Minimal perfect hash functions in large scale bioinformatics Problem
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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

References

Hash functions
- a, b, c, d, e : hashable elements (e.g. strings, images, etc.)
- \[ h(x) = \text{hash function} \]
- \[ h(a, b, c, d, e) = \{h(a), h(b), h(c), h(d), h(e)\} \]

Hash functions

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

Quasi-dictionary
- Put a fingerprint in the value and check it at the query
- False positive rate:
  \[ \frac{2^{k+1} - f}{2^{k+2}} - \frac{1}{2^{k+2}} \]

Short Read Connector tools

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

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...

Less pressure on your machine!