



Bloocoo, a memory efficient read corrector

Gaëtan Benoit, Dominique Lavenier, Claire Lemaitre, Guillaume Rizk

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Motivations

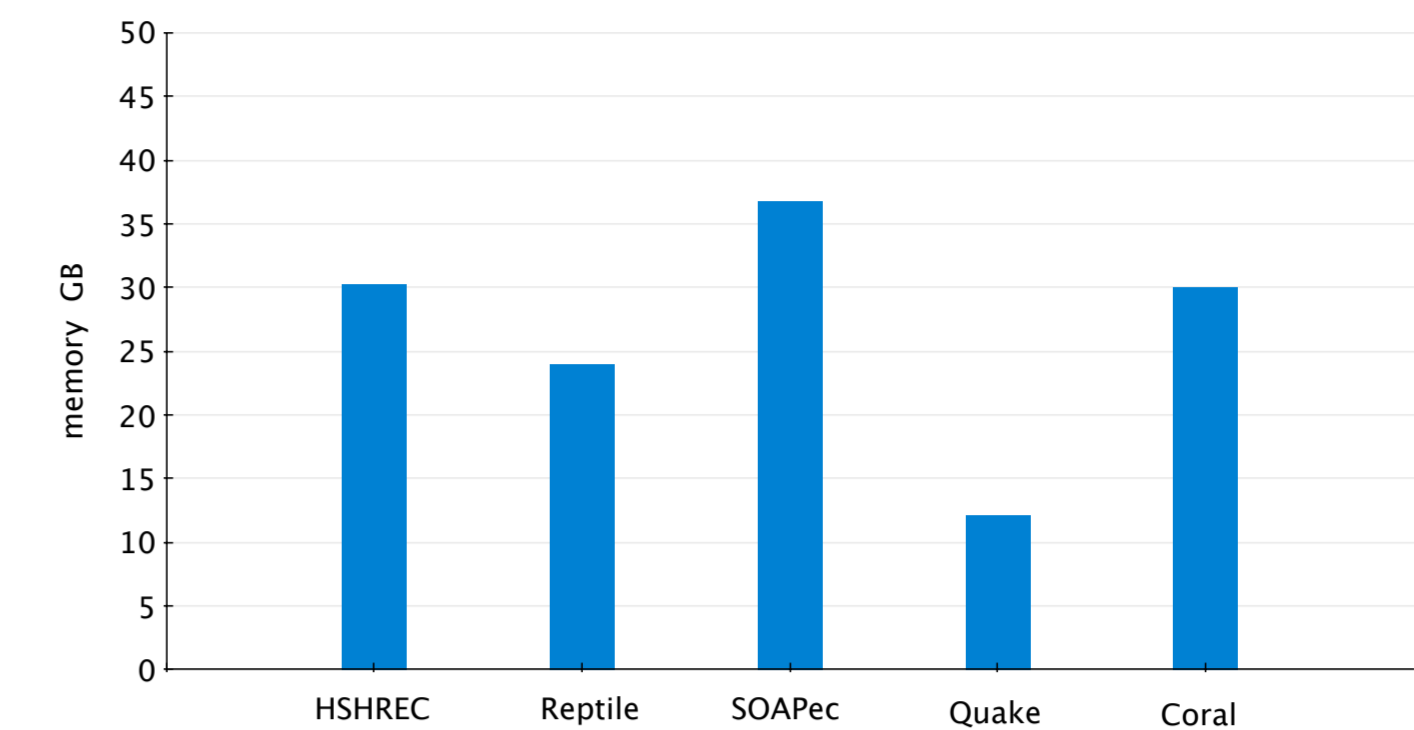
Next generation sequencing technologies generate a high amount of short DNA sequences, but may contain imperfections.

Some applications, such as assembly, yield better results with high quality data, triggering the need for short-read correction software.

