DSB2022
fimpera: low memory counting Approximate Membership Query
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Inria Rennes

context

context

fimpera

context

fimpera

results

Summary

context

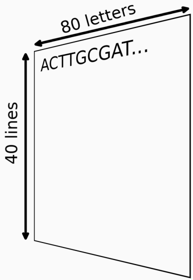
fimpera

results

Some context

My dream:

- to index (large) genomic datasets
- to query those indexed datasets



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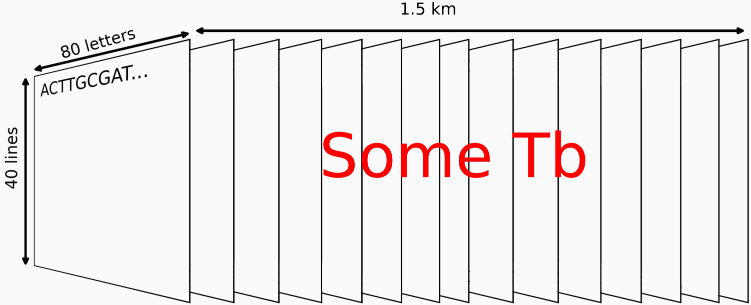

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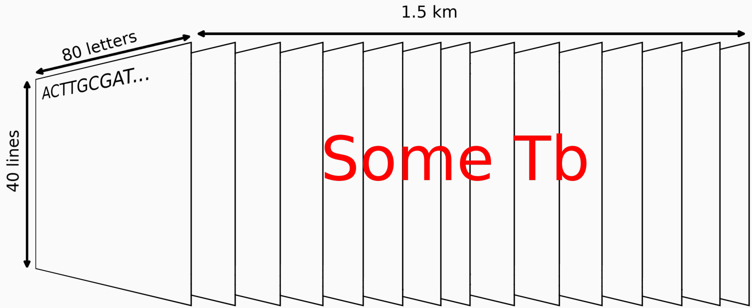

Camille Marchet, Christina Boucher, Simon J Puglisi, Paul Medvedev, Mikaël Salson, and Rayan Chikhi. **Data structures based on k-mers for querying large collections of sequencing data sets.** Genome Research, 31(1):1–12, 2021.

Challenges

- indexation time
- **abundance storage**
- **index size**
- query time
- **false positive rate**

How to compare sequences

- extract every subsequence of size *k* (*k*-mers)
- count *k*-mers
- index them along with their abundance
- query abundance of every *k*-mer from your queried sequence

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Main idea of fimpera

Let’s consider the 13-mer ‘datastructure’. Its 11-mers are:

- ‘datastructu’ (abundance: 5)
- ‘atastructur’ (abundance: 2)
- ‘tastructure’ (abundance: 4)

$\Longrightarrow$ abundance of ‘datastructure‘ can’t be more than 2.

Some notations

Rather than indexing k-mers, **let's index s-mers**, $s < k$.
Let's introduce $z = k - s$, so that a k-mer is made of $z + 1$ smaller s-mers.

A k-mer is said 'found' iif the $z + 1$ s-mers composing it are found in the filter.

Indexation with fimpera

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$(*)$ e.g. counting Bloom filter

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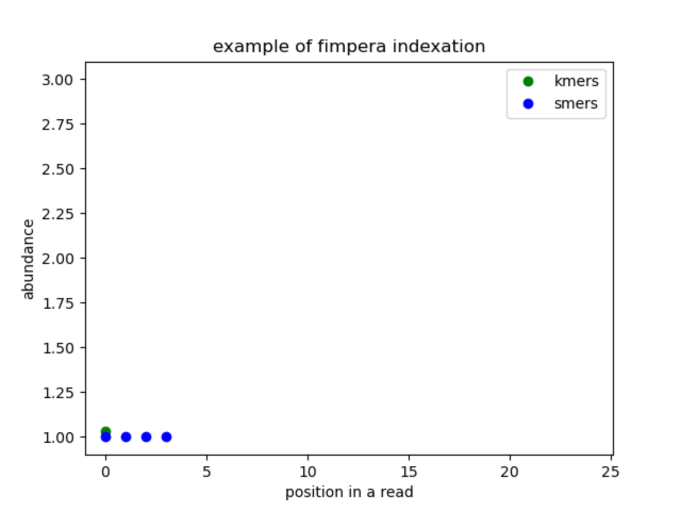

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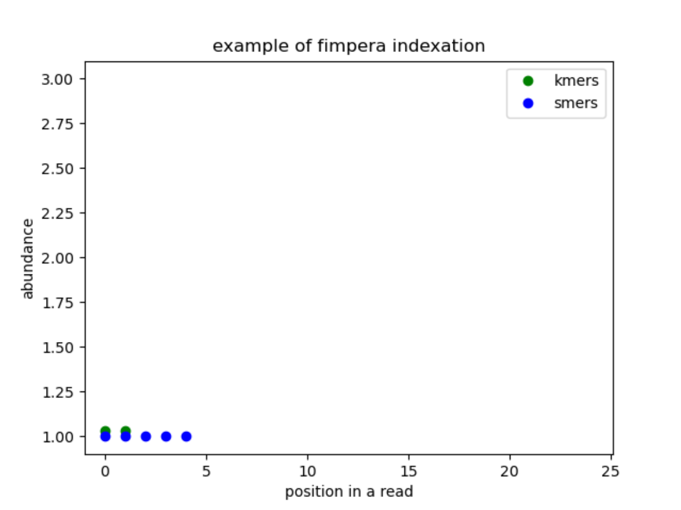

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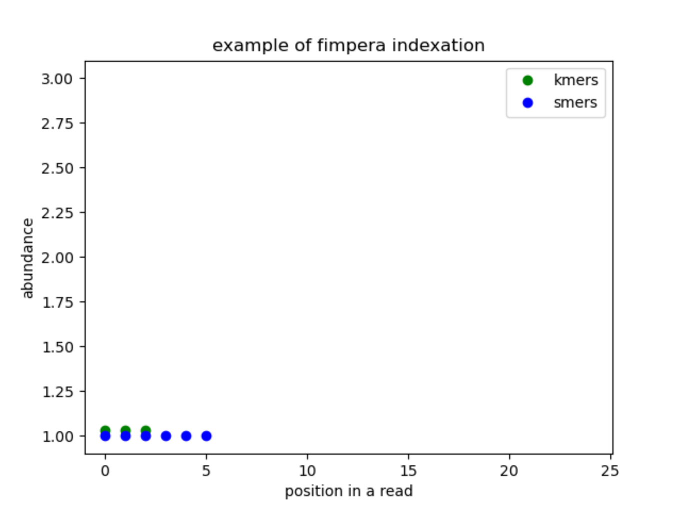

