Scalability is a critical challenge in data science ft. Twitter

Professor Bioinformatics and Computational Biology
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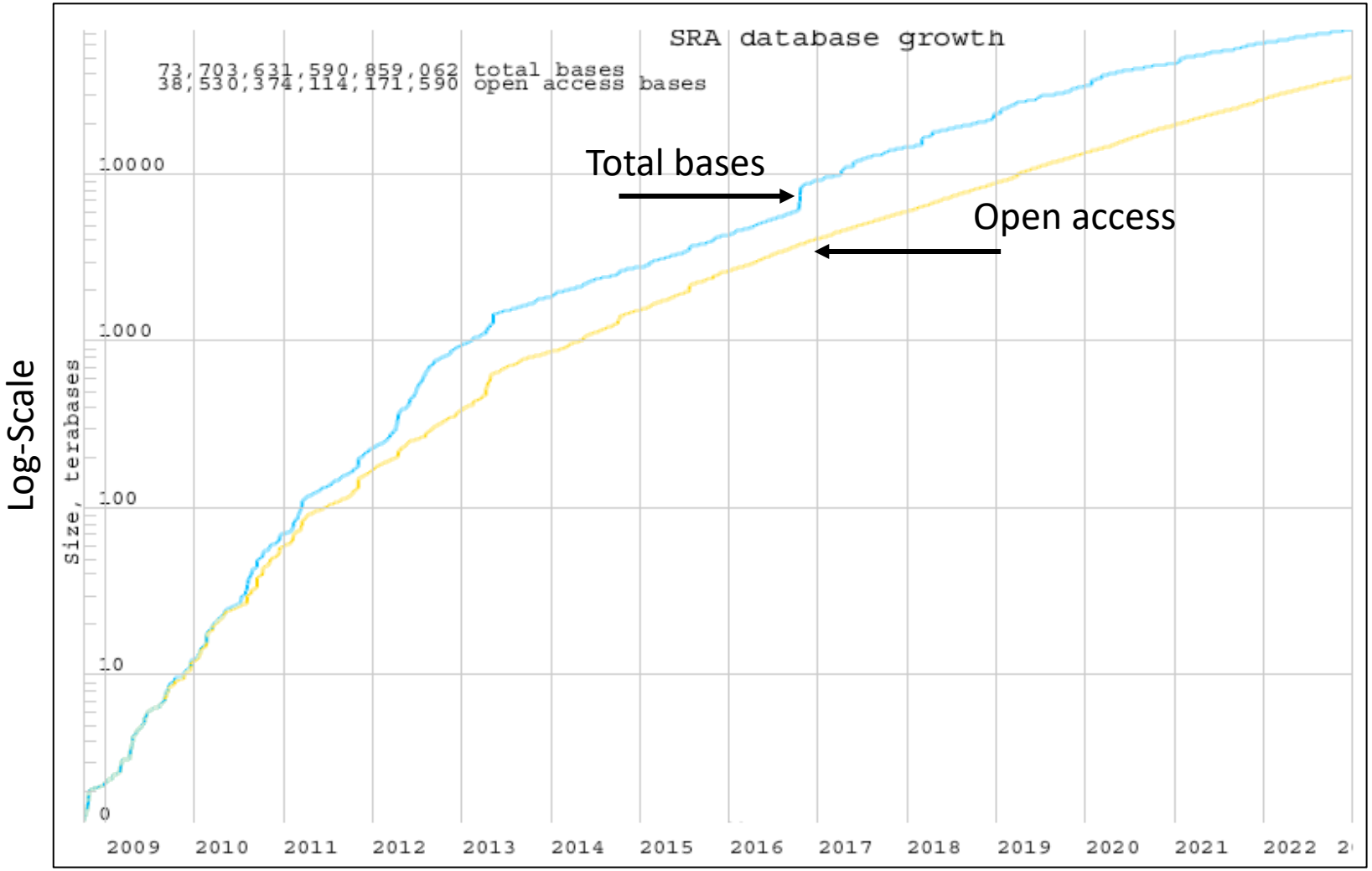
Sequence Read Archive (SRA) growth

