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Minimal perfect hash functions in large scale bioinformatics Problem

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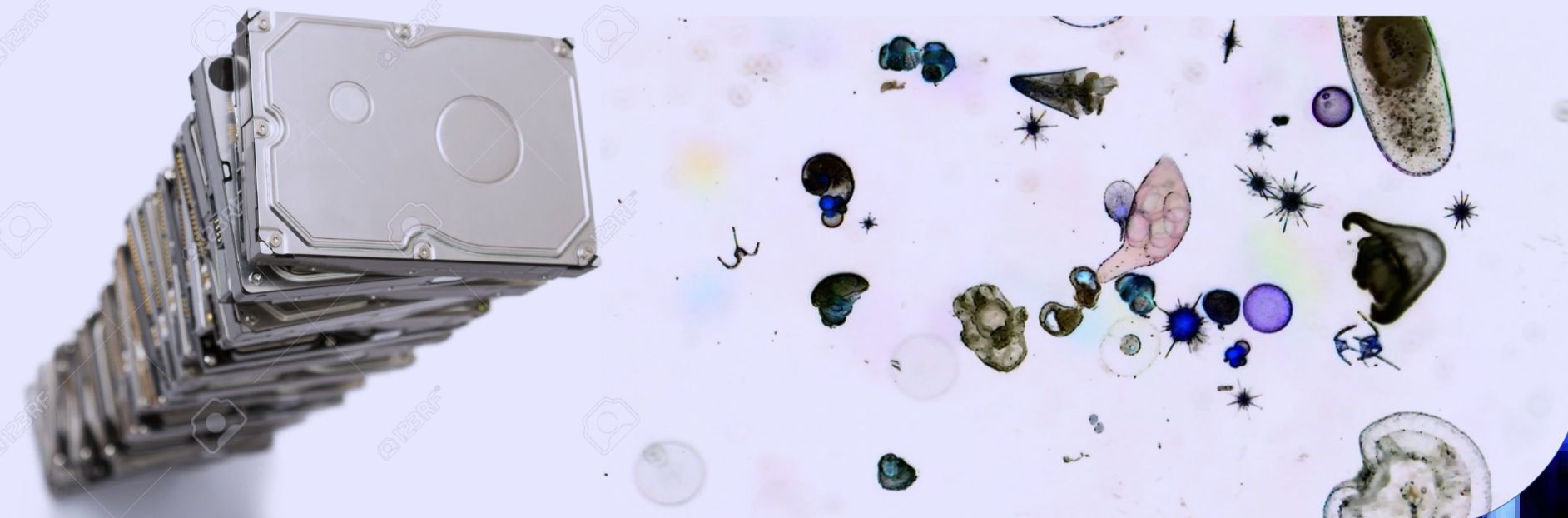
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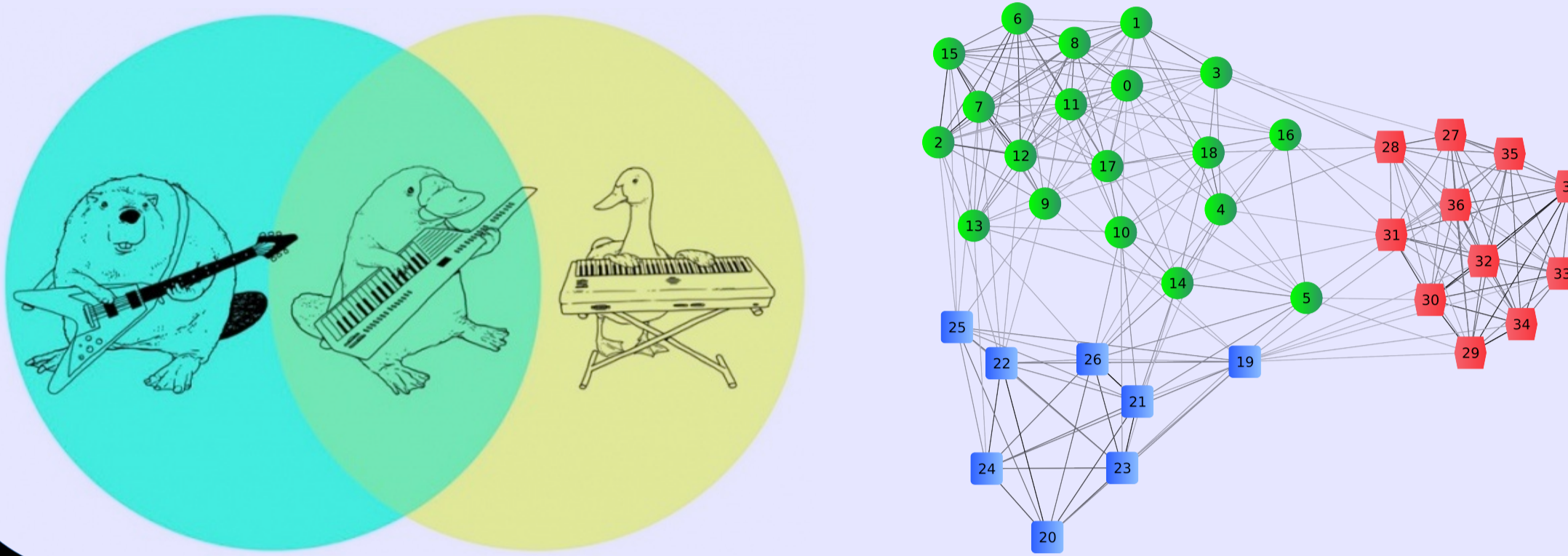
(Meta)Genomic Data

