Pangenomic k-mer distribution estimation

At low memory cost

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Context

- Project Logan, compression of unitigs

Introduction

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- Compress a Human pangenome

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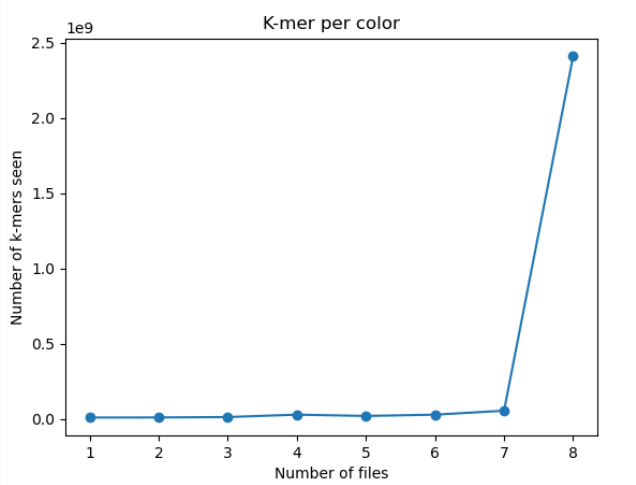
- Computing k-mer distribution accross pangenome
- Need to count k-mers once per file accross every files



Existing tools

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- Gene based tools
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- K-mer based tools
  - Pangrowth [1]
  - That's all....

Specificities

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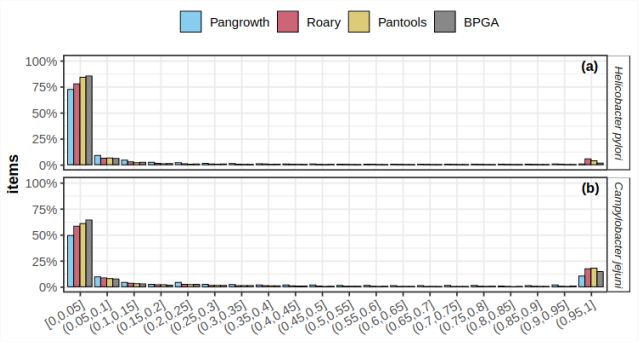
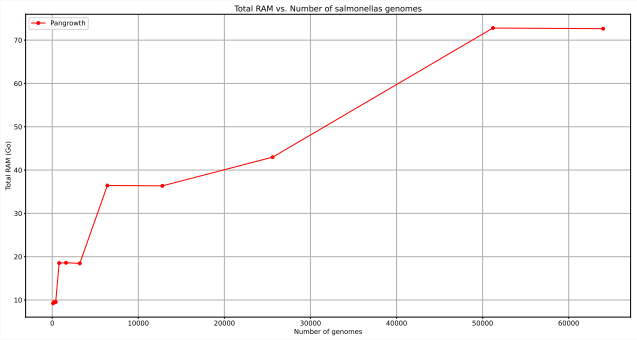
- Compared with gene based methods, gives a similar output
- uses the histogram to estimate pangenome ”openness”
- Does not scale easily



