# Dynamic quasi-minimal perfect hash function for k-mers



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February 5, 2020

# Background and Motivation

A MPHF is an injective function 
$$h:\{s_1,\ldots,s_n\} 
ightarrow [1,n]$$

| Static   | Dynamic |  |  |  |  |  |
|--|---------|--|--|--|--|--|
| Applications:  |         |  |  |  |  |  |
| - Meraculous [Chapman et al. PloS one (2011)]          |         |  |  |  |  |  |
| - BCALM2 [Chikhi et al. Bioinformatics (2016)]         |         |  |  |  |  |  |
| - pufferfish [Almodaresi et al. Bioinformatics (2018)] |         |  |  |  |  |  |
| Implementations:                                       |         |  |  |  |  |  |

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- BBHash [Limasset et al. SEA (2017)]
- EMPHF [Belazzougui et al. DCC (2014)]

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#### **Static**

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## Implementations:

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- EMPHF [Belazzougui et al. DCC (2014)]

## Dynamic

## Applications:

– vg

[Garrison et al. Nature (2018)]

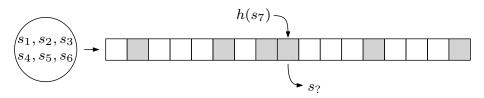
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#### Implementations:

- ?

# Challenge

#### How to retrieve an element when a collision occurs?

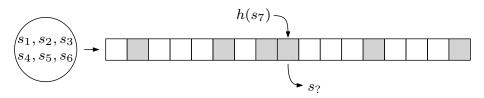


Our idea: combine a MPHF with a fully-dynamic de Bruijn graph

Our result: a dynamic MPHF for k-mers

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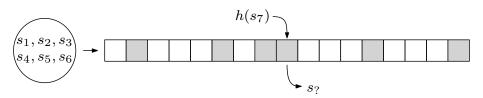
combine a MPHF with a fully-dynamic de Bruijn graph

Our result:

a dynamic MPHF for k-mers

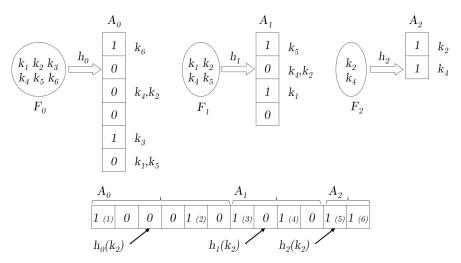
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How to retrieve an element when a collision occurs?



Our idea: combine a MPHF with a fully-dynamic de Bruijn graph

Our result: a dynamic MPHF for k-mers



[Image taken from Limasset et al. SEA (2017)]

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# Fully Dynamic de Bruijn graph

- bit matrices IN and OUT
- forest  ${\mathcal F}$  of spanning trees
- list R of roots



[Belazzougui et al. SPIRE (2016); Crawford et al. Bioinformatics (2018)]

# Fully Dynamic de Bruijn graph

- bit matrices IN and OUT
- forest  ${\mathcal F}$  of spanning trees
- list R of roots



|                    |   | Ι | N |   | OUT |   |   |   | $k_2$      |
|--------------------|---|---|---|---|-----|---|---|---|------------|
|                    | A | C | G | T | A   | C | G | T | $k_3$      |
| $\frac{1}{1(k_3)}$ | 0 | 0 | 0 | 0 | 0   | 0 | 0 | 1 | $k_1$      |
| $2(k_1)$           | 0 | 0 | 0 | 0 | 1   | 1 | 1 | 0 | G          |
| $3(k_4)$           | 0 | 1 | 0 | 0 | 0   | 0 | 0 | 0 | CF         |
| $4 (k_2)$          | 1 | 0 | 0 | 0 | 0   | 0 | 0 | 0 | $k_5$      |
| $5 (k_5)$          | 0 | 0 | 1 | 1 | 0   | 0 | 0 | 0 | $k_4$      |
|                    |   |   |   |   |     |   |   |   | D /1- 1- \ |

$$R = \langle k_1, k_3 \rangle$$

[Belazzougui et al. SPIRE (2016); Crawford et al. Bioinformatics (2018)]

- the MPHF is a list of bit vectors (blocks)
- whenever we insert an element, we update the dBG
- the new elements are always added to the last block
- a new block is created if:
  - a) the last block is too "full"
  - b) a collision occurs in the last block
- if a collision occurs:
  - 1. recreate the element by visiting the dBG
  - 2. insert both elements