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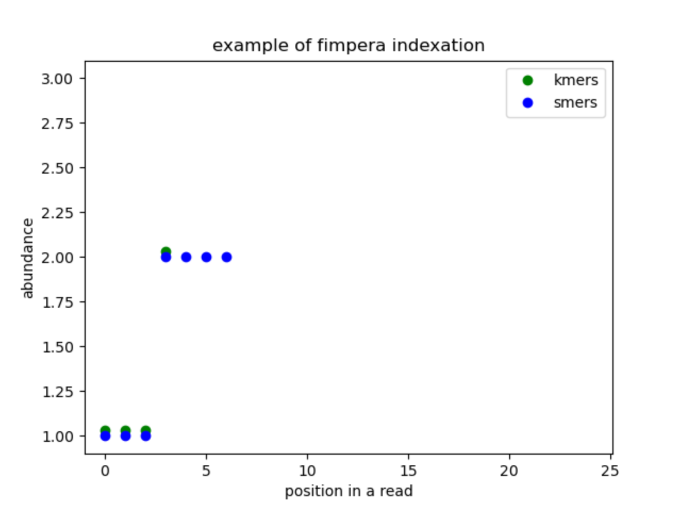

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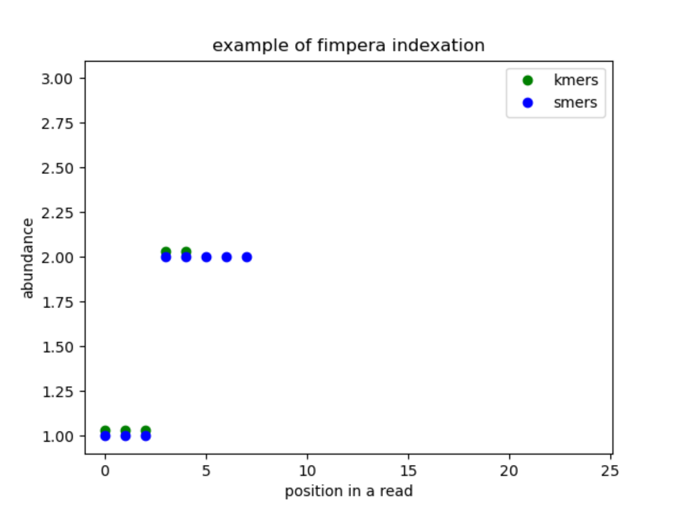

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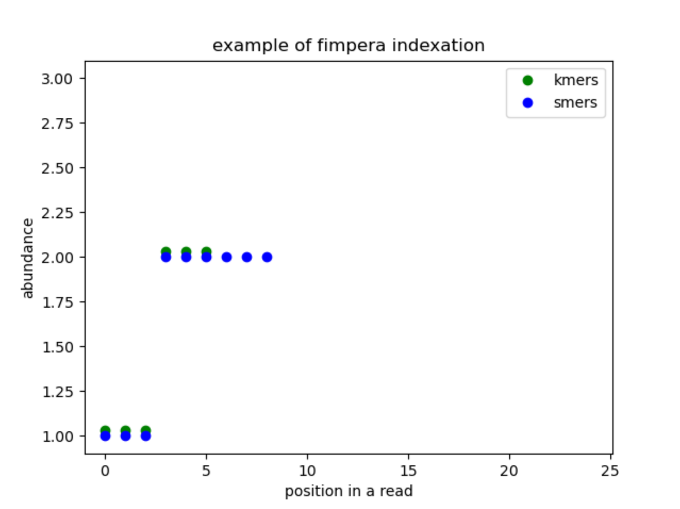

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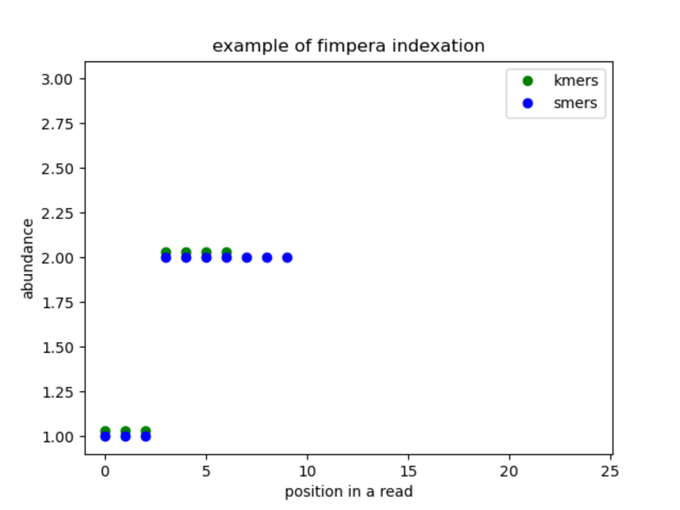

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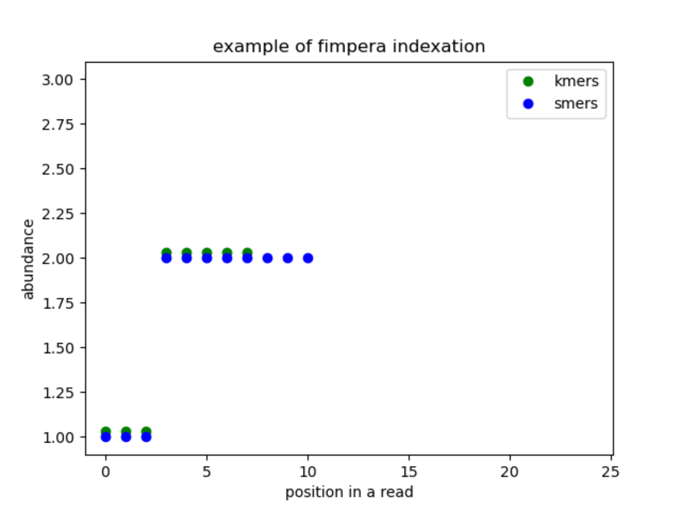