SRA contains a lot of *diversity information*



Data from: https://www.ncbi.nlm.nih.gov/Traces/sra/sra_stat.cgi

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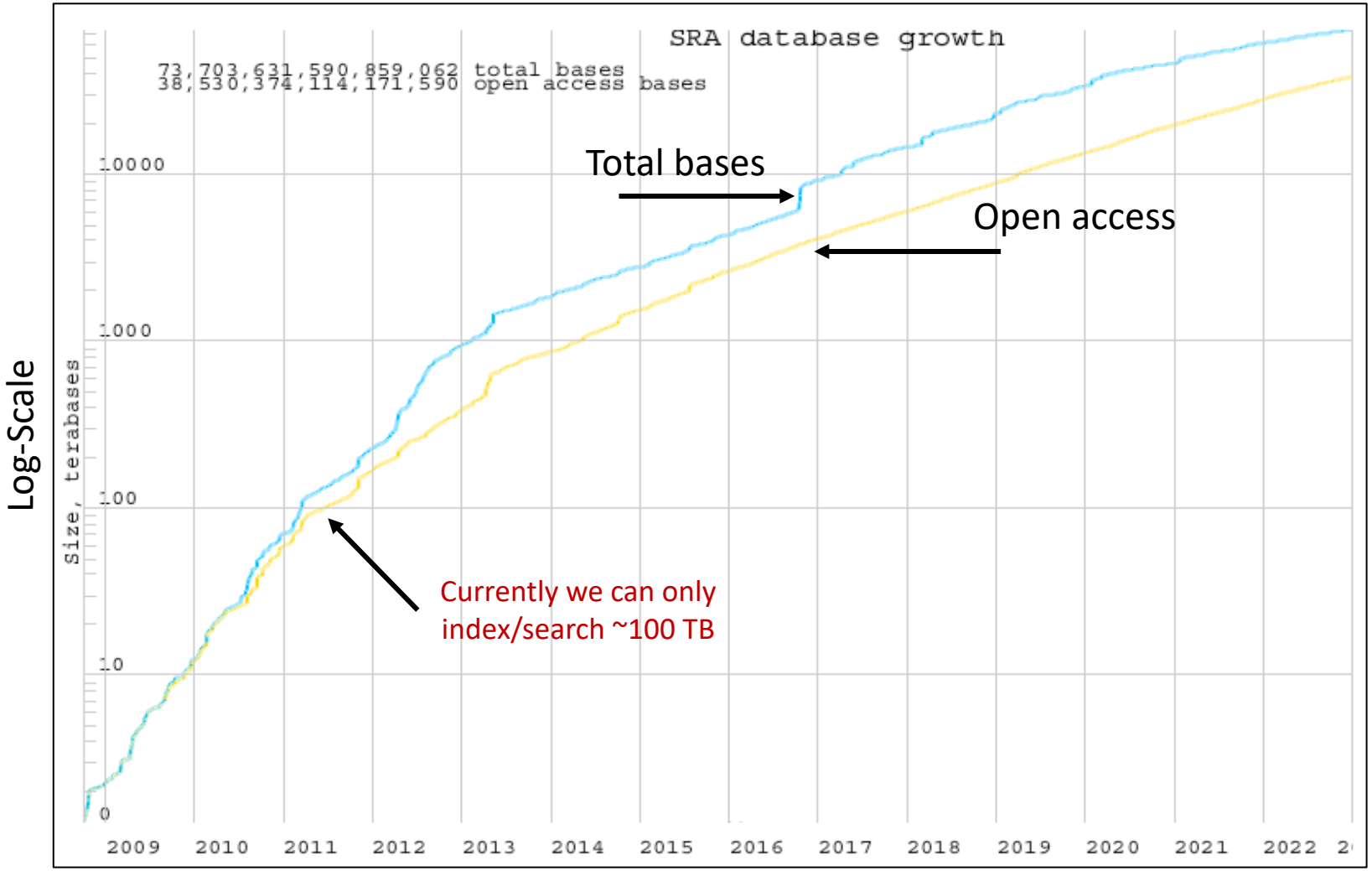