Billions of short sequences of hundreds of base pairs, from one or multiple genomes



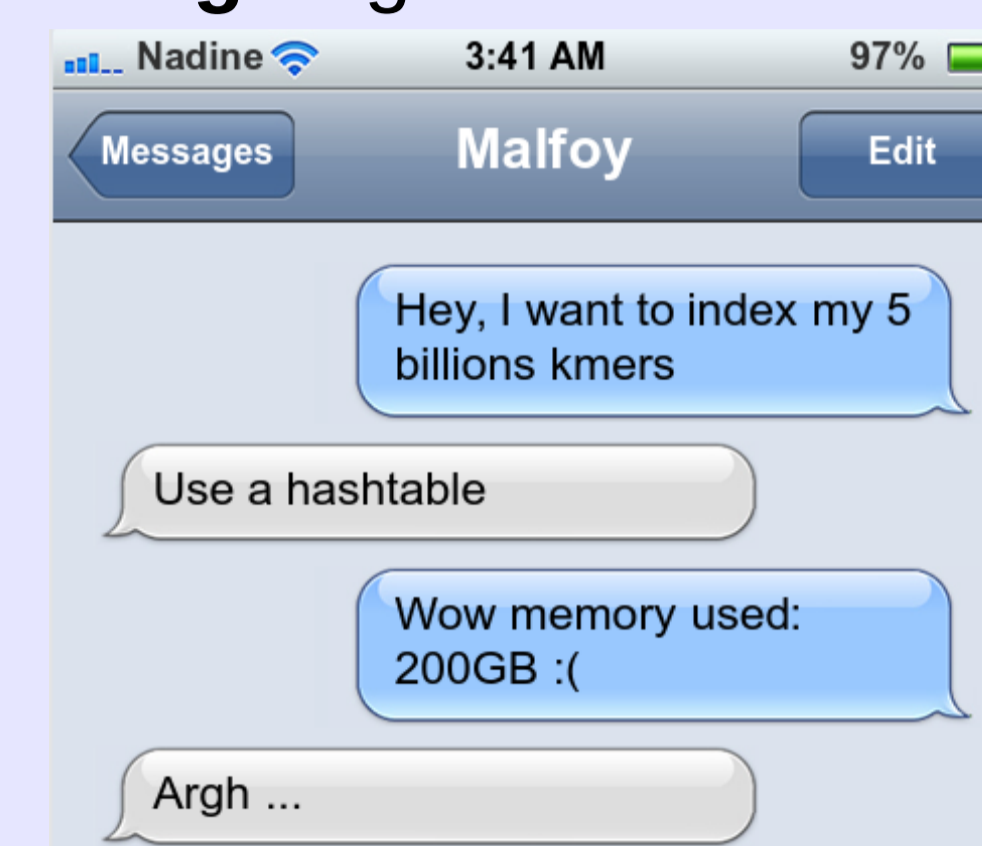
Questions

Dataset comparison :
Detection of similar reads **inter** or **intra** datasets



Problem

Indexing huge set of elements

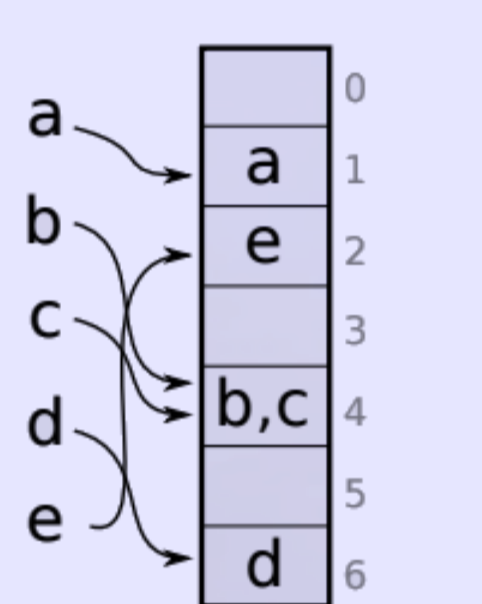


Hash functions

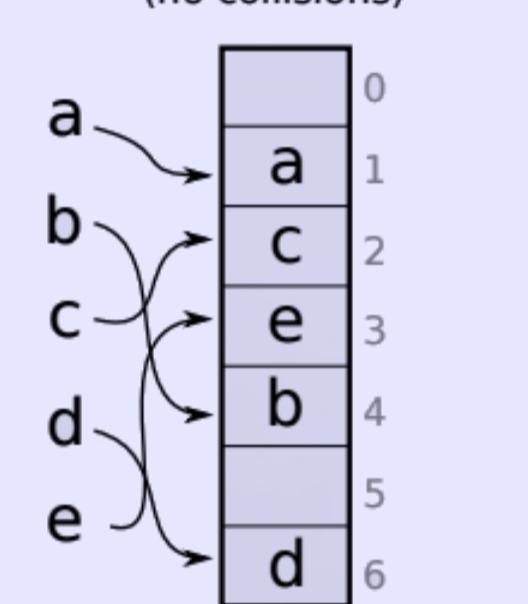
a,b,c,d,e : hashable elements (e.g. strings, integers, etc..)

→ : hash function
: image [0;m] of hash function (e.g. indices of buckets in a hash table)

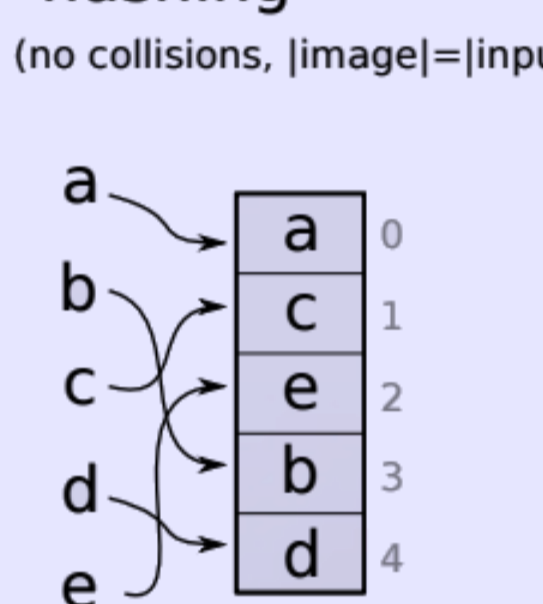
Classical hashing



Perfect hashing (no collisions)