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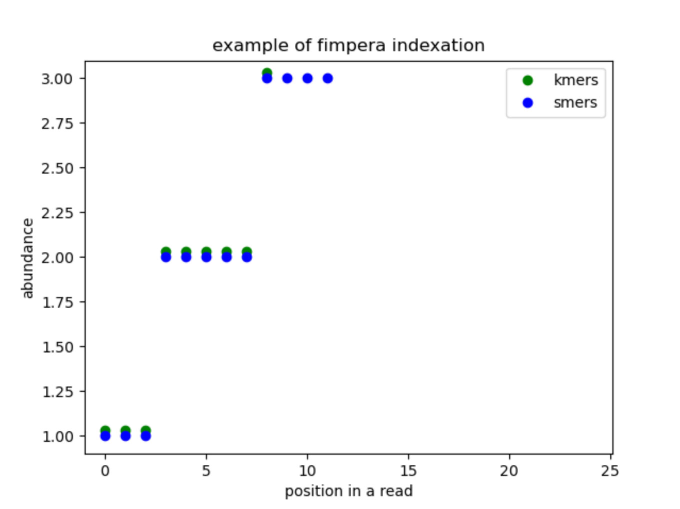

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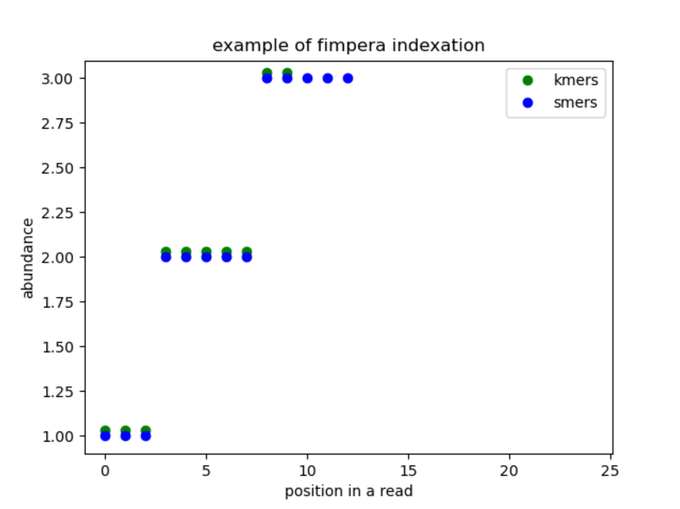

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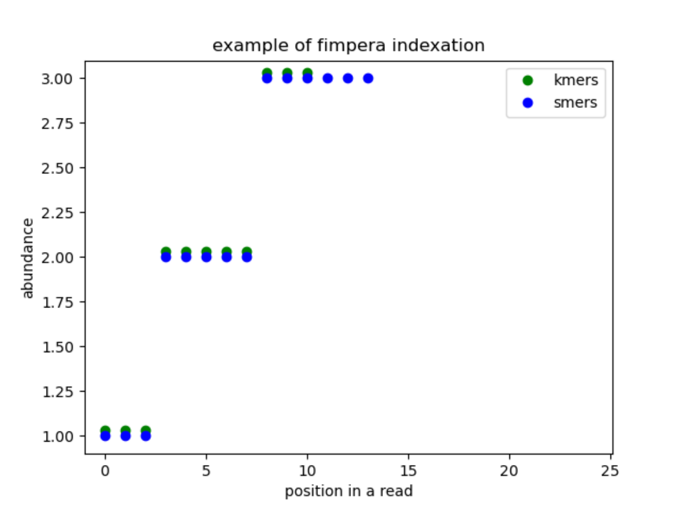

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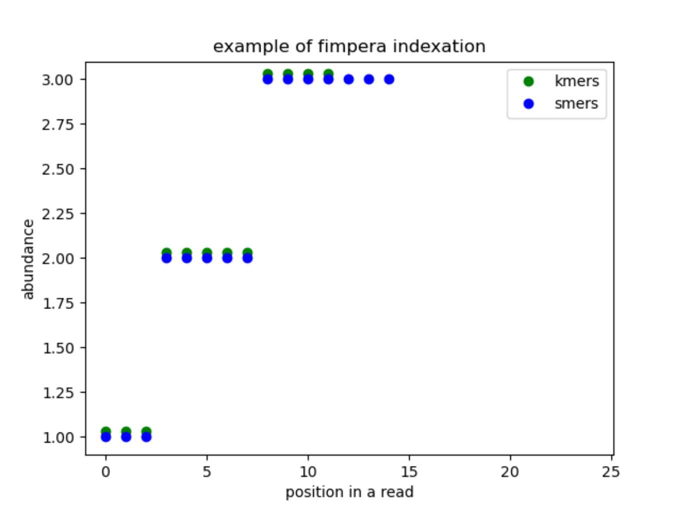

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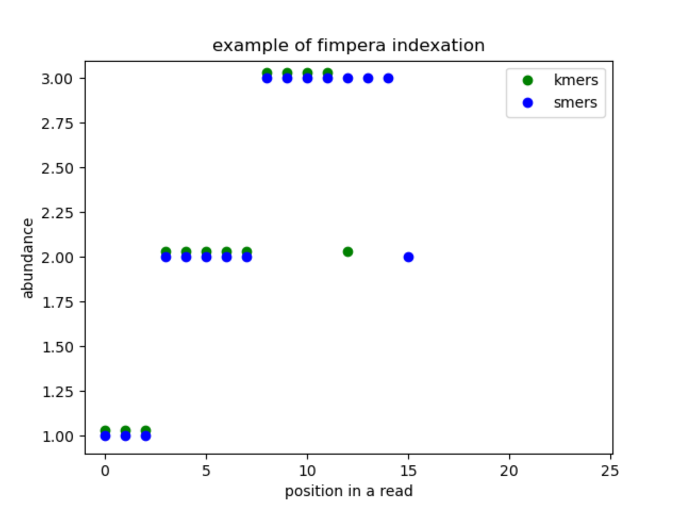

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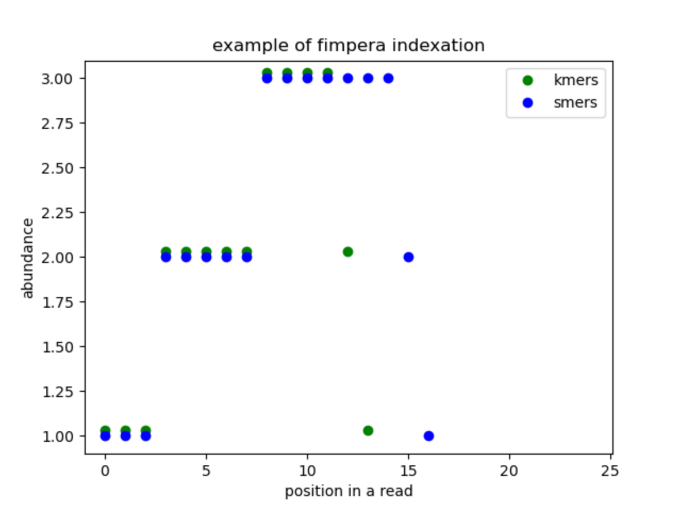