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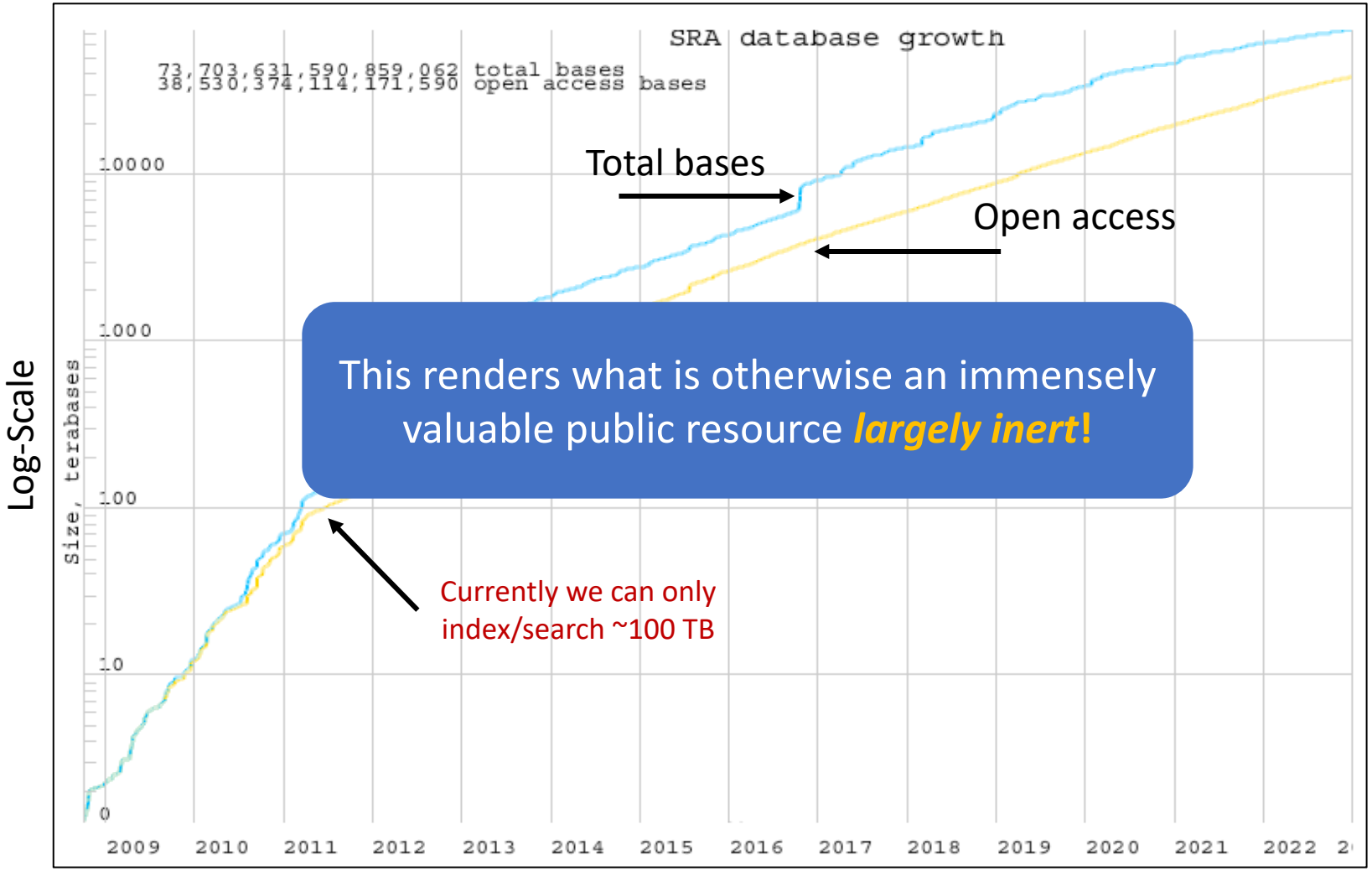

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Searches over SRA will enable complex biological analysis

- **What if I find a new putative disease-related transcript, and want to see if it appeared in other biological samples?**
- **What if I discover a new fusion event in a particular cancer subtype and want to know if it is common among samples with this subtype?**
- **What if I find an unexpected bacterial contaminant in my data; which other samples might contain this?**