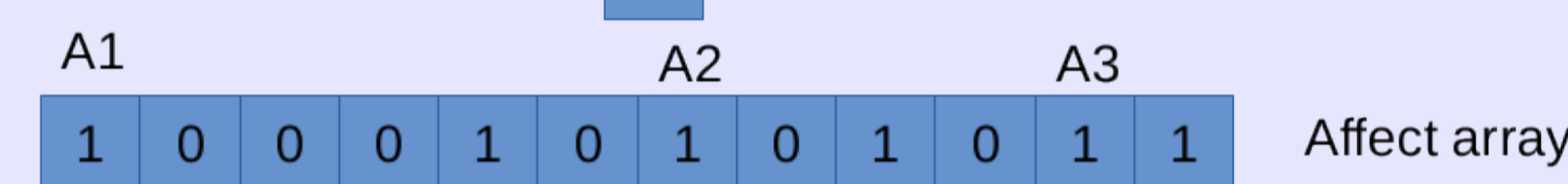
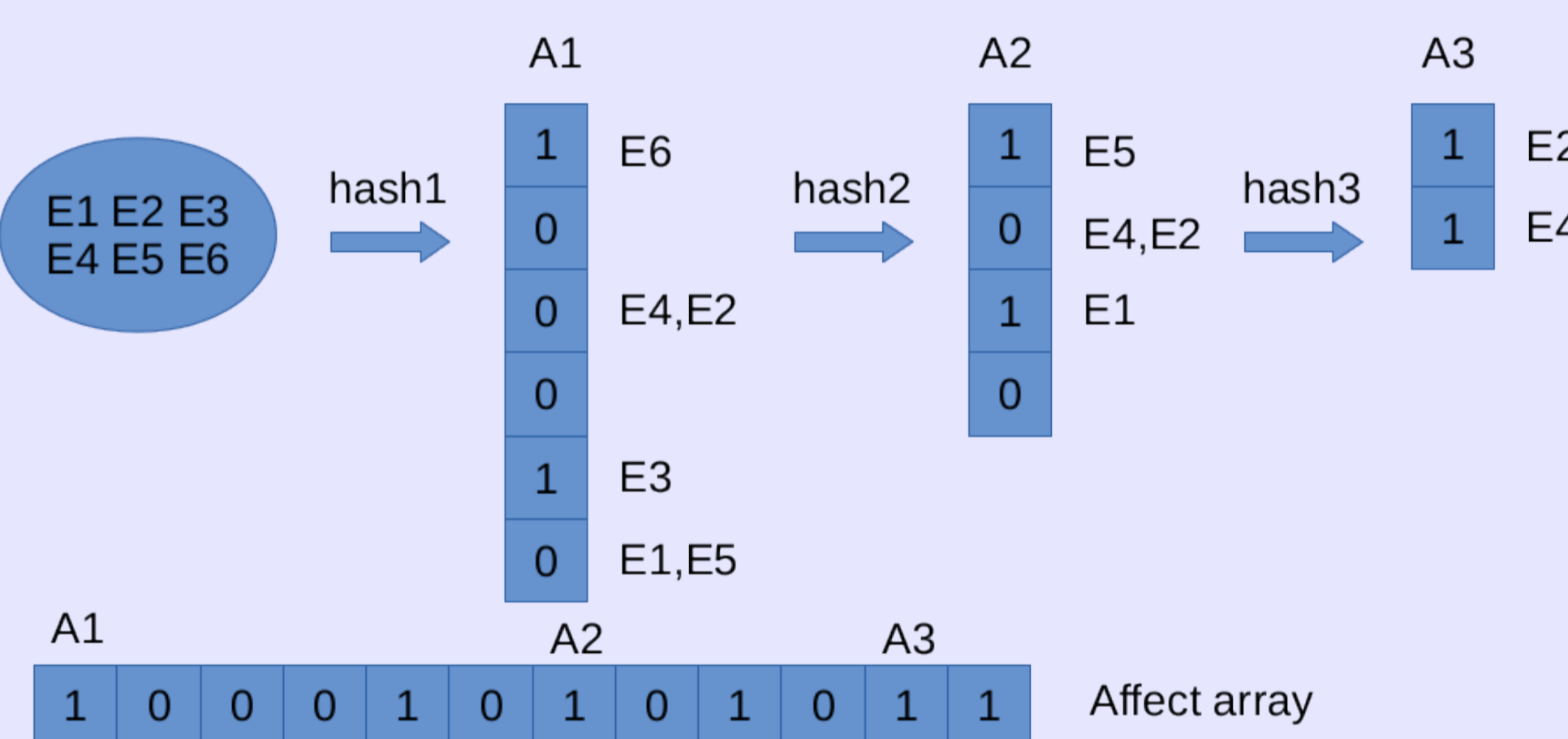


