Minimal perfect hash functions in large scale bioinformatics Problem

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Minimal perfect hash functions in large scale bioinformatics

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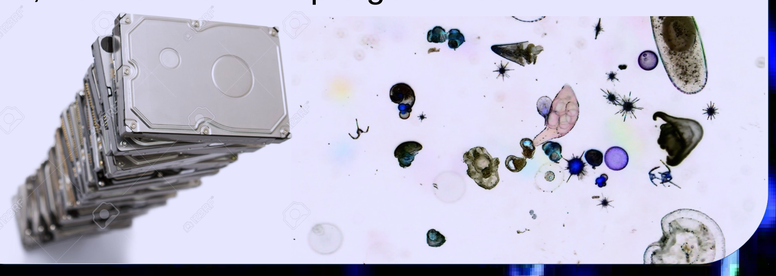
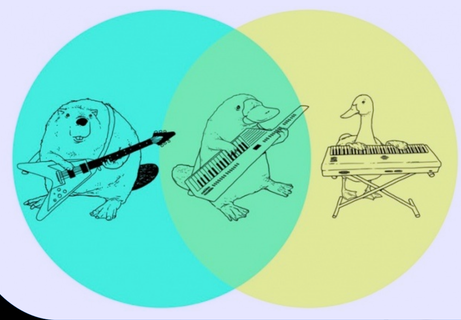
(Meta)Genomic Data

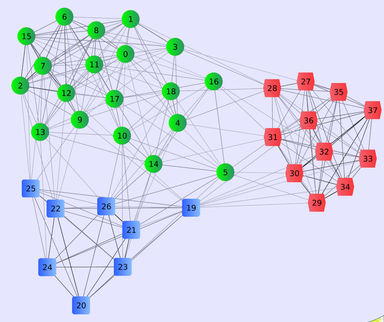
Billions of short sequences of hundreds of base pairs, from one or multiple genomes



Questions

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





Problem

Indexing huge set of elements

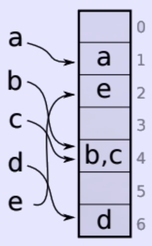
Hash functions

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

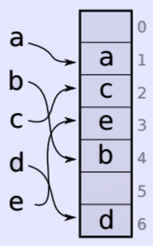
⟶ : hash function

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

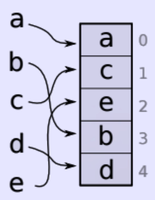
Classical hashing

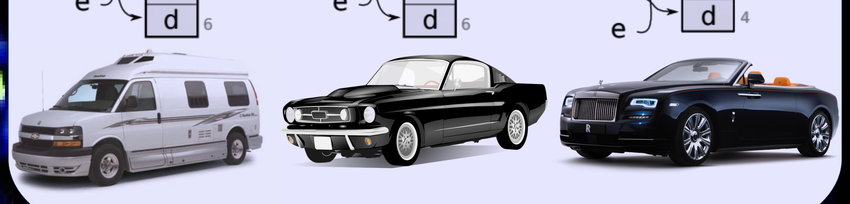


Perfect hashing (no collisions)



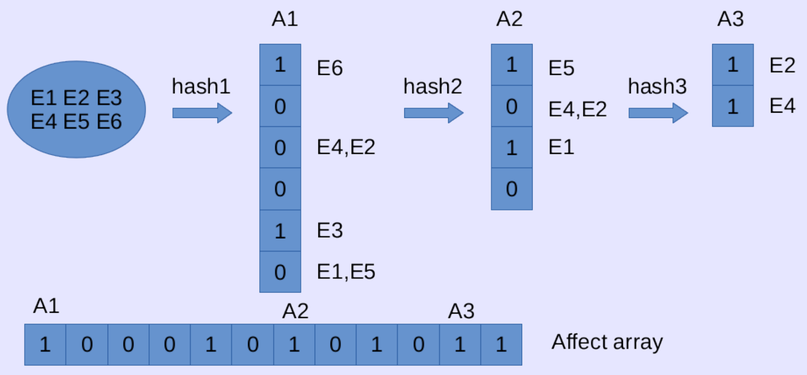
Minimal perfect hashing (no collisions, |image|=|input|)





BBhash library

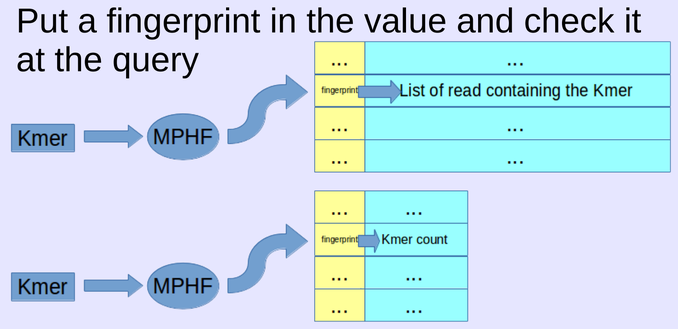
-Memory efficient (less than 3bits per key)
-Fast query (200ns)
-Fast to construct (even for billions elements)



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 :