⚒ A set of tools to index and search large-scale biological data

Our lab: enabling scalable data science

_K_-mer processing
Squeakr
[Bioinformatics 2017]

Weighted de Bruijn graphs
deBGR
[ISMB 2017, Bioinformatics 2017]

Colored de Bruijn graphs
Rainbowfish
[WABI 2017]

Sequence search over SRA

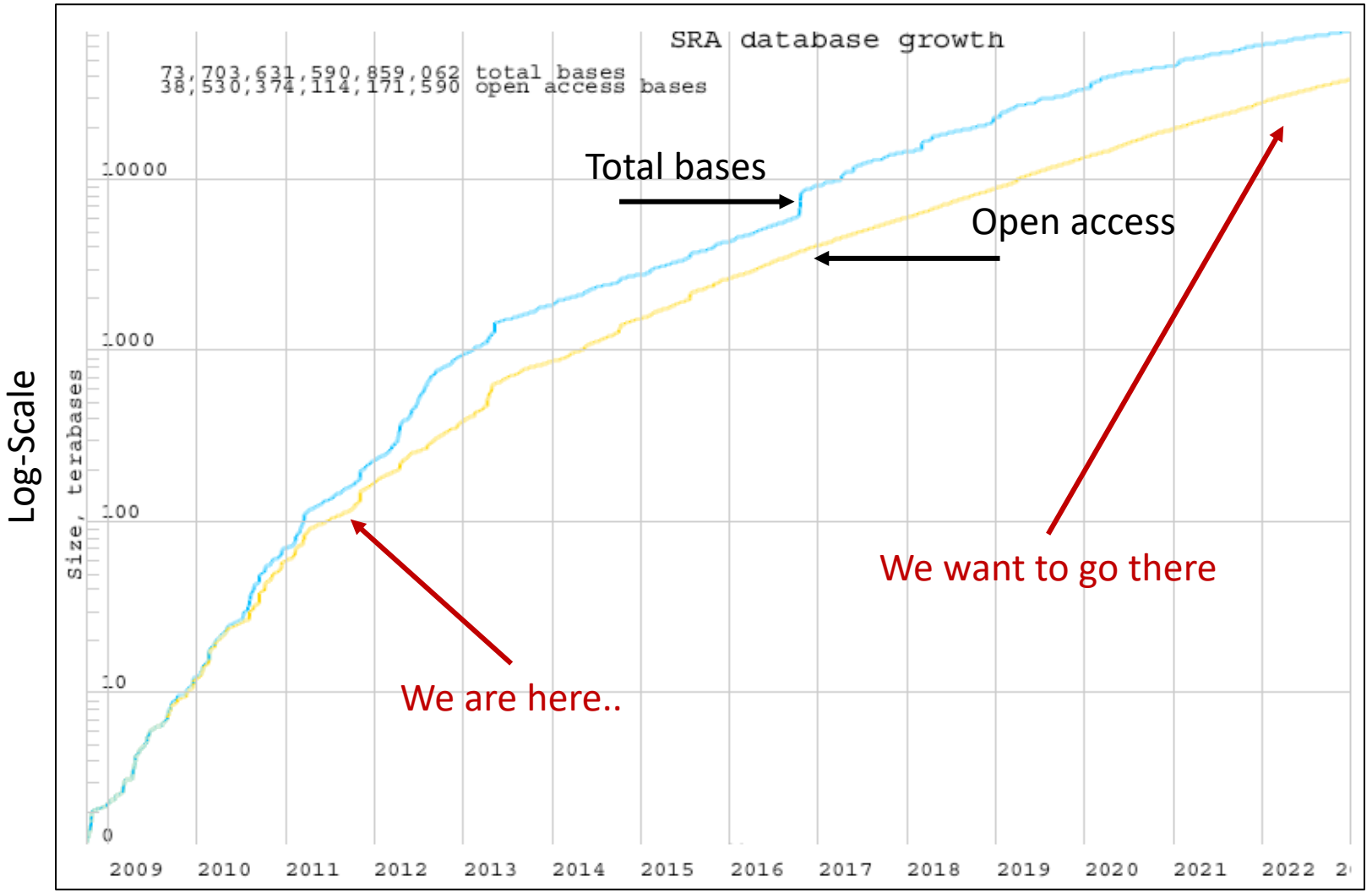
- Mantis [RECOMB 2018, Cell Systems 2018]
- Mantis-MST [RECOMB 2019, JCB 2020]
- Mantis-LSM [Bioinformatics 2022]