Minimal perfect hashing (no collisions, |image|=|input|)



BBhash library

- Memory efficient (less than 3bits per key)
- Fast query (200ns)
- Fast to construct (even for billions elements)

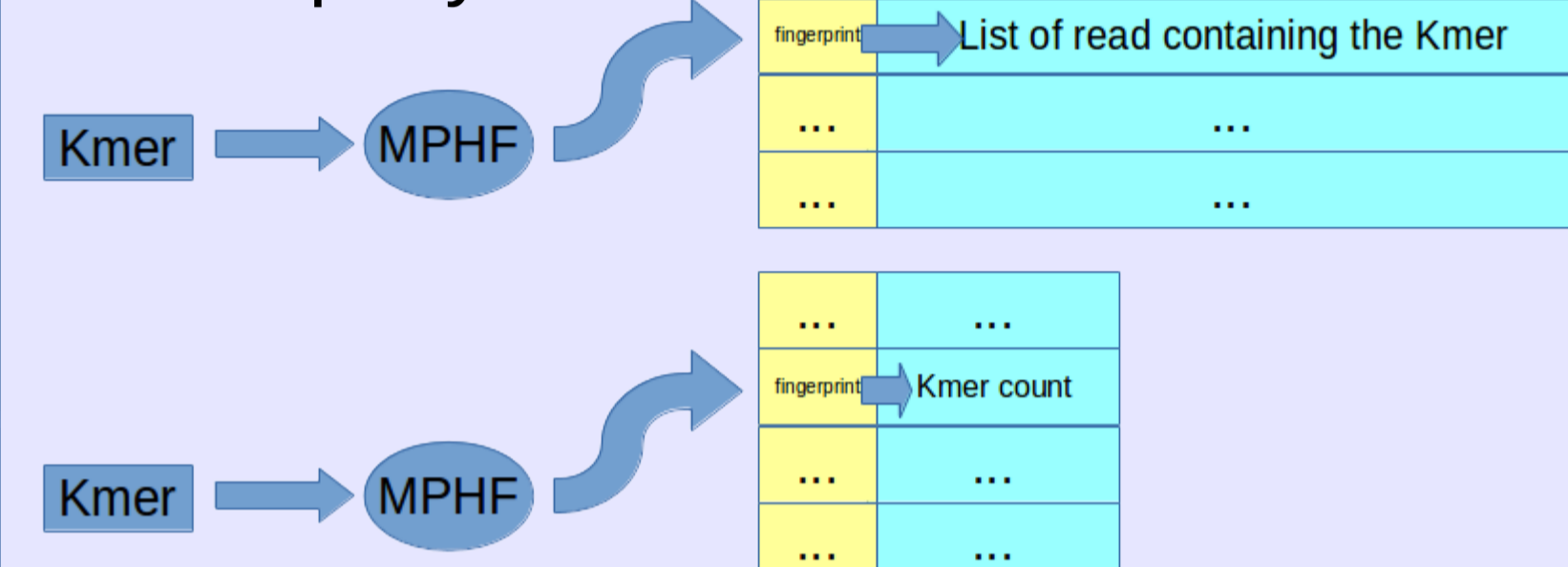


BUT

- No membership operation
- A 'stranger' key can be associated to a value

Quasi-dictionary

Put a fingerprint in the value and check it at the query



False positive rate :

$$\frac{2^{(2*k-f)} - 1}{2^{2*k}} \approx \frac{1}{2^f}$$

Memory consumption :