A word on scalability



Memory is critical

- A 96GB RAM machine is >4x price 16GB on AWS

K-mer Layers Estimation using Bloom filters

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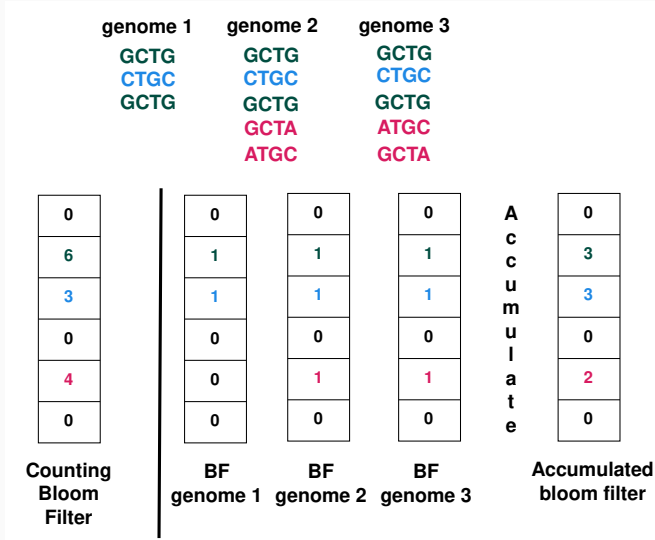
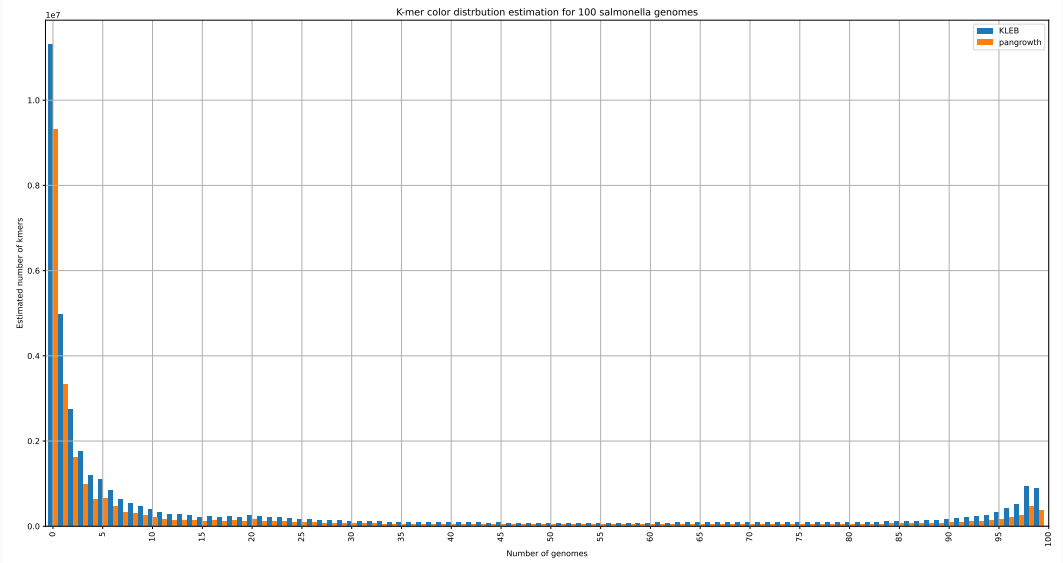
- Accumulated Bloom Filter
  - Novel data structure
  - Between Counting bloom filters [3] and Agregating bloom filters [4]

