Freemont, James McDonald, and Thomas Heinis. Oligoarchive: Using dna in the dbms storage hierarchy. In CIDR, 2019.
[2] Morten E Allentoft, Matthew Collins, David Harker, James Haile, Charlotte L Oskam, Marie L Hale, Paula F Campos, Jose A Samaniego, M Thomas P Gilbert, Eske Willerslev, et al. The half-life of dna in bone: measuring decay kinetics in 158 dated fossils. Proceedings of the Royal Society B: Biological Sciences, 279(1748):4724–4733, 2012.
[3] Robert N Grass, Reinhard Heckel, Michela Puddu, Daniela Paunescu, and Wendelin J Stark. Robust chemical preservation of digital information on dna in silica with error-correcting codes. Angewandte Chemie International Edition, 54(8):2552–2555, 2015.

Background of DNA storage

- **Nucleotides**: molecules form the building blocks of DNA.
  - Adenine (A) ←→ Thymine (T)
  - Cytosine (C) ←→ Guanine (G)

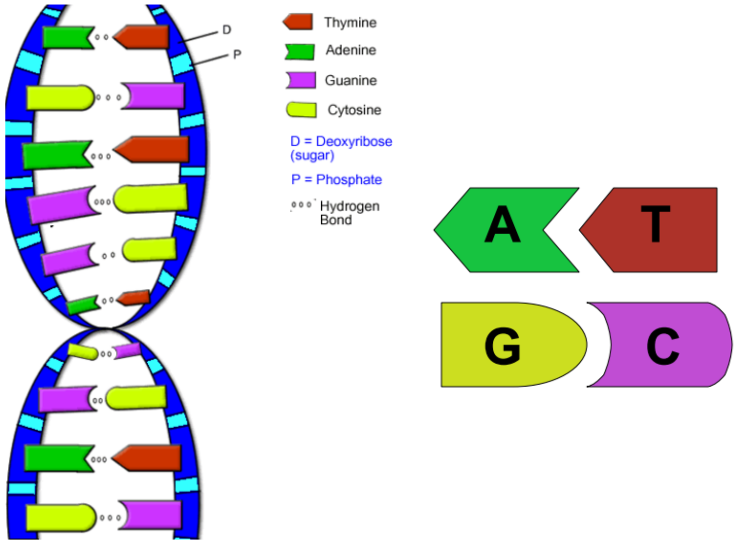


Figure 1

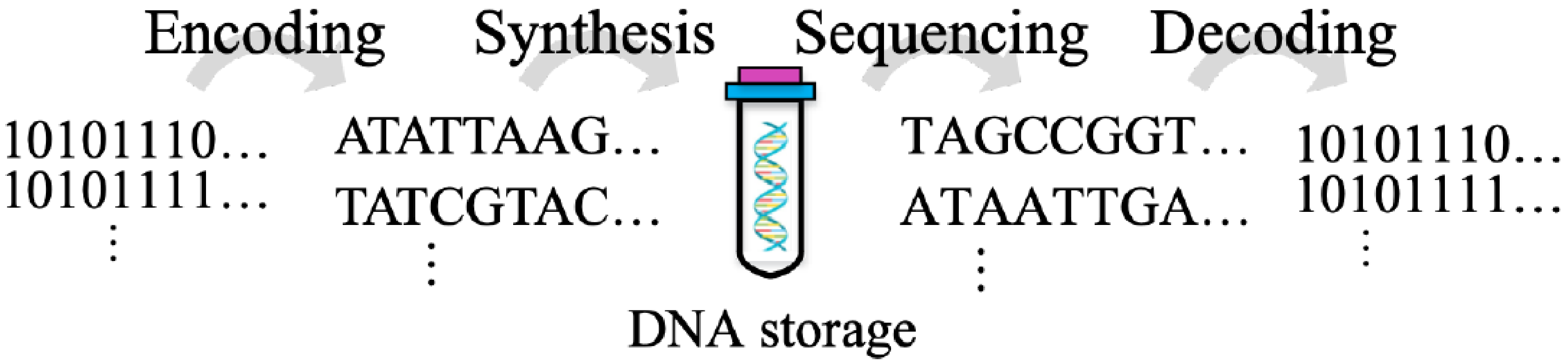
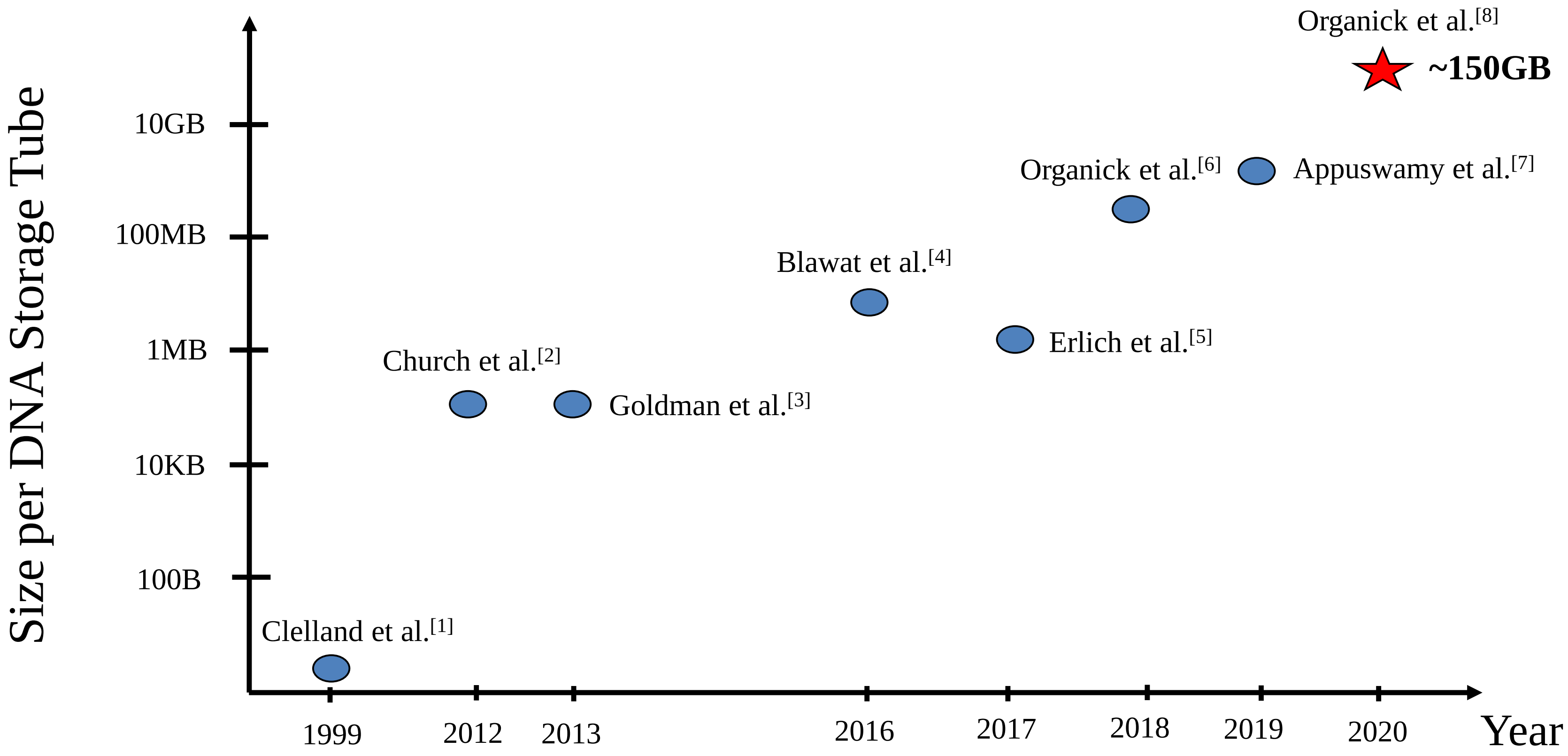