GPU-accelerated distributed _k_-mer processing
DEDUKT
[IPDPS 2021]

Pangenome index
VariantStore
[Genome Biology 2021]

Exascale metagenomic assembly
MetaHipMer*
[PPoPP 2023, ACDA 2023]

What's next



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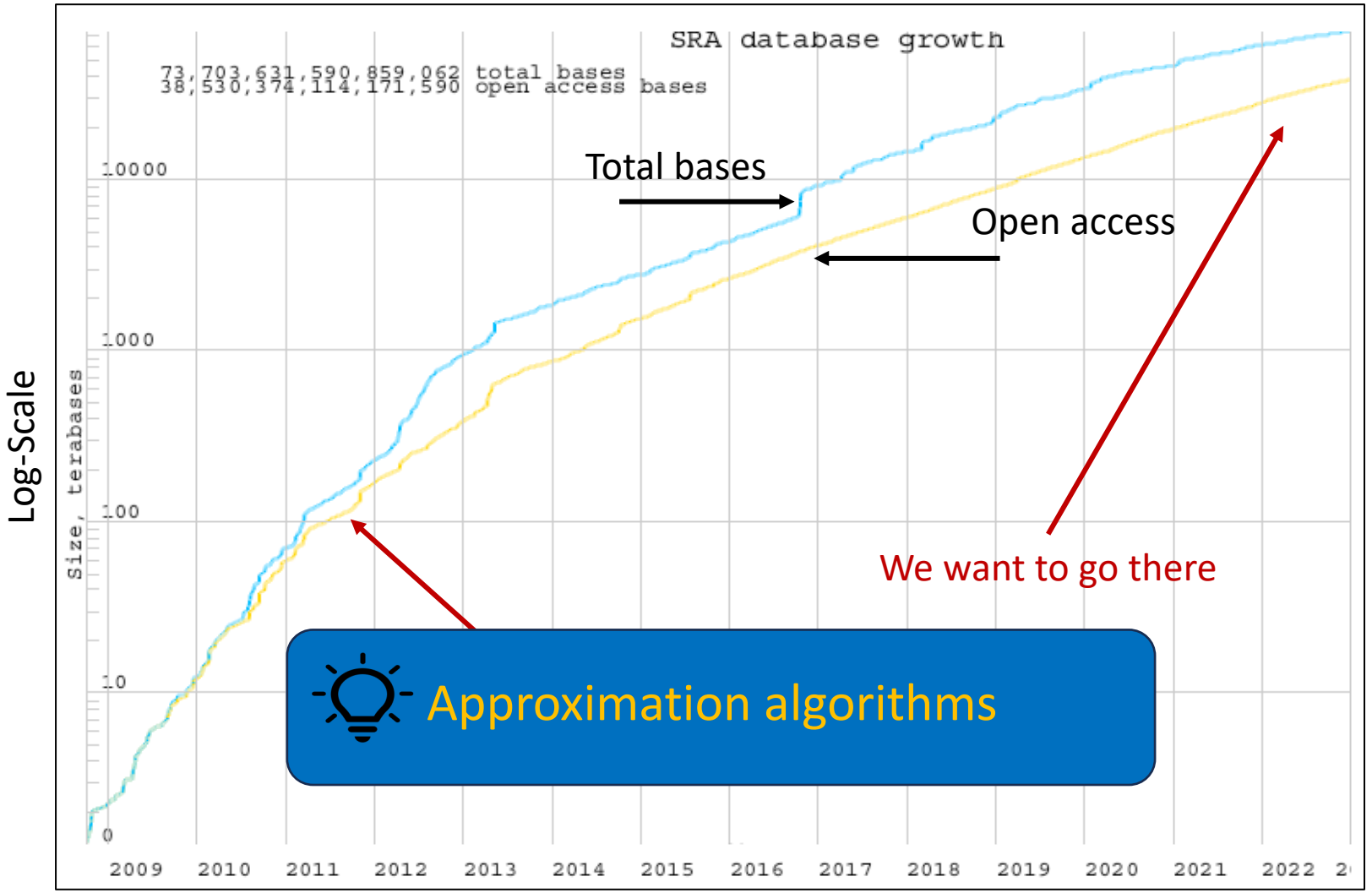

