# FRACTIONAL HITTING SETS & SUPERSAMPLER

EFFICIENT AND LIGHTWEIGHT GENOMIC DATA SKETCHING

Timothé Rouzé, Igor Martayan, Camille Marchet & Antoine Limasset July 25, 2023









# Introduction

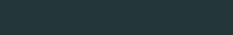


#### **INTRODUCTION**



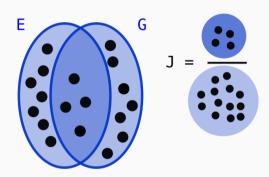
# **Problems**

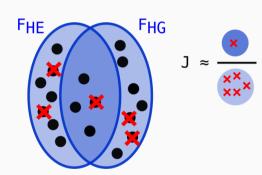
- keeps increasing
- · large scale analysis not possible



**PRELIMINARIES** 

# JACCARD INDEX



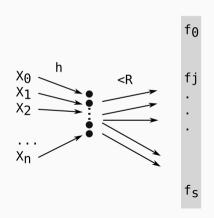


# **Bottom Minhash in MASH**

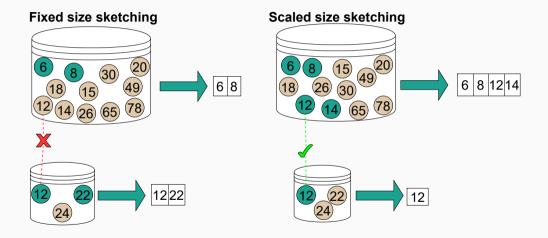
sketch

# $X_0$ $X_1$ $X_2$ $X_1$ $X_1$ $X_2$ $X_1$ $X_2$ $X_1$ $X_1$ $X_2$ $X_1$ $X_1$ $X_2$ $X_1$ $X_2$ $X_1$ $X_1$ $X_2$ $X_1$ $X_2$ $X_1$ $X_1$

# Scaled MinHash in Sourmash sketch



#### FIXED VS SCALED SIZE SKETCHING



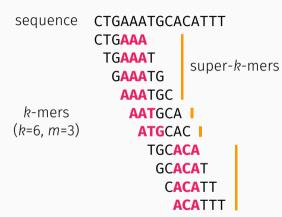


#### MINIMIZERS & SUPER-K-MERS

#### Minimizer

smallest *m*-mer of a *k*-mer according to some order (e.g. lexicographical)

width parameter: w = k - m + 1



### MINIMIZERS & SUPER-K-MERS

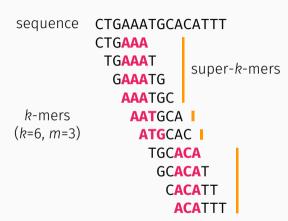
#### Minimizer

smallest *m*-mer of a *k*-mer according to some order (e.g. lexicographical)

width parameter: w = k - m + 1

# Super-k-mer

run of consecutive *k*-mers sharing the same minimizer



We use minimizers as a footprint for selecting super-k-mers

We want a sparse minimizer set

# Density

$$d = \frac{\text{\#selected minimizers}}{\text{\#m-mers}}$$

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```
TGTTGTGCTATT
sequence
           TGTTGT
            GTTGTG
             TTGTGC
 k-mers
              TGTGCT
(k=6, m=3)
               GTGCTA
                TGCTAT
                 GCTATT
selected
           * * * ** *
minimizers
      high density
 (lexicographical order)
```

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sequence TGTTGTGCTATT TGTTGT **GTTGTG** TTGTGC k-mers TGT**GCT** (k=6, m=3)**GTGCTA TGCTAT** GCTATT selected \* \* \* \*\* \* minimizers high density (lexicographical order)

sequence TGTTGTGCTATT TGT**TGT** GT**TGT**G TTGTGC k-mers **TGT**GCT (k=6, m=3)**GTGCTA** TGCTAT **GCTATT** selected minimizers low density (TGT < CTA < ...)

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sequence
           TGTTGTGCTATT
                              sequence
                                        TGTTGTGCTATT
           TGTTGT
                                        TGTTGT
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                                         GTTGTG
             TTGTGC
                                           TTGTGC
 k-mers
                               k-mers
              TGTGCT
                                            TGTGCT
(k=6, m=3)
                             (k=6, m=3)
               GTGCTA
                                             GTGCTA
                 TGCTAT
                                              TGCTAT
                  GCTATT
                                               GCTATT
 selected
                              selected
           * * * ** *
minimizers
                             minimizers
      high density
                                    low density
 (lexicographical order)
                                  (TGT < CTA < ...)
```

low density  $\iff$  long super-k-mers

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 $d = \frac{\text{\#selected minimizers}}{\text{\#m-mers}}$ 