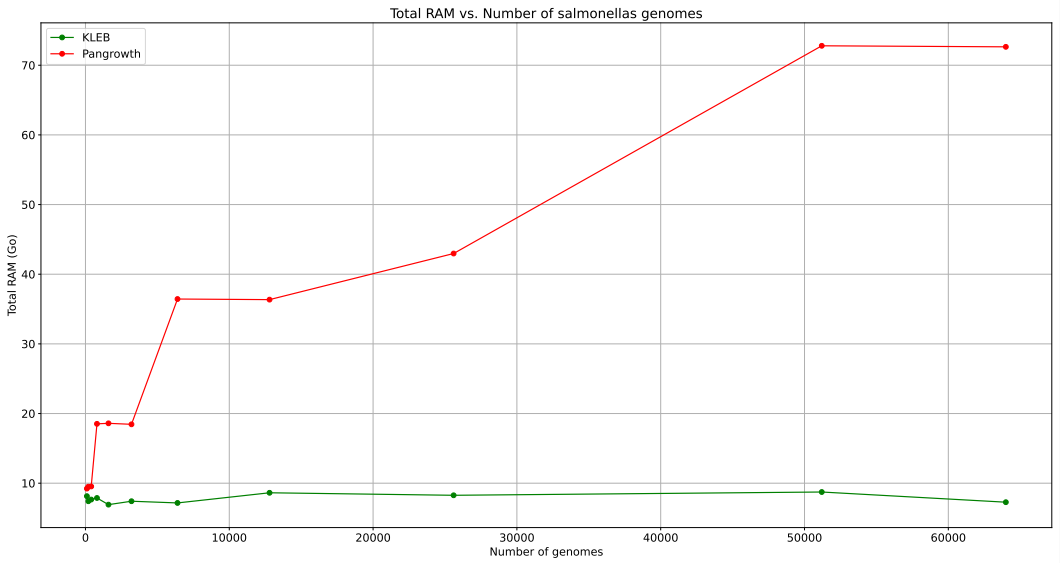
Accumulated bloom filter



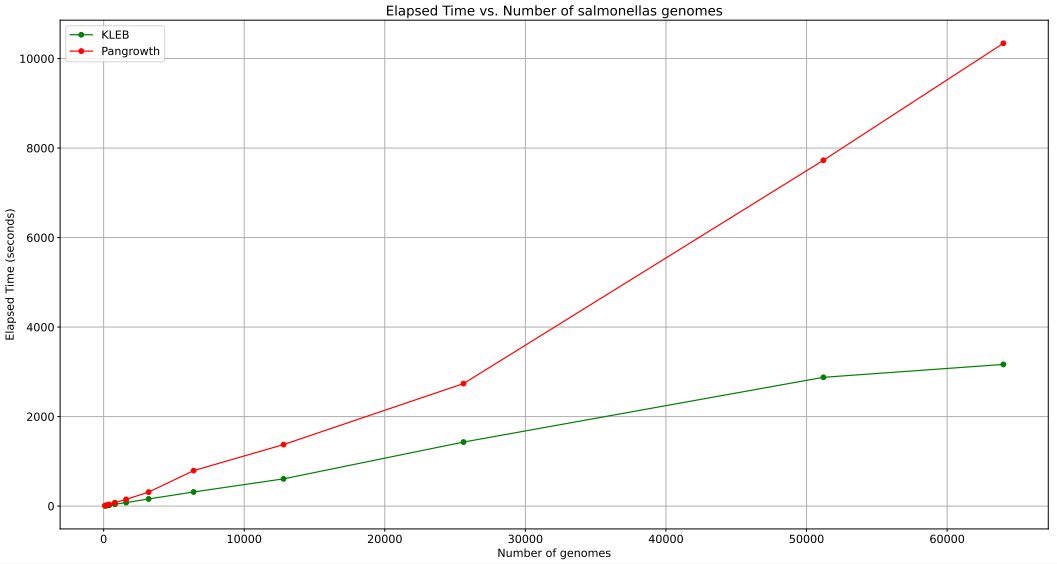
Histogram comparison



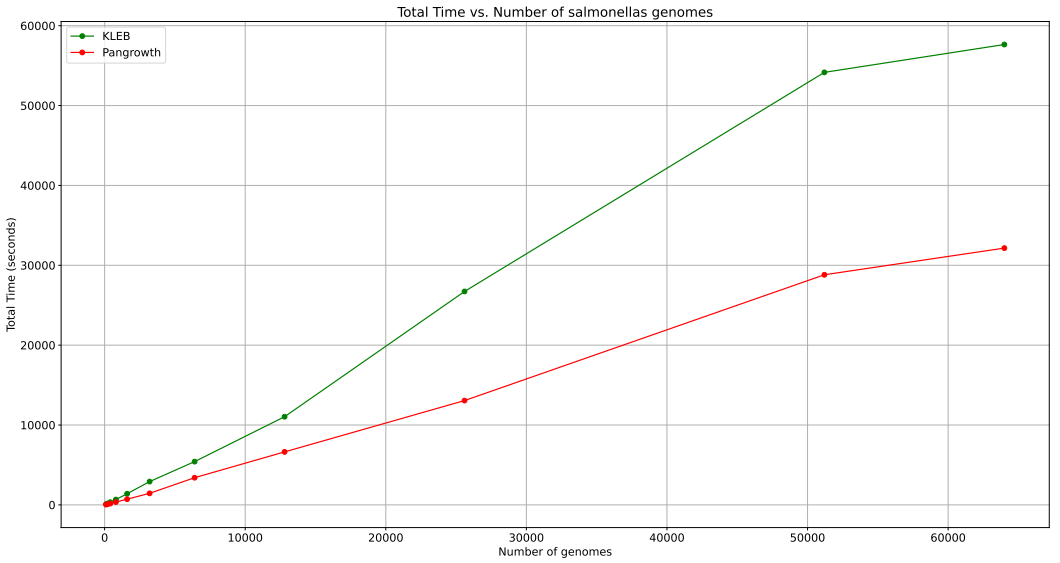
Memory consumption



Elapsed time on increasing number of genomes



CPU TIME (WIP)


Total Time vs. Number of salmonellas genomes
KLEB
Pangrowth
Total Time (seconds)
Number of genomes
0
10000
20000
30000
40000
50000
60000

Take home messages

- K-mer distribution
  - Gain better understanding on species
  - Guidance for genomic data compression
- Perspectives
  - Better qualitative analysis
  - Improve computational time
  - LSH methods

- KLEB
  - Arbitrarily lighter in memory
  - handling of big collections of genomes
  - still a work in progress
  - independant of k value

Appendix

References I

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