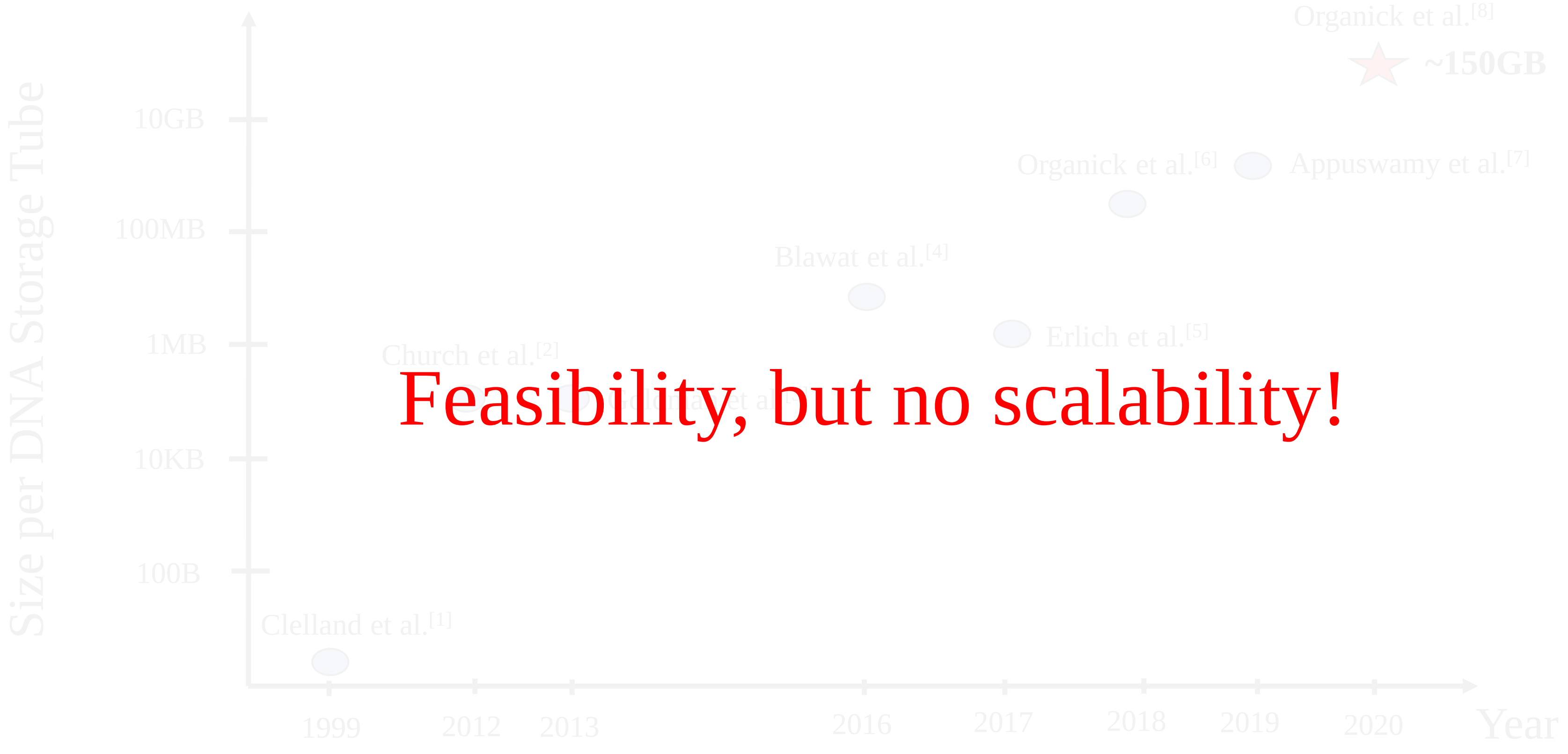
Figure 1 from https://www.genome.gov/Pages/Education/Modules/BasicsPresentation.pdf

Existing Work



[1] Clelland, C. T., Risca, V. & Bancroft, C. Hiding messages in DNA microdots. Nature 399, 533–534 (1999).
[2] Church, G. M., Gao, Y. & Kosuri, S. Next- generation digital information storage in DNA. Science ***337****, 1628–1628 (2012)*
[3] Goldman, N. et al. Towards practical, high- capacity,low- maintenance information storage in synthesized DNA. Nature 494, 77–80 (2013).
[4] Blawat, M. et al. Forward error correction for DNA data storage. Procedia Comput. Sci. 80, 1011–1022 (2016)
[5] Erlich, Y. & Zielinski, D. DNA Fountain enables a robust and efficient storage architecture. Science 355, 950–954 (2017).
[6] Organick, L. et al. Random access in large- scale DNA data storage. Nat. Biotechnol. 36, 242–248 (2018).
[7] Appuswamy, Raja, et al. "OligoArchive: Using DNA in the DBMS storage hierarchy." CIDR. 2019.
[8] Organick, Lee, et al. "Probing the physical limits of reliable DNA data retrieval." Nature communications 11.1 (2020): 1-7.