Optimal density: d = 1/w

When using a random order, the expected density is  $\frac{2}{w+1}$ 

```
TGTTGTGCTATT
sequence
                             sequence
                                        TGTTGTGCTATT
           TGTTGT
                                        TGTTGT
            GTTGTG
                                         GTTGTG
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                                          TTGTGC
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#### **UNIVERSAL HITTING SETS & DENSITY LOWER BOUND**

# Universal Hitting Set (UHS)

set *S* of *m*-mers s.t. every run of *w* consecutive *m*-mers has  $\geq$  1 element in *S* 



# Universal Hitting Sets & Density Lower Bound

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In any UHS, the density is  $\geqslant \frac{1.5}{w+1}$  (i.e. the density factor is  $\geqslant$  1.5)

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Can we cross this lower bound by relaxing some constraints?



# FRACTIONAL HITTING SETS

Instead of covering every k-mer, we cover a fraction f of them

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In practice, we select minimizers smaller than a certain threshold t

$$t = \left[1 - (1 - f)^{1/w}\right] \cdot 4^m$$

minimizers  $\leq t$  are called small minimizers

# Density upper bound

Given a covering fraction f, assuming  $m > (3 + \varepsilon) \log_4 w$ ,

$$d \leqslant \frac{2f}{w+1} + o(1/w)$$

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- $\ominus$  not very meaningful as  $f \to 0$ (since most k-mers are not covered) Is there a more meaningful metric?

#### RESTRICTED DENSITY UPPER BOUND FOR SMALL MINIMIZERS

# Restricted density upper bound

Given a covering fraction f, assuming  $m > (3 + \varepsilon) \log_4 w$ , when restricting to k-mers containing small minimizers,

$$d \leq 2 \cdot \frac{f + (1 - f) \ln(1 - f)}{f^2(w + 1)} + o(1/w)$$

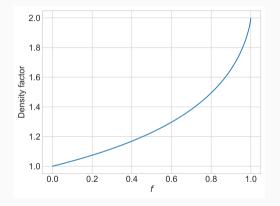
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- below the  $\frac{1.5}{w+1}$  barrier for  $f \le 0.8$
- approaches optimal density as  $f \rightarrow 0$



#### PROPORTION OF MAXIMAL SUPER-K-MERS

# Proportion of maximal super-k-mers

The average proportion of maximal super-k-mers is

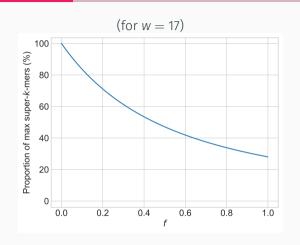