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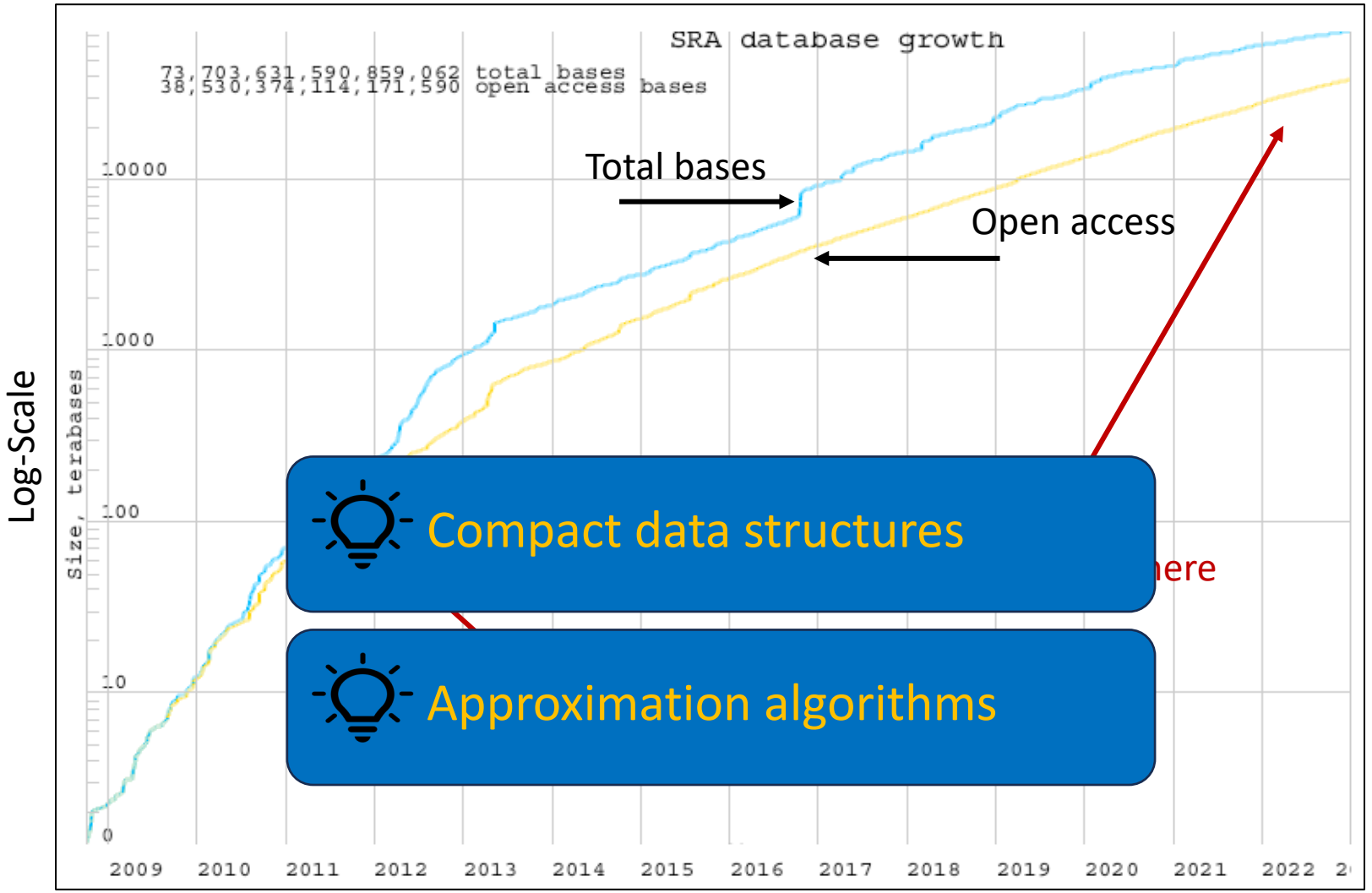