Existing Work



Feasibility, but no scalability!

[1] Clelland, C. T., Risca, V. & Bancroft, C. Hiding messages in DNA microdots. Nature 399, 533–534 (1999).
[2] Church, G. M., Gao, Y. & Kosuri, S. Next- generation digital information storage in DNA. Science 337, 1628–1628 (2012)
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Our Contributions

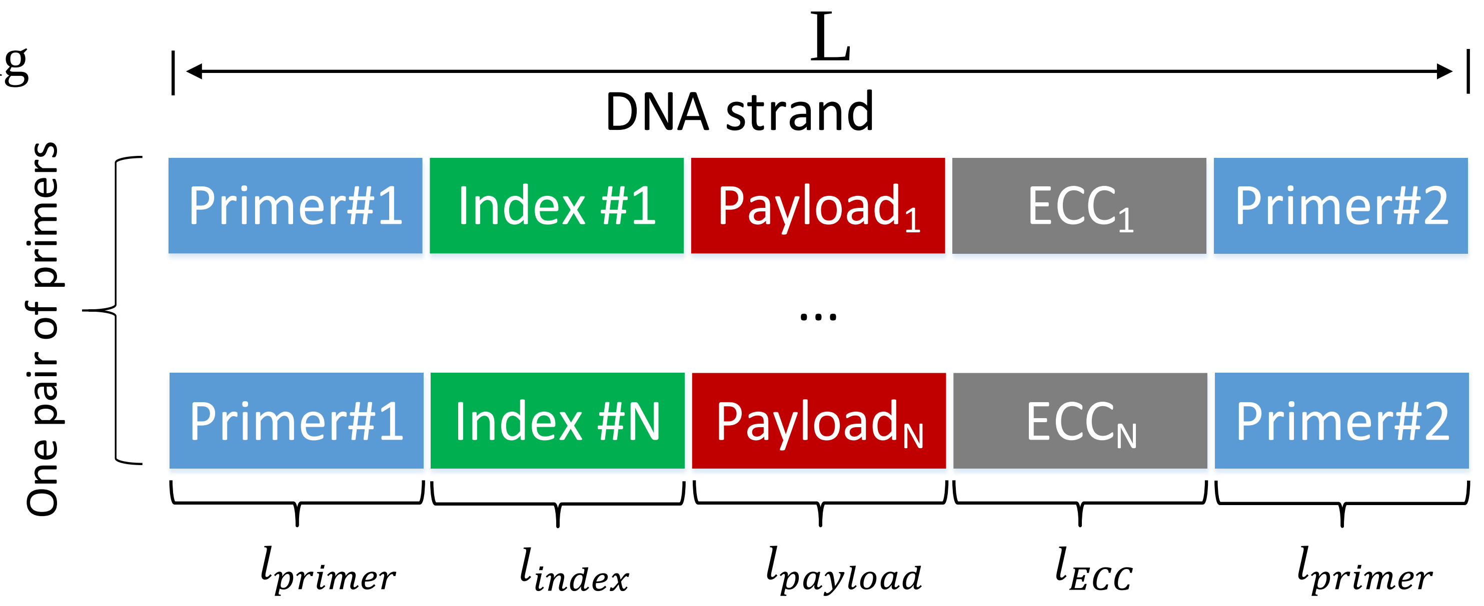
- Investigate the effect of different factors on the capacity of DNA storage (in-house simulator)
- Analyze trade-offs between different factors and scalability of DNA storage
- How to index the whole world's data in DNA storage

Factors and Modeling of DNA Storage

- **Primer**: is used to read data out (sequencing process based on Polymerase Chain Reaction (PCR))
- **Index**: distinguishes DNA strands in the same primer pair
- **Payload**: useful information
- **ECC**: corrects errors from synthesis and sequencing processes