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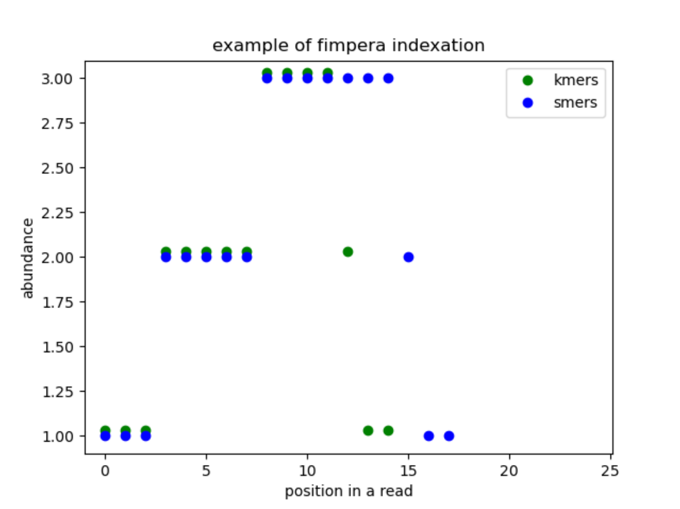

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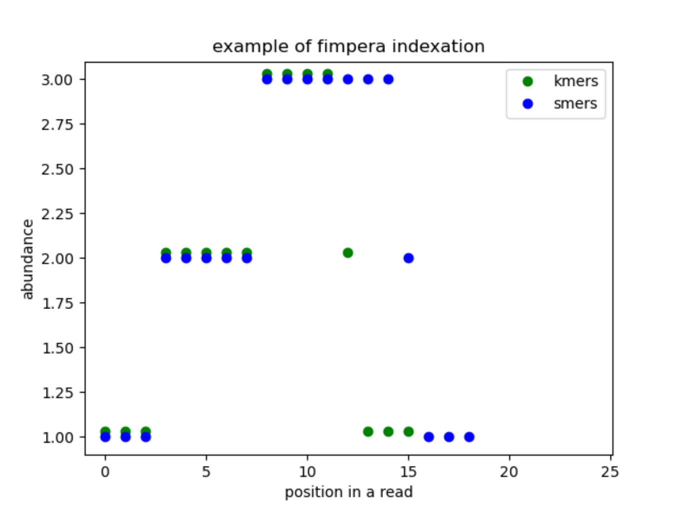

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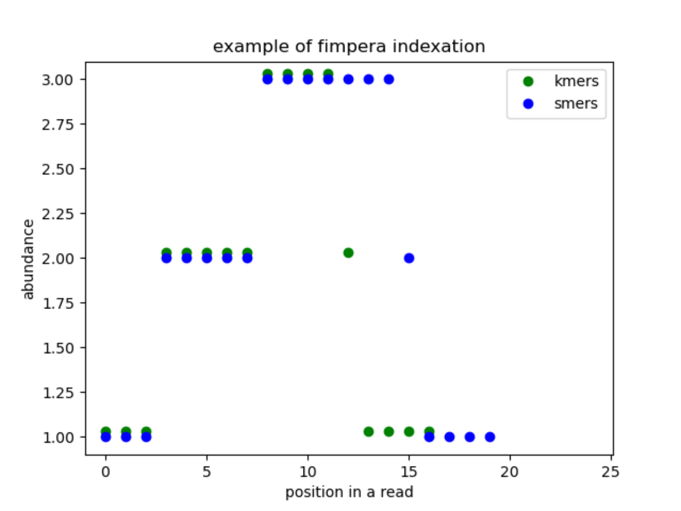

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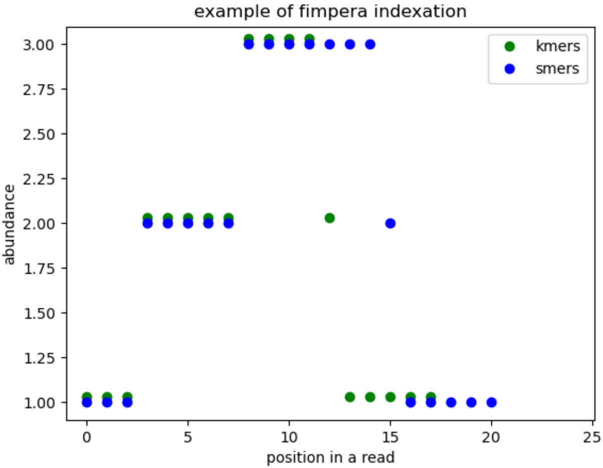

Query on fimpera

- query abundance of every *s*-mers
- compute *k*-mers abundance (min of *s*-mers abundance)

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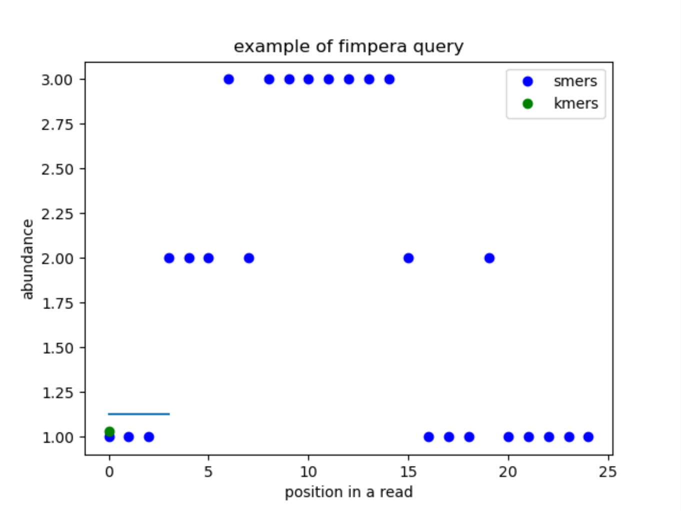

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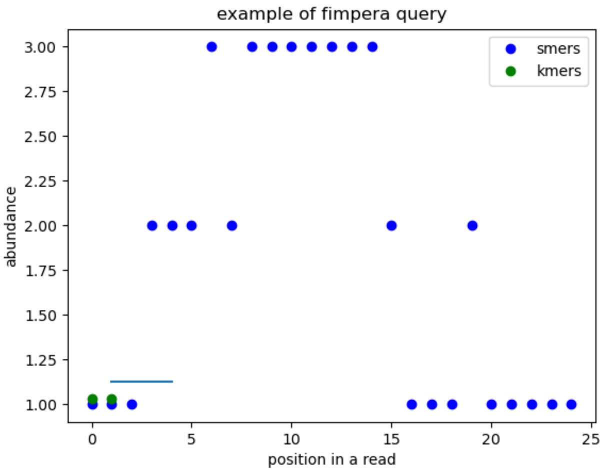