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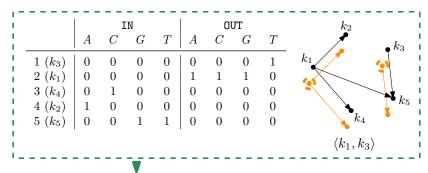
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## Structure overview



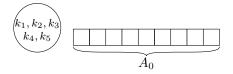


 $dBG^1$ : bit matrices + forest + roots

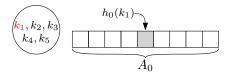
<sup>1</sup> Belazzougui et al. SPIRE (2016)

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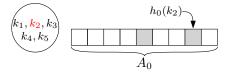


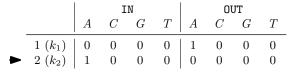






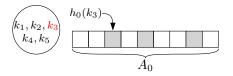


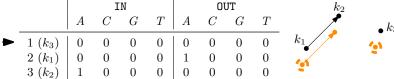






 $\langle k_1 \rangle$ 

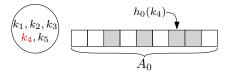




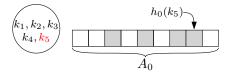




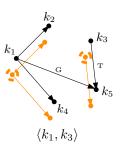
 $\langle k_1, k_3 \rangle$ 

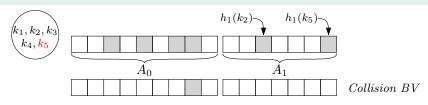


|                       |           |   | I | N |   | OUT |   |   |   | $k_2$                      |
|-----------------------|-----------|---|---|---|---|-----|---|---|---|----------------------------|
|                       |           | A | C | G | T | A   | C | G | T | $k_3$                      |
|                       | $1 (k_3)$ | 0 | 0 | 0 | 0 | 0   | 0 | 0 | 0 | $k_1$                      |
|                       | $2(k_1)$  | 0 | 0 | 0 | 0 | 1   | 1 | 0 | 0 |                            |
| $\blacktriangleright$ | $3(k_4)$  | 0 | 1 | 0 | 0 | 0   | 0 | 0 | 0 | C                          |
|                       | $4(k_2)$  | 1 | 0 | 0 | 0 | 0   | 0 | 0 | 0 | <b>\</b>                   |
|                       |           |   |   |   |   |     |   |   |   | $k_4$                      |
|                       |           |   |   |   |   |     |   |   |   | $\langle k_1, k_3 \rangle$ |



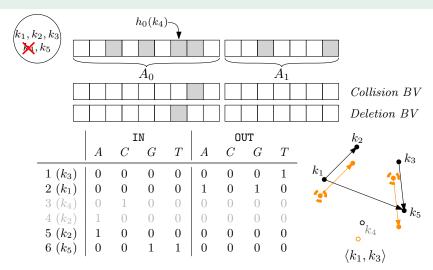
|   |   | I | N |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|
|   | A | C | G | T | A | C | G | T |
| $ \begin{array}{c} 1 \ (k_3) \\ 2 \ (k_1) \\ 3 \ (k_4) \\ 4 \ (k_2) \end{array} $ | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
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|             | $3(k_4)$  | 0 | 1  | 0 | 0 | 0   | 0 | 0 | 0 | 1.                         |  |  |
|             | $4(k_2)$  | 1 | () | 0 | 0 | 0   | 0 | 0 | 0 | $k_5$                      |  |  |
| <b>&gt;</b> | $5(k_2)$  | 1 | 0  | 0 | 0 | 0   | 0 | 0 | 0 | $k_4$                      |  |  |
| <b>&gt;</b> | $6 (k_5)$ | 0 | 0  | 1 | 1 | 0   | 0 | 0 | 0 | $\langle k_1, k_3 \rangle$ |  |  |

## Deletion



#### Dynamic implementation of

- quasi-minimal perfect hash function for k-mers
- de Bruijn graph

#### 0Qs

- is it reasonable and efficient in practice?
- can we also find good theoretical bounds?
- how many shifts should we allow?
- when should we create a new block?
- worst case:  $2^{b-1}$  insertions in the last block (but in practice?)

[b blocks]

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– when should we rebuild everything? can we reuse some parts?

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# Thank You! Questions? Suggestions? Idea?

Wanna help us?