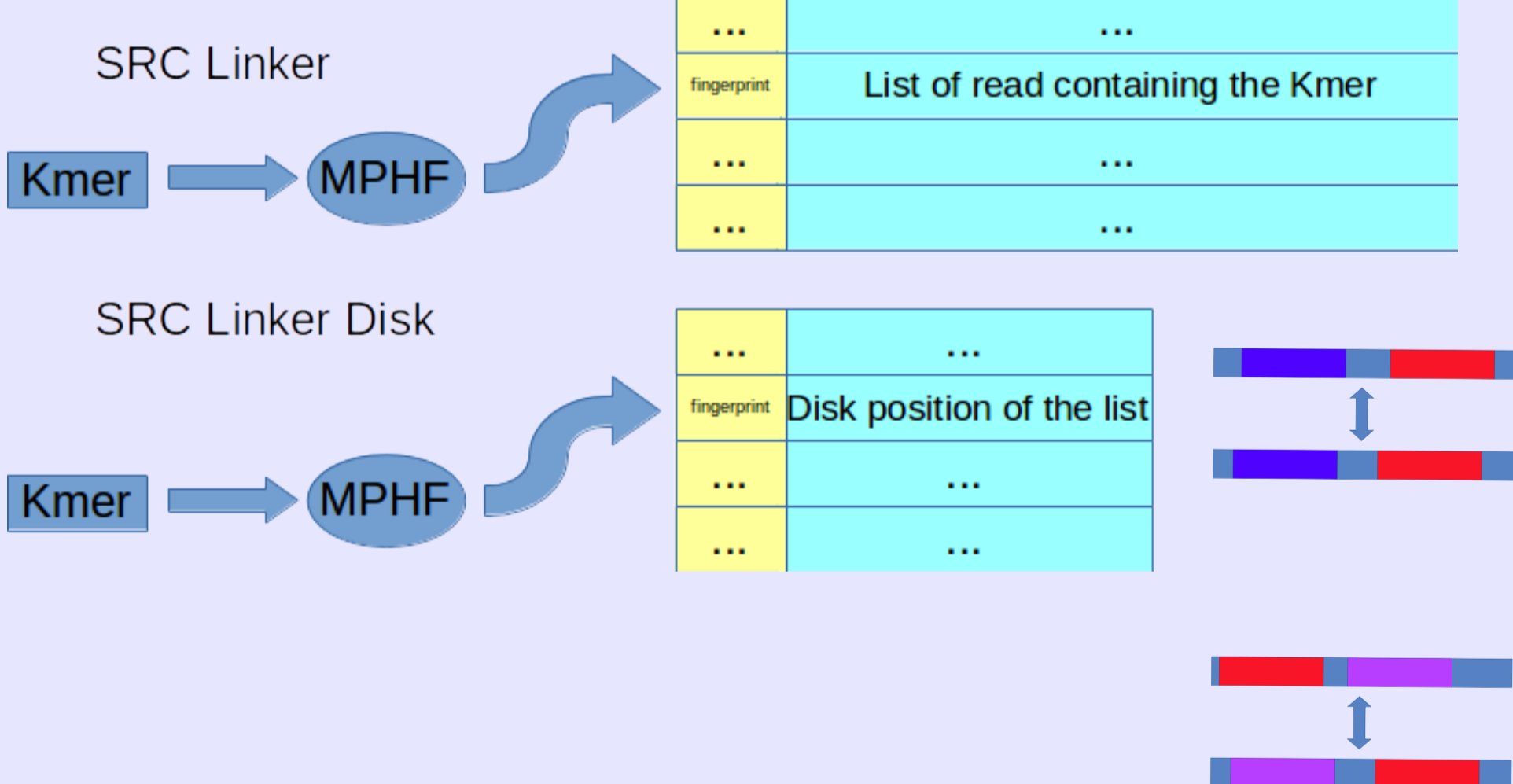
- Bit/elements : 10 FP rate: 1/10²
- Bit/elements : 20 FP rate: 1/10⁵
- Bit/elements : 30 FP rate: 1/10⁸

Short Read Connector tools

Given A and B sets of reads :