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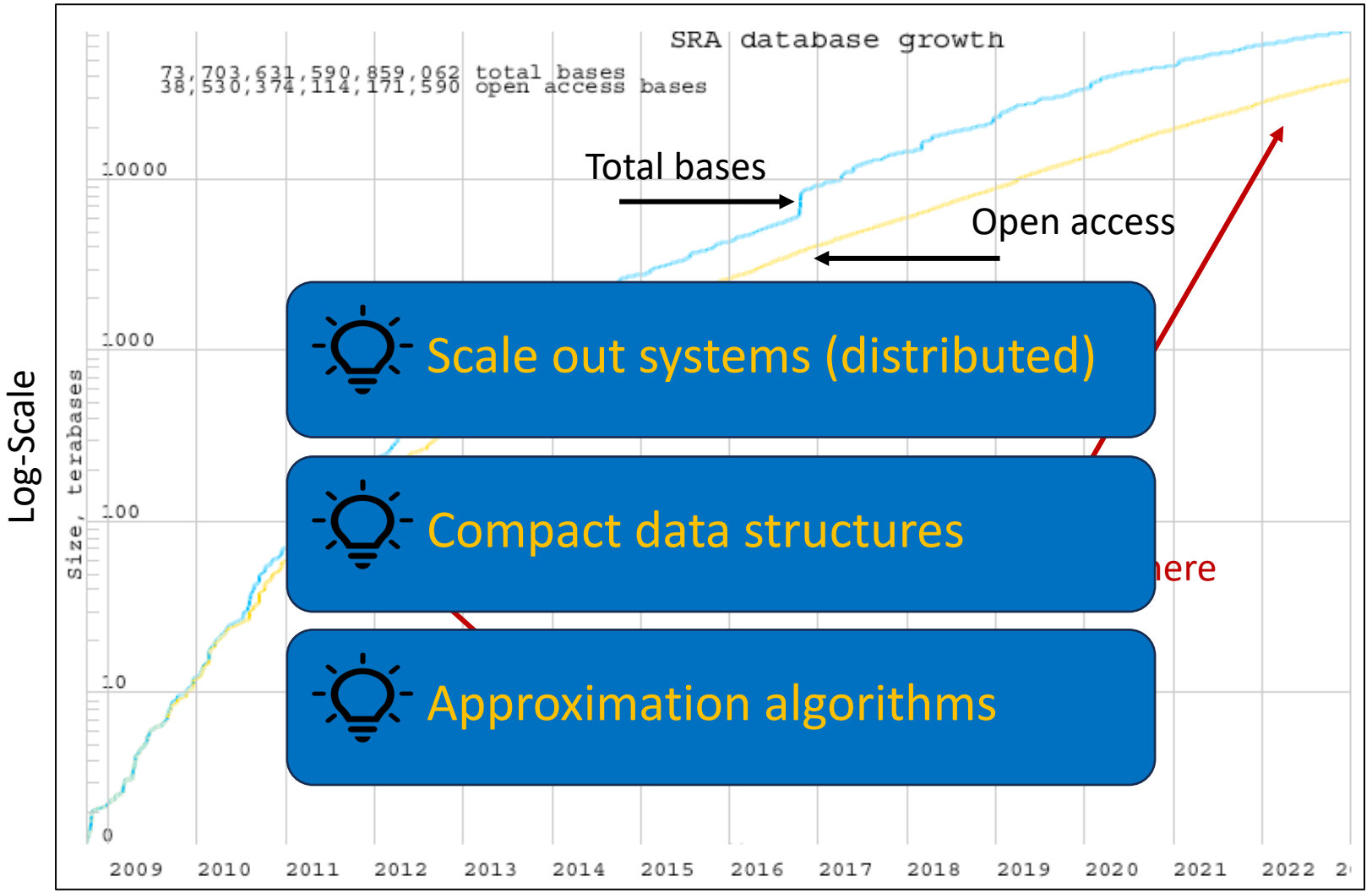