- **PF (primer factor)**: **N** DNA strands attached to the same primer pair
- **Coding density**: useful information (bit)
  $Info = coding\ density\ * l_{payload}$

- **Solubility**
- **Droplet volume**
- **...**



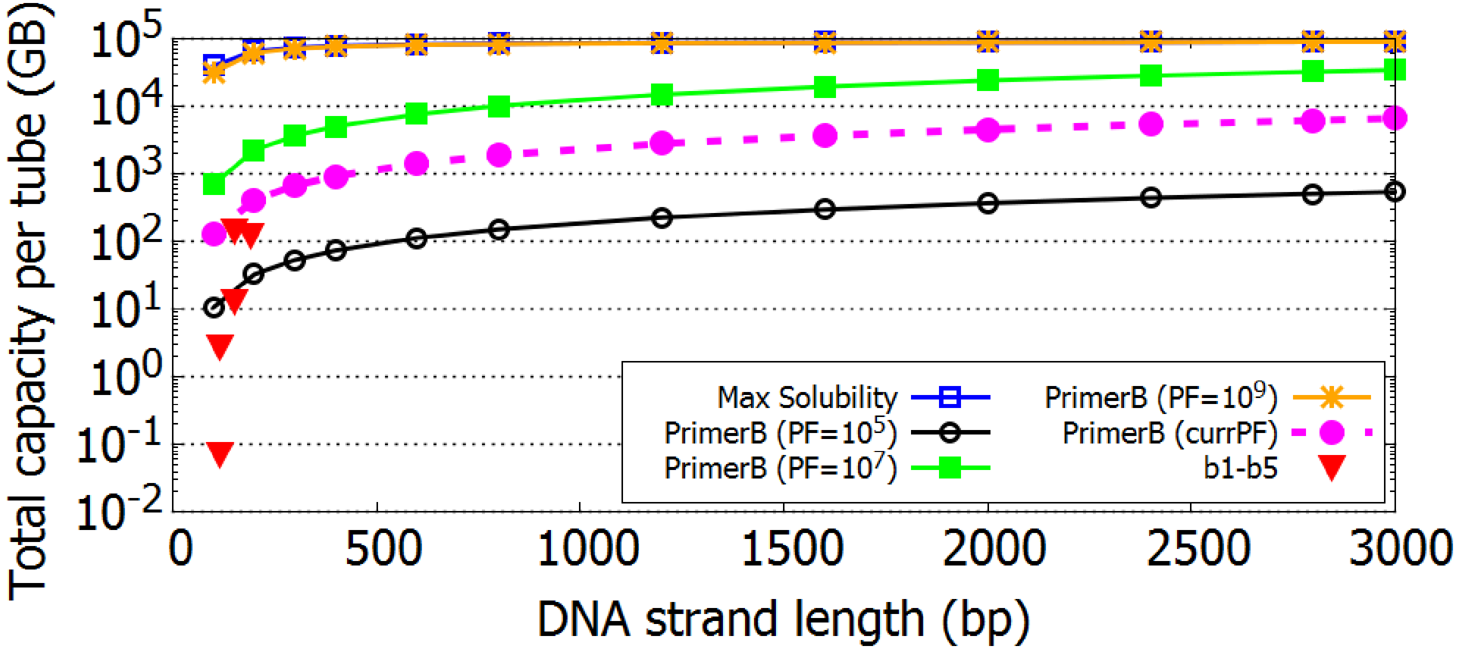
$$L = l_{primer} * 2 + l_{index} + l_{payload} + l_{ECC}$$

(l_{primer} is about 18 – 25 bp)

DNA Storage Trade-offs: varying DNA length (L)