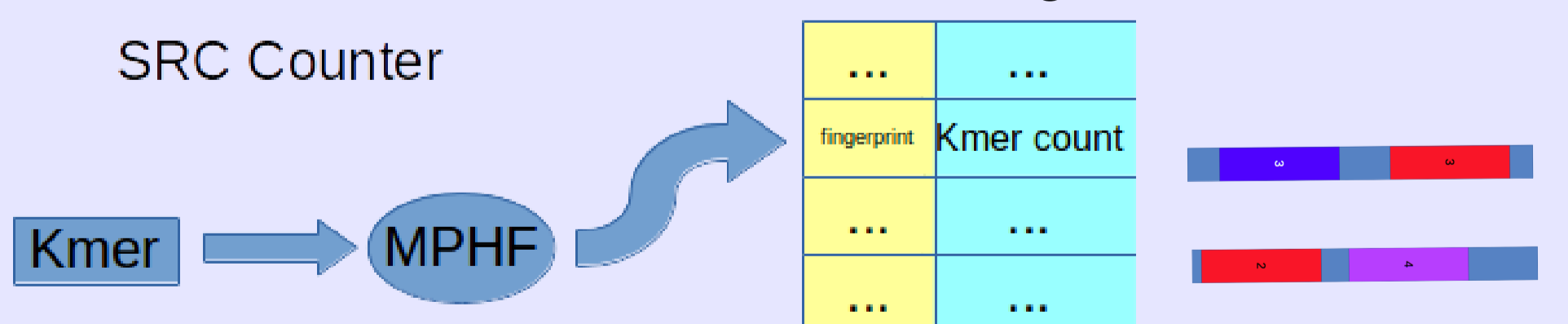
SRC Linker :

Output reads in A that has T Kmers that appear in set B.