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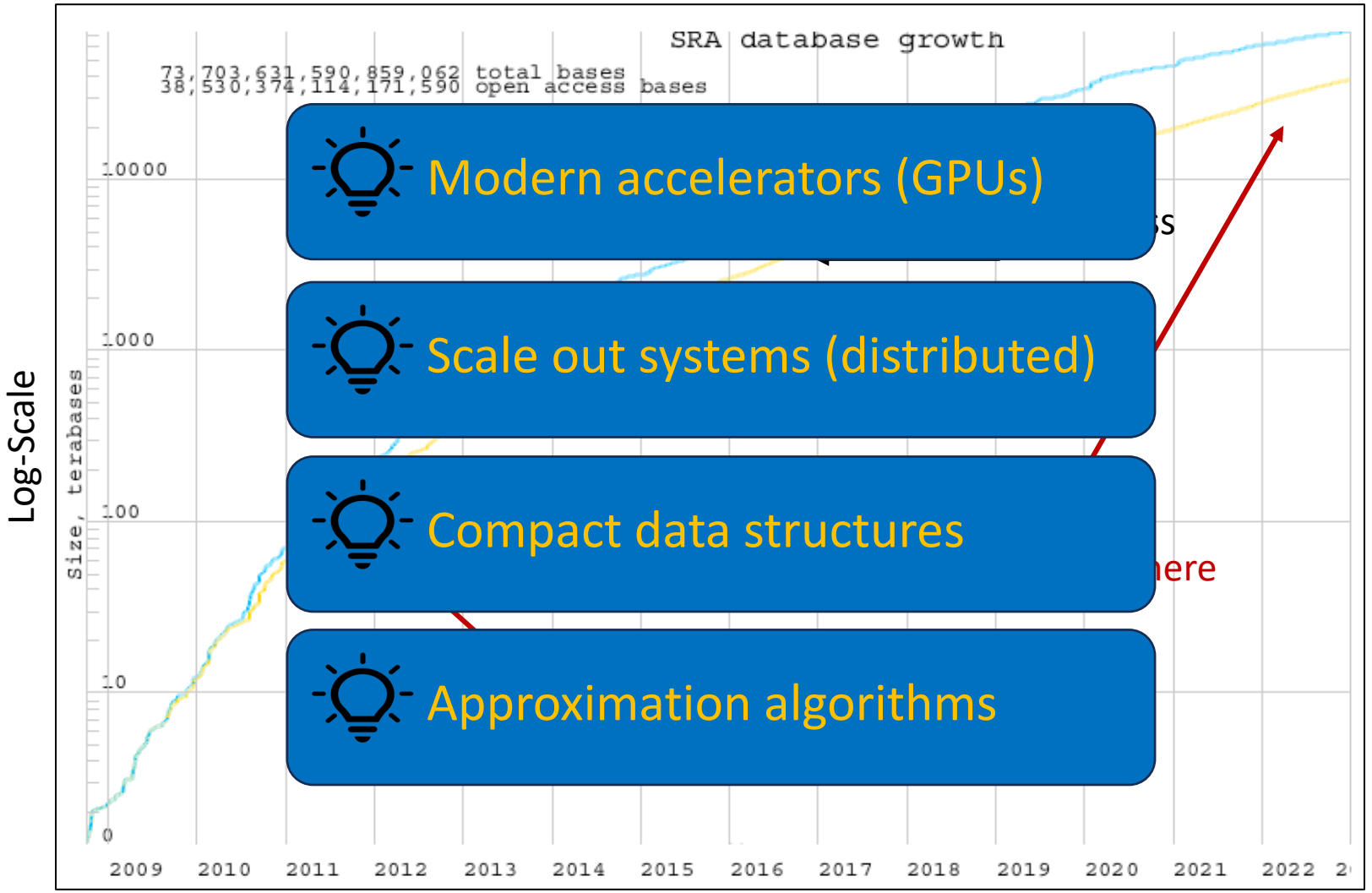

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