Error correction – common methods

- Exploits high depth of coverage
- Multiple sequence alignment
- Suffix tree
- Kmer frequency spectrum

Most methods use large amount of memory
And therefore limited to small datasets

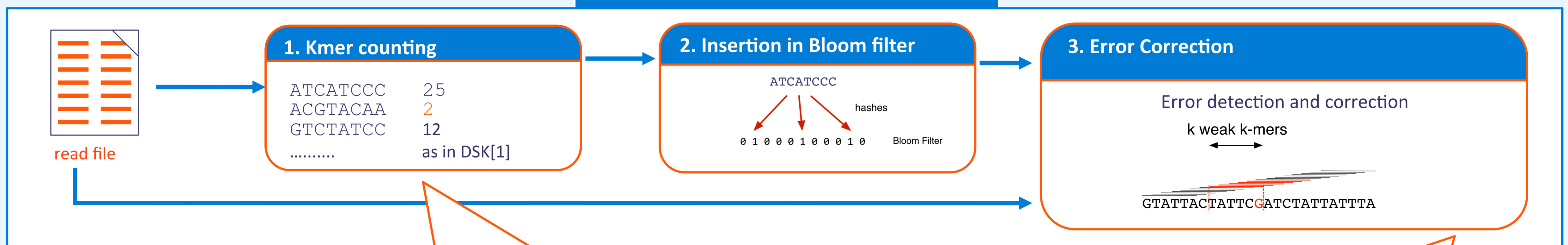


Memory used on a 56x *D.Melanogaster* dataset (98M reads) on state-of-the-art methods. From *A survey of error-correction methods, 2013* [3]