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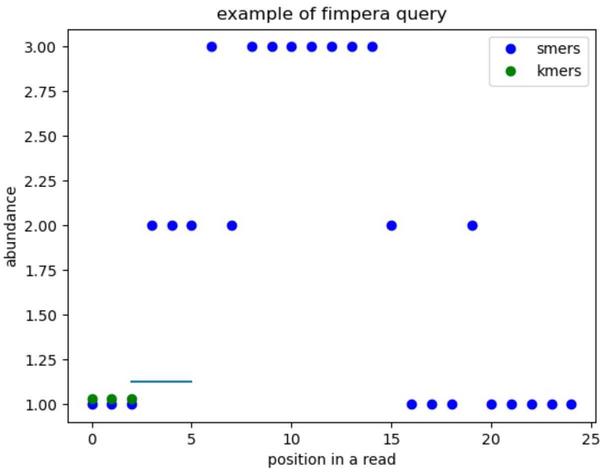

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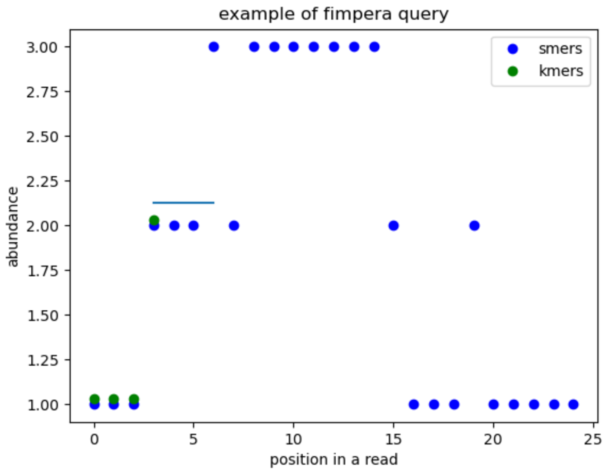

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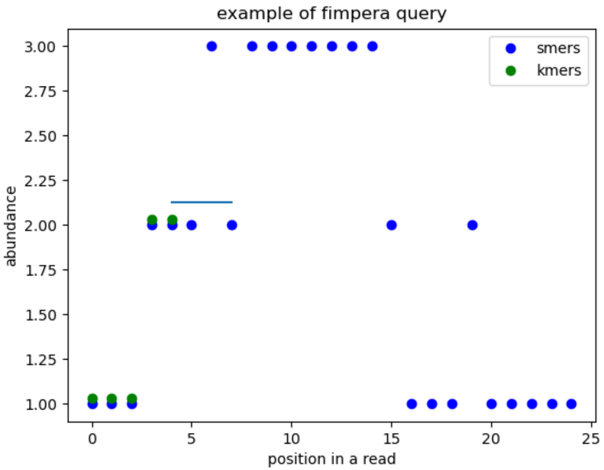

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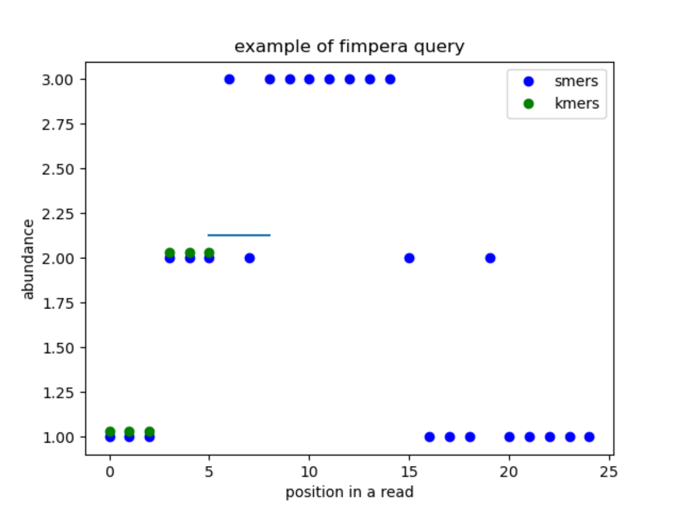

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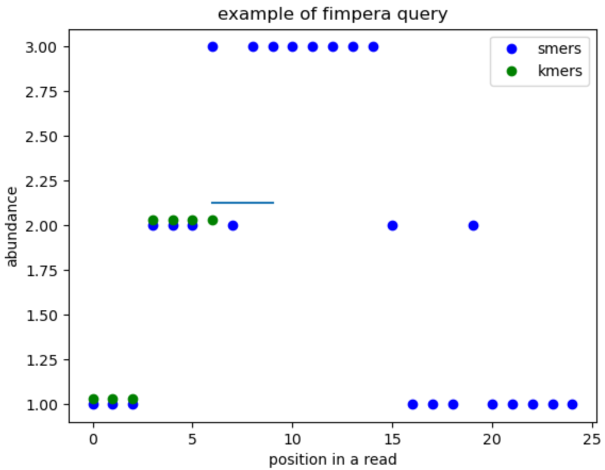

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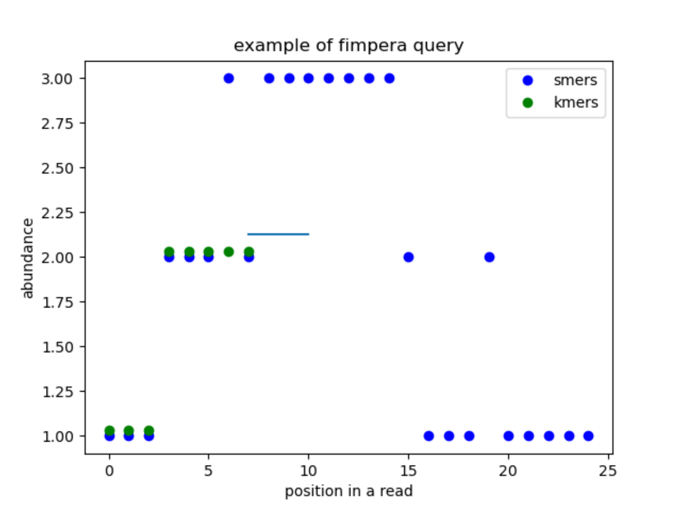