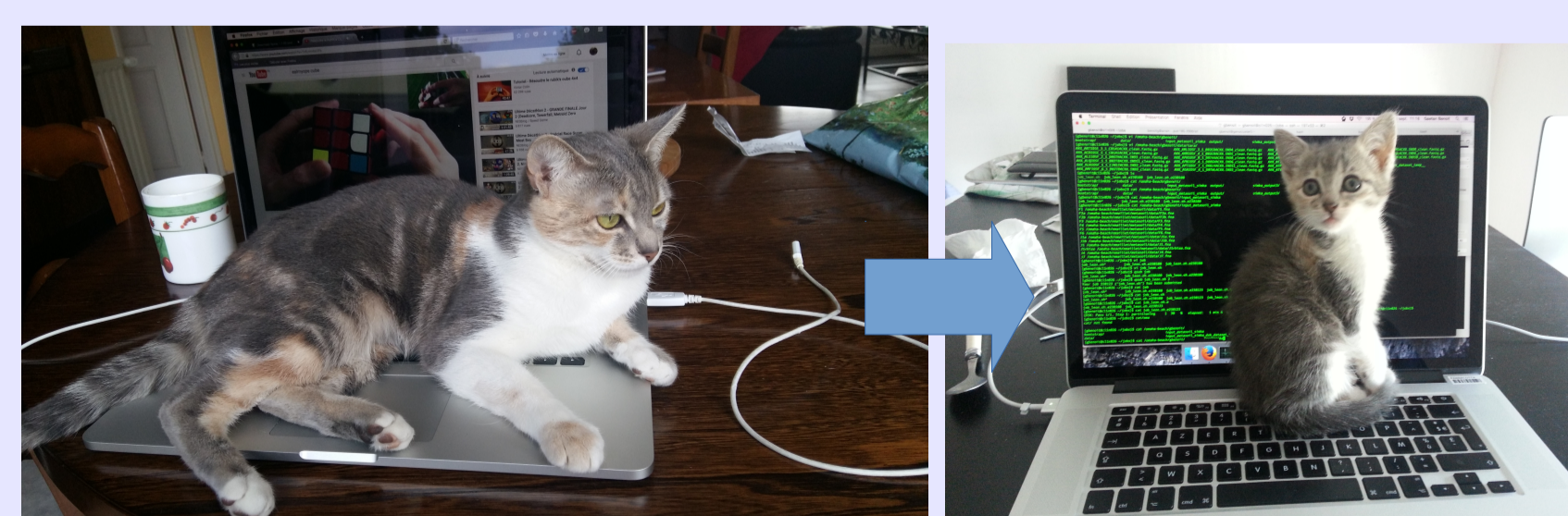
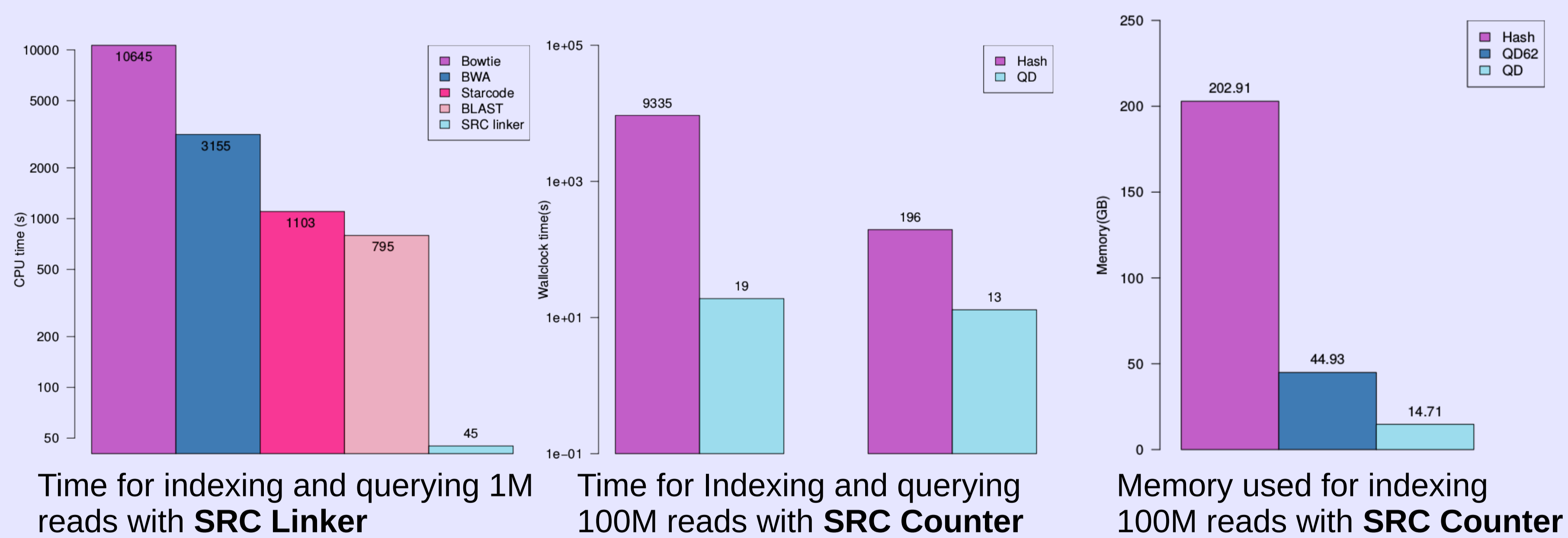


SRC Counter

Output reads in A that has T Kmers in common with the reads of B and estimate their coverage.



Results



Less pressure on your machine !

Still have to assess the qualitative aspects of our methods ...

References

- Bowtie2**
Langmead, Ben, and Steven L. Salzberg. "Fast gapped-read alignment with Bowtie 2." *Nature methods* 9.4 (2012): 357-359.
- BWA**
Li, Heng, and Richard Durbin. "Fast and accurate short read alignment with Burrows-Wheeler transform." *Bioinformatics* 25.14 (2009): 1754-1760.
- Starcode**
Zotile, Eduard, Pol Cuscó, and Guillaume J. Filion. "Starcode: sequence clustering based on all-pairs search." *Bioinformatics* 31.12 (2015): 1913-1919.
- BLAST**
Altschul, Stephen F., et al. "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." *Nucleic acids research* 25.17 (1997): 3389-3402.
- SRC**
<http://arxiv.org/pdf/1605.08319.pdf>

Links

- Bbhash library :**
github.com/rizkg/BBHash
- Quasi-dictionary :**
github.com/pierrepeterlongo/quasi_dictionary
- Short Read Connector :**
github.com/GATB/connector

QR code



Team