No tool able to handle large whole genome re-sequencing data files

Methods

Bloocoo



Kmer spectrum creation

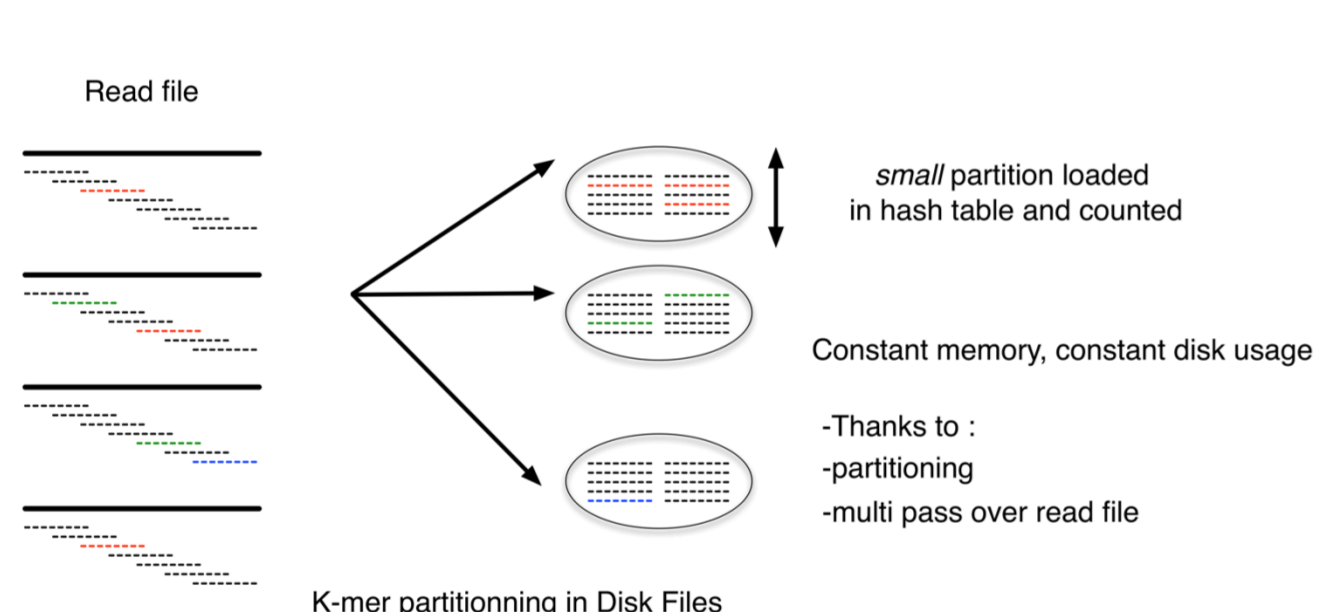
Read file



Bloom filter of solid kmers

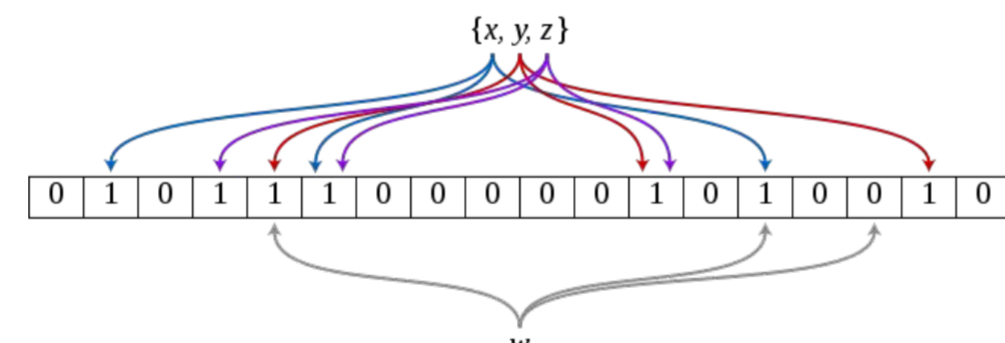
Kmer counting and insertion of solid kmers in Bloom filter : GATB library

DSK: disk streaming of kmers [1]

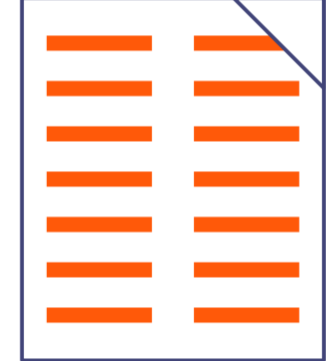
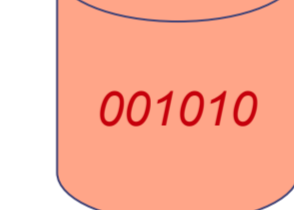
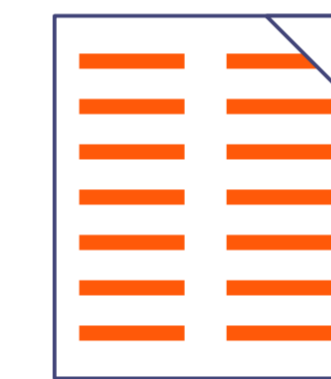


Bloom filter

- Keep solid kmers (with abundance above threshold)
- Insert them in a bloom filter
- Fast cache-coherent implementation
- 11 bits/kmer → 0.5% false positives