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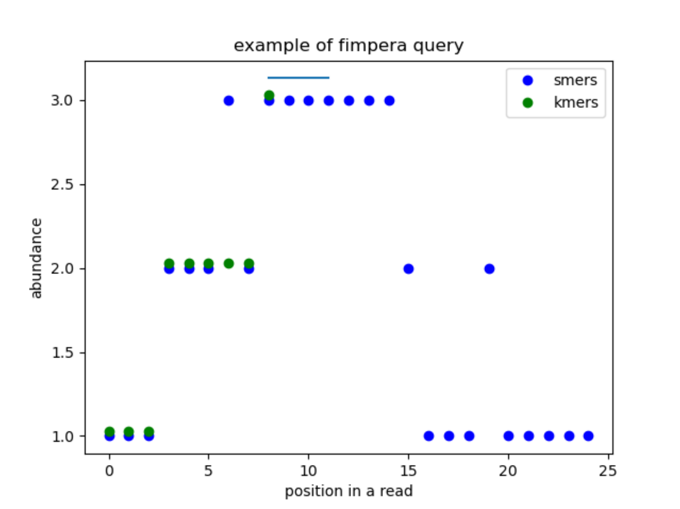

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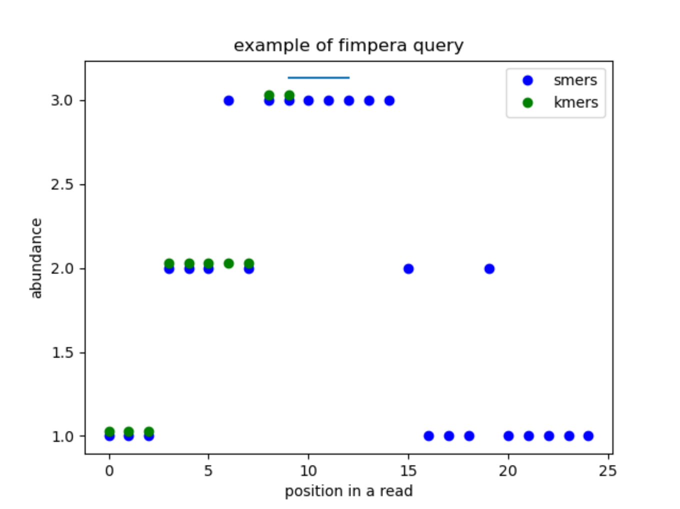

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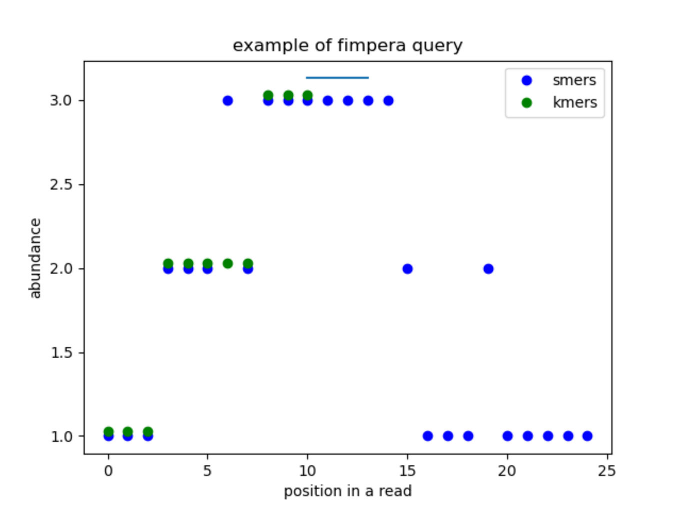

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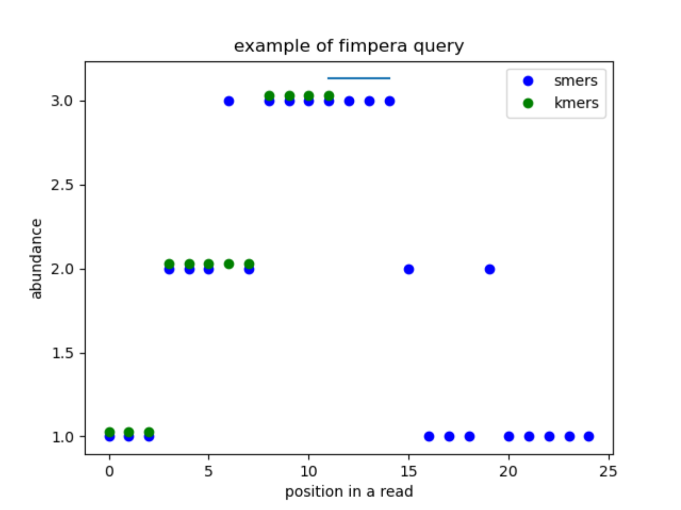

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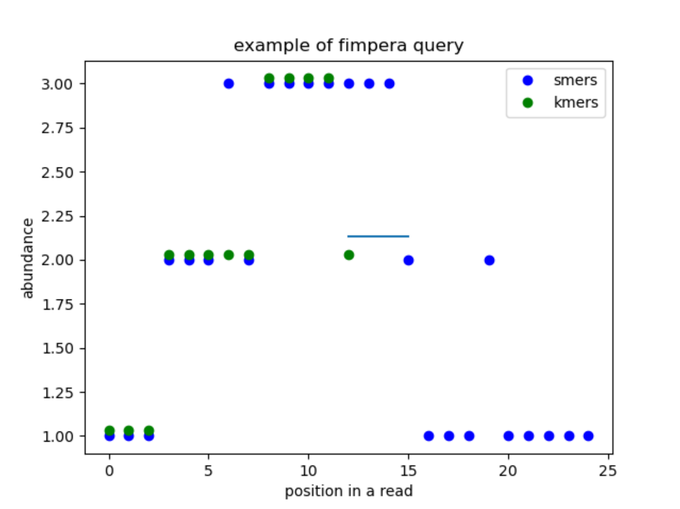

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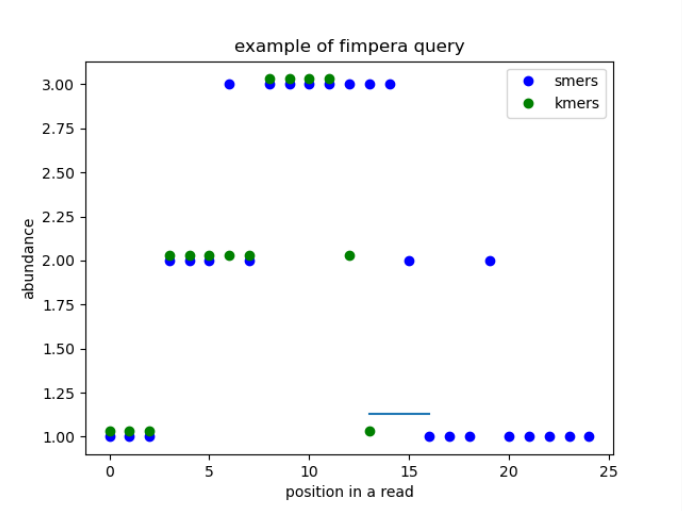