L ↑ ⟹ l_{ECC} ↑ $l_{payload}$? l_{index} →

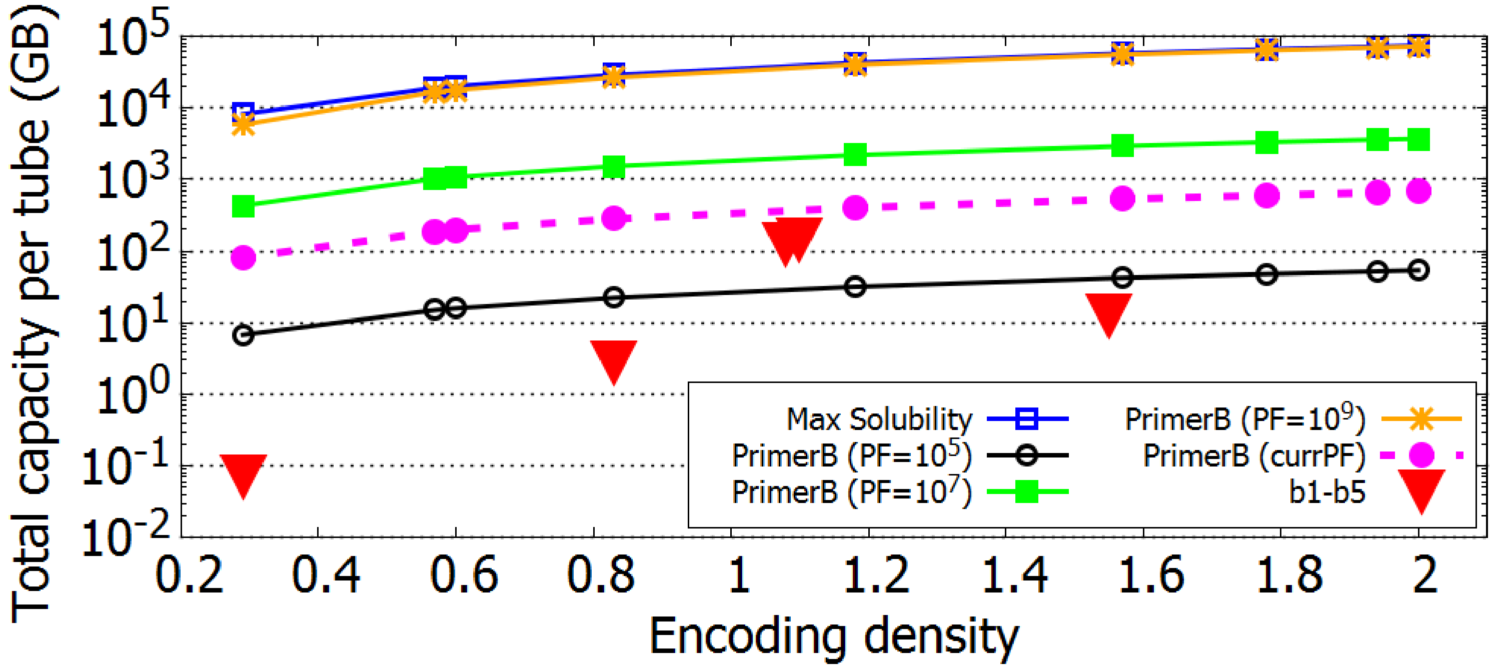
L = 100 – 3000 bp



DNA Storage Trade-offs: varying coding density

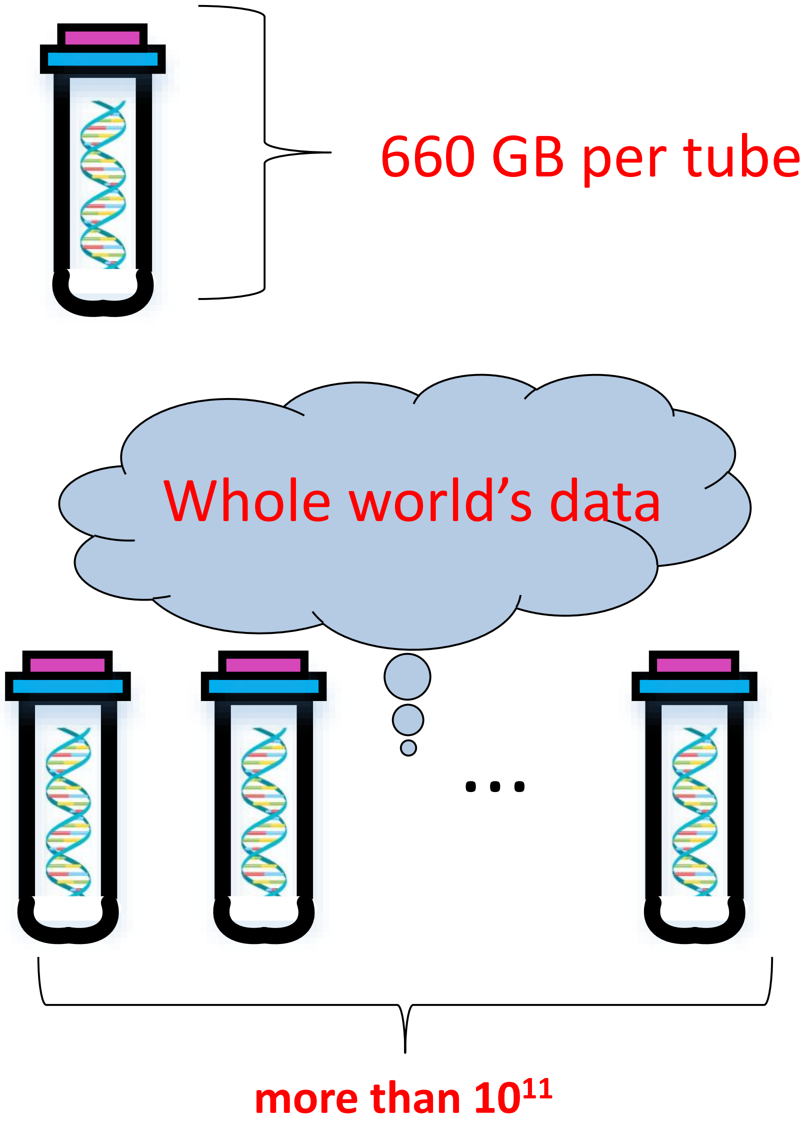
Coding density ↑ ⇒ l_{ECC} ↑ $l_{payload}$ ↓ l_{index} →

Coding = 0.29 - 2



Store the Whole World's Data based on Today's Technology

Factor	Value
Whole world's data (ZB)	44
DNA Strand Length(bp)	300
Primer length (bp)	20
Coding density	1
ECC	15%
Tube size (mL)	1.7
Max DNA solubility in liquid (mg/mL)	500
Droplet size (mL)	0.001
PF	1.55*10E6



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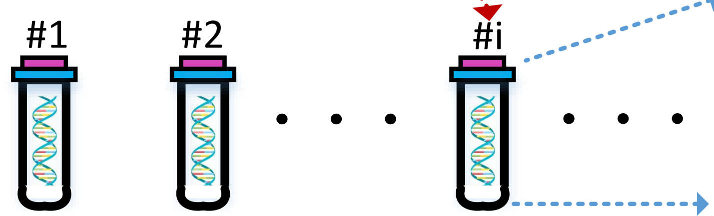
DNA Storage Indexing

Block-based storage device:

Request OFFSET mod $capacity_{tube}$



len

External index:

$offset_1$	Primer pair #1
…	…