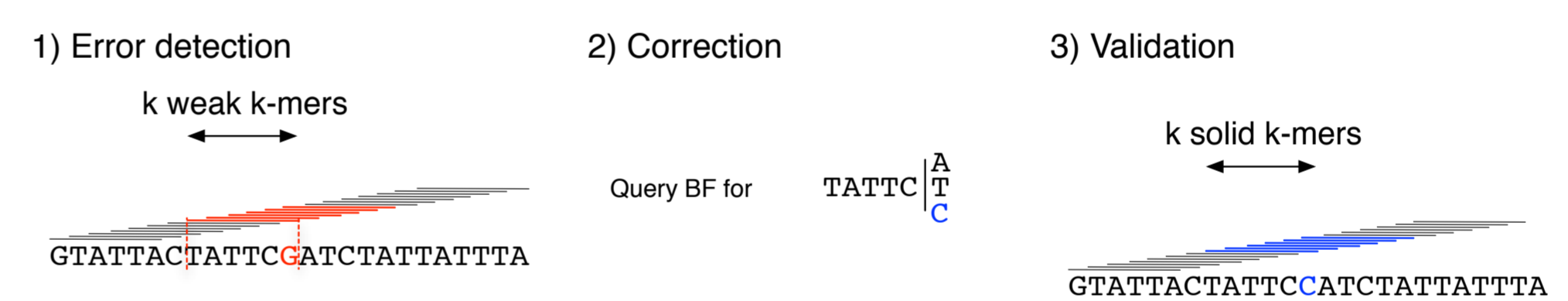


Correction

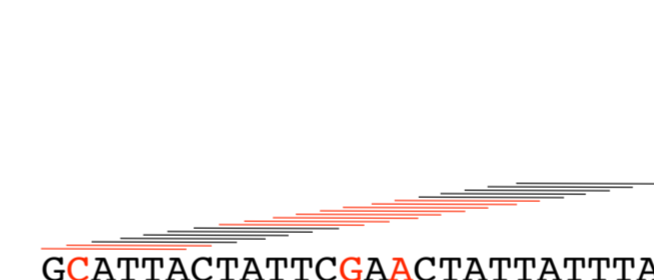


Corrected read file

Identify and correct errors by querying the bloom filter for solid kmers



Complex cases



- multistage correction
- vote algorithm
- indel correction (ion torrent homopolymers)

Results

Simulated data:

- Simulated read sets on *C.elegans*
- 1% error rate, 40 x, 100 bp, 40 M reads

Comparison with Musket[2], Racer [4], SOAPec [5], Bless [6]

Software	Recall (%)	Precision (%)	Memory (GB)	Time (sec)
Bloocoo 1.0	95.8	99.5	0.8	681
Musket 1.1	97.9	99.6	7.8	3280
Racer 1.01	97.2	78.5	31.2	2041
SOAPec 2.02	76	99.7	12.7	17203
Bless 0.17	97.2	98.8	0.2	7620

Real «big» data :

- Human NA12878, 2.8 G reads ~ 100x
- 440 GB fasta file
- ~ 2 billion errors corrected
- Requiring only 3.8GB of memory, executed in ~ 30 h

Easy integration in GATB assembly pipeline

Minia assembly on the real *C. elegans* dataset SRX026594 (70x) with and without error-correction.

Dataset	N50	Misassemblies
Original	4783	36
Bloocoo corrected	7634	26
Musket corrected	7749	29

Bloocoo:

- ★ Able to correct large datasets
- ★ Easy integration in the GATB assembly pipeline
- ★ Time/memory scalable on big datasets
- ★ Works also on indel errors (ion torrent)

References:

- [1] Rizk, G., Lavenier, D., & Chikhi, R. (2013). DSK: k-mer counting with very low memory usage. *Bioinformatics*, btt020.
- [2] Liu, Yongchao, Jan Schröder, and Bertil Schmidt. "Musket: a multistage k-mer spectrum-based error corrector for Illumina sequence data." *Bioinformatics* 29.3 (2013): 308-315.
- [3] Yang, X., Chockalingam, S. P., & Aluru, S. (2013). A survey of error-correction methods for next-generation sequencing. *Briefings in bioinformatics*, 14(1), 56-66.
- [4] Ilie, L., & Molnar, M. (2013). RACER: Rapid and accurate correction of errors in reads. *Bioinformatics*, btt407.
- [5] Li R, Zhu H, Ruan J et al. De novo assembly of human genomes with massively parallel short read sequencing. *Genome research* 2010;20:265-272.
- [6] Heo, Y., Wu, X. L., Chen, D., Ma, J., & Hwu, W. M. (2014). BLESS: Bloom filter-based error correction solution for high-throughput sequencing reads. *Bioinformatics*, btu030.

Download and use Bloocoo

<http://gatb.inria.fr/software/bloocoo/>

C++, Open Source, released under A-GPL license

Publication: E. Drezen, G. Rizk, R. Chikhi, C. Deltel, C. Lemaître, P. Peterlongo, D. Lavenier
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Bioinformatics, 2014

Download this poster:

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