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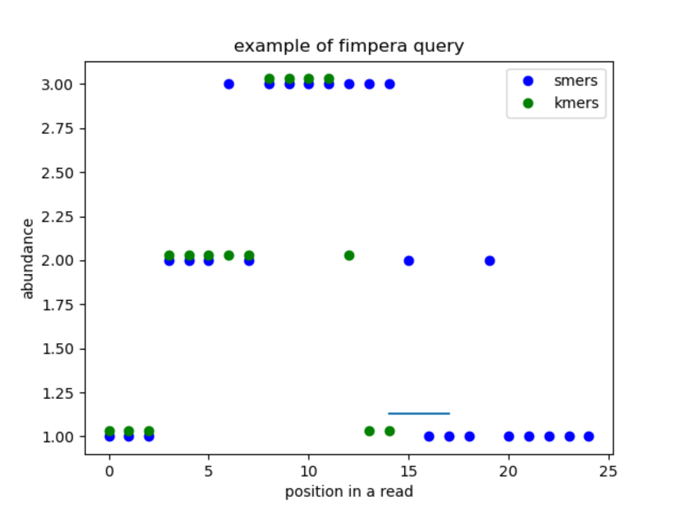

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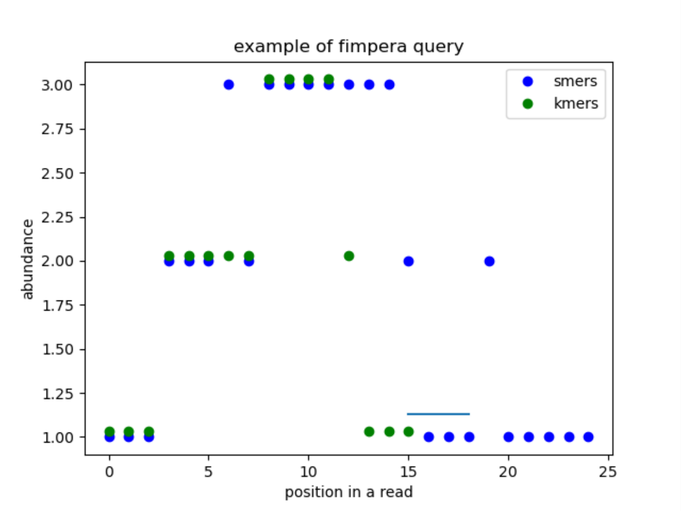

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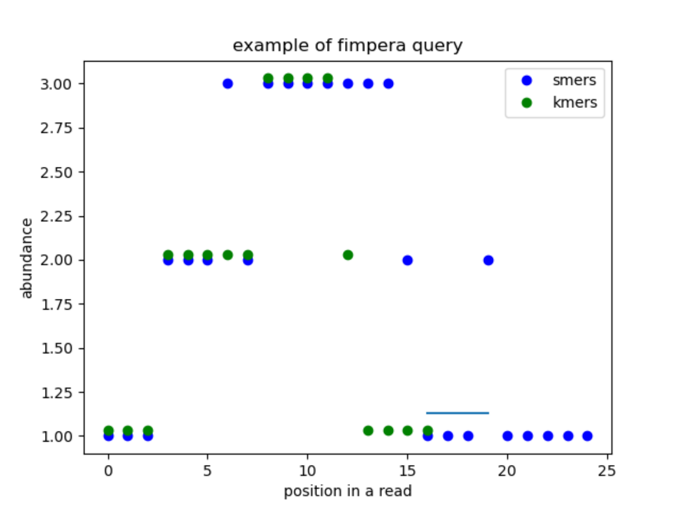

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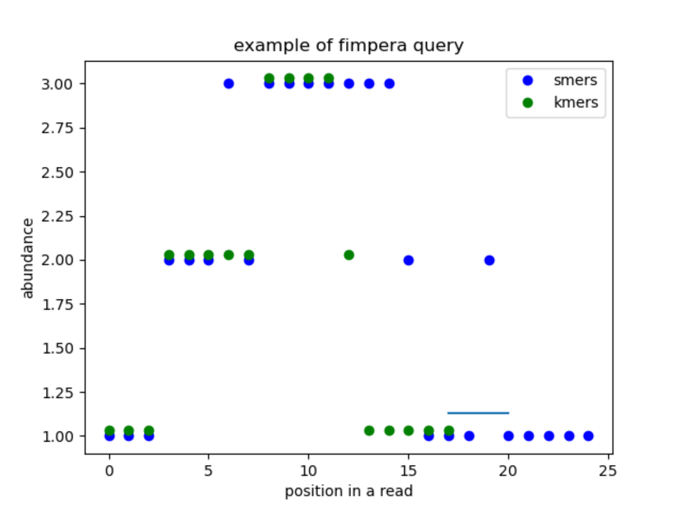

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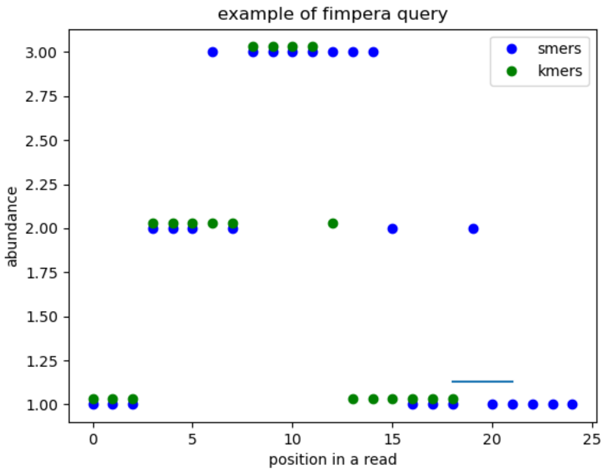