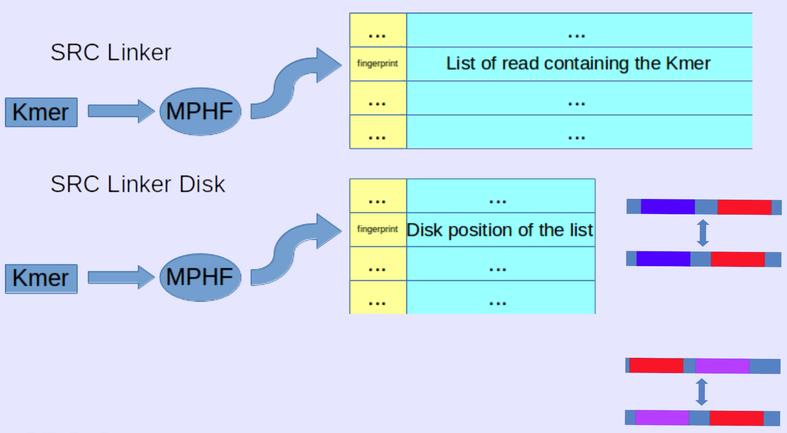
$$\frac{2^{(2*k-f)}-1}{2^{2*k}} \approx \frac{1}{2^f}$$

Memory consomption :
Bit/elements : 10 FP rate: $1/10^2$
Bit/elements : 20 FP rate: $1/10^5$
Bit/elements : 30 FP rate: $1/10^8$
...

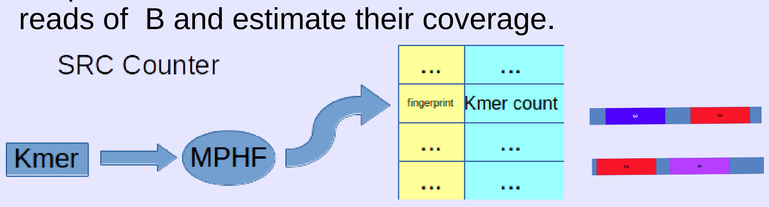
Short Read Connector tools

Given A and B sets of reads :

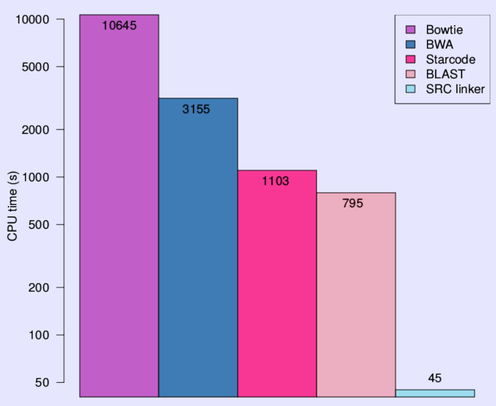
SRC Linker :
Output reads in A that has T Kmers that apear in set B.



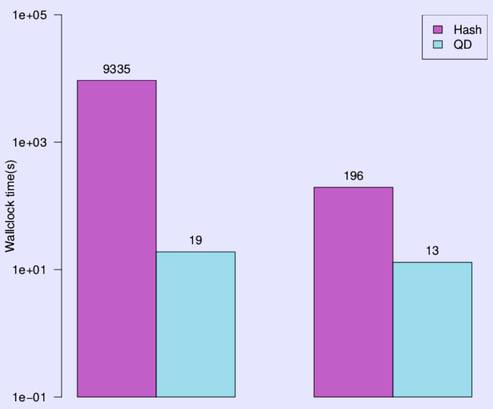
SRC Counter
Output reads in A that has T Kmers in common with the reads of B and estimate their coverage.



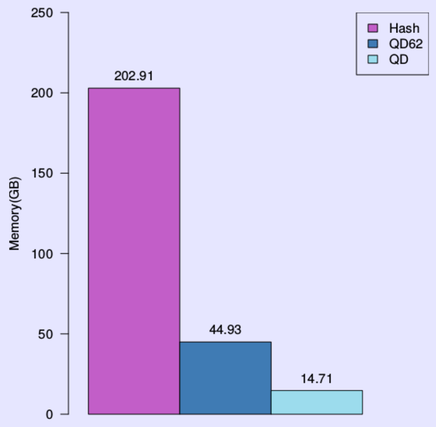
Results



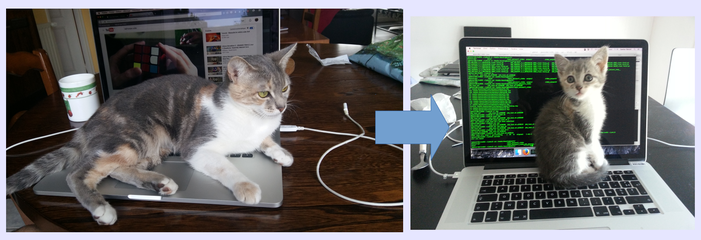
Time for indexing and querying 1M reads with **SRC Linker**



Time for Indexing and querying 100M reads with **SRC Counter**



Memory used for indexing 100M reads with **SRC Counter**



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
Zorita, 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.

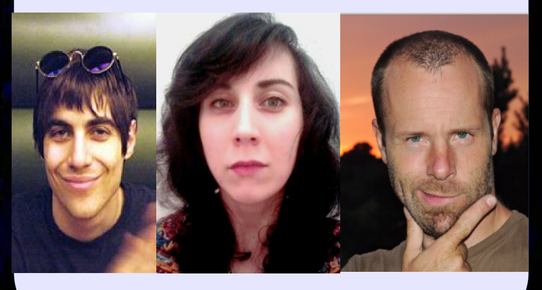
SRC
http://arxiv.org/pdf/1605.08319.pdf

Links

Bbhash library :
github.com/rizkg/BBHash

Quasi-dictionary :
github.com/pierrepeterlongo/quasi_dictionary

Short Read Connector :
github.com/GATB/rconnector

QR code

Team