$offset_i$	Primer pair #i
…	…
$offset_M$	Primer pair #M

len * # of entries * # of tube ~77 TB

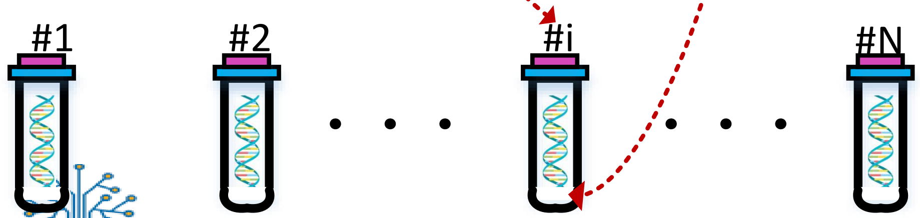
Object-based storage device:

len

External index:

ID_1	Tube #1	Primer pair #1	$Index_{start1}$	$Index_{end1}$
…	…	…	…	…
ID_i	Tube #i	Primer pair #j	$Index_{starti}$	$Index_{endi}$
…	…	…	…	…
ID_M	Tube #N	Primer pair #M	$Index_{startM}$	$Index_{endM}$

Request Global ID/Key



len * # of IDs ~7.17*10^5 TB

Indexing for the object-based storage device is more challenging

Conclusion

- Modeling of DNA storage based on different factors
- Investigate the trade-offs between different factors
- Scalability of DNA storage
- Introduce simple schemes to index the whole world’s data in DNA storage

Thanks!

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