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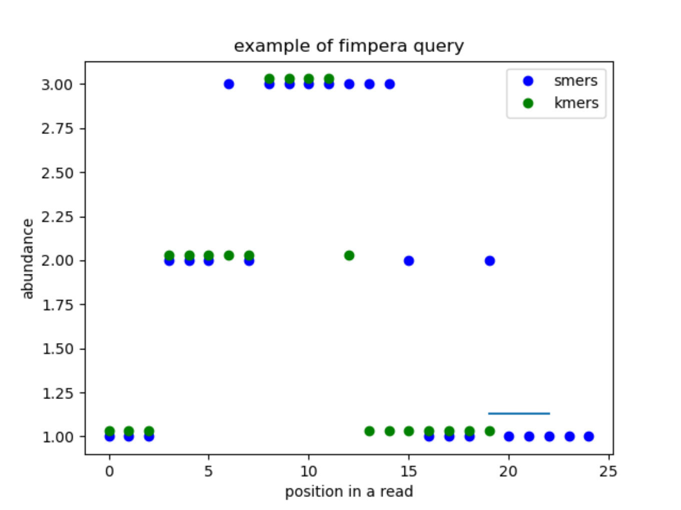

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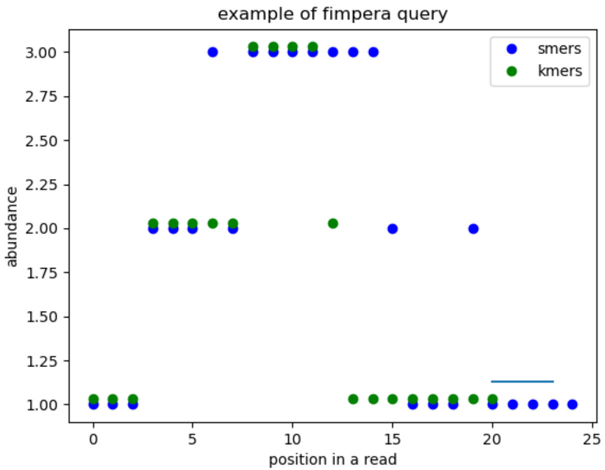

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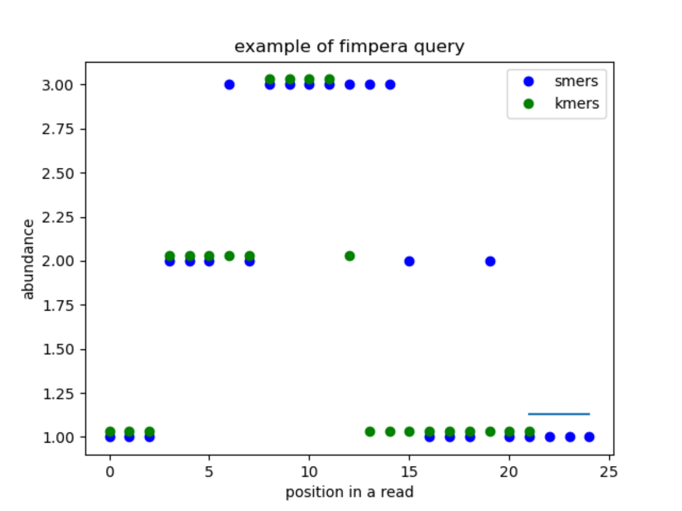

limitation of fimpera

For a chosen k, if z is too high, then fimpera will index and query very small s-mers. In such case, the probability of having indexed all those s-mers is *high*.

Example of construction overestimation

- indexing ‘ACTGAC’ with $s = 3$
- indexed s-mers include ‘GAC’, ‘ACT’ and ‘CTG’
- k-mer ‘GACTG’ would be found with the abundance of ‘ACTGAC’

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Data used

- two fastq files from the TARA ocean dataset (metagenomic)
- one is indexed
- 1,000,000 reads are queried from the second

fimpera’s effect on false positive rate

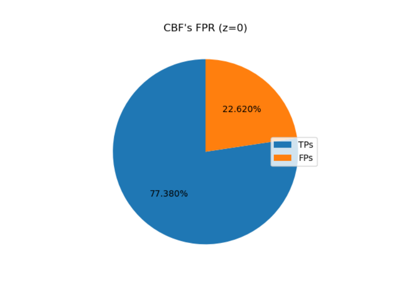

Figure 1: proportion of false positive calls **without** fimpera

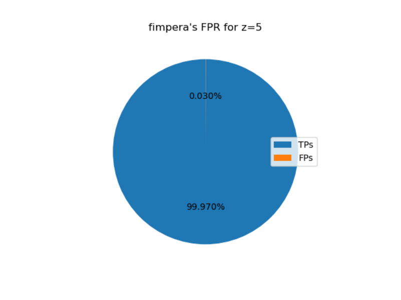

Figure 2: proportion of false positive calls **with** fimpera

fimpera’s effect on abundance correctness

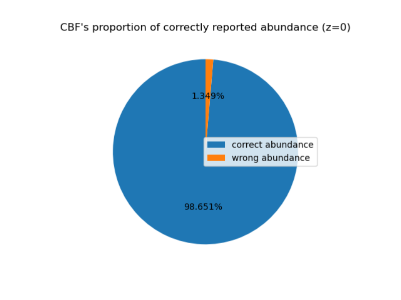

Figure 3: proportion correct abundance calls **without** fimpera

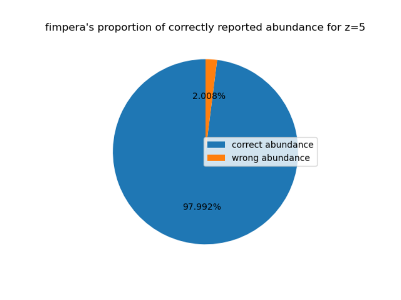

Figure 4: proportion correct abundance calls **with** fimpera

fimpera's effect on abundance error

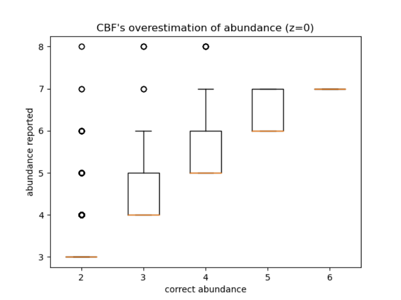

Figure 5: overestimations **without** fimpera

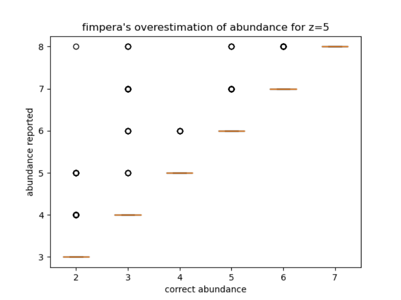

Figure 6: overestimations **with** fimpera