$$\left[ \left( 1 - \frac{1}{w} \right) \frac{f}{1+f} \right]^2 + \frac{1 - f(1 - 2/w)}{1+f}$$

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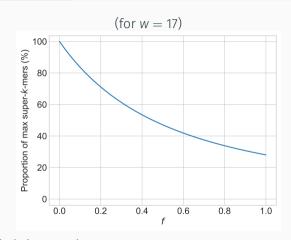


#### PROPORTION OF MAXIMAL SUPER-K-MERS

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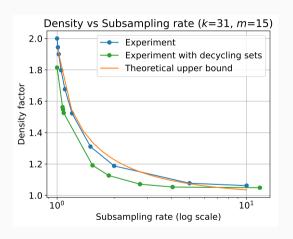
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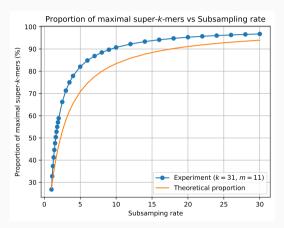
$$\left[ \left( 1 - \frac{1}{w} \right) \frac{f}{1+f} \right]^2 + \frac{1 - f(1 - 2/w)}{1+f}$$



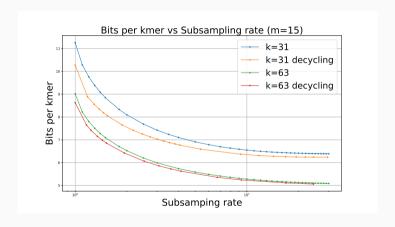
How accurate is it in practice?

#### COMPARISON WITH EXPERIMENTAL RESULTS



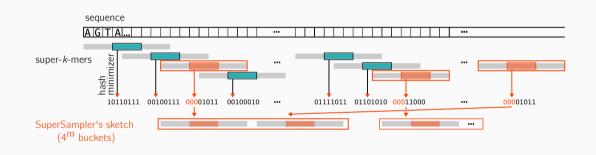


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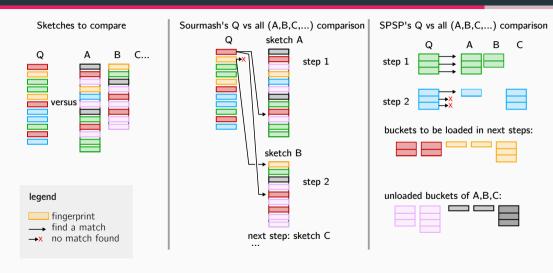




# SUPERSAMPLER'S SKETCHES



#### SKETCH COMPARISON





# PERFORMANCE COMPARISON ON DISSIMILAR DATA (REFSEQ)

# Computational time

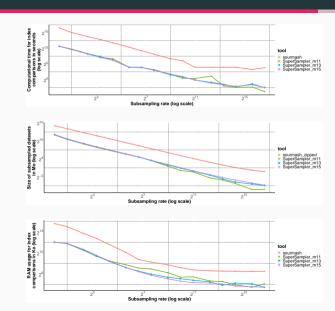
50× faster

# Disk usage

20× lighter

# RAM usage

6× less RAM



# PERFORMANCE COMPARISON ON SIMILAR DATA (SALMONELLAS)

# Computational time

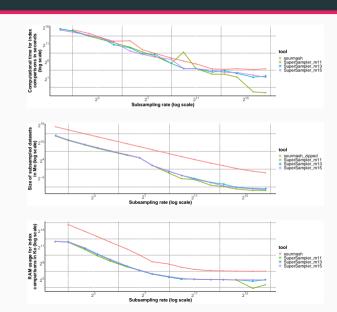
7× faster

# Disk usage

50× lighter

# RAM usage

6× less RAM





#### TAKE HOME MESSAGES

- · Super-k-mers
  - robust fingerprints
  - · low memory cost
- Fractional Hitting Sets
  - generalization of UHS
  - · lower density
  - longer super-k-mers
  - can be combined w/ existing UHS

- · Go check out our posters!
  - Igor Martayan's poster (#123) on the theory behind FHS
  - My poster about SuperSampler (#147), if you want to have a chat with me!
- If you want to dig deeper into FHS and SuperSampler, go checkout our preprint:





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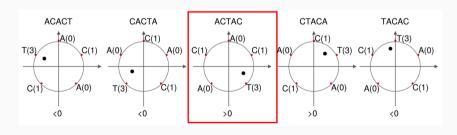
David Pellow, Lianrong Pu, Baris Ekim, Lior Kotlar, Bonnie Berger, Ron Shamir, and Yaron Orenstein. Efficient minimizer orders for large values of k using minimum decycling sets. bioRxiv. pages 2022–10. 2022.

#### **DECYCLING SETS**

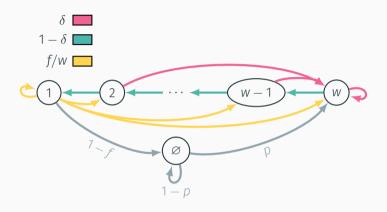
# Decycling set

set S of m-mers whose removal make the De Bruijn graph acyclic

- if at least one m-mer is in S, take it in your UHS
- · otherwise, use a random order to select a minimizer



# SUPER-K-MERS' MARKOV CHAIN



- state i: small minimizer starts at i in the k-mer
- state  $\varnothing$ : no small minimizer in the k-mer