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Bloocoo: a memory efficient read corrector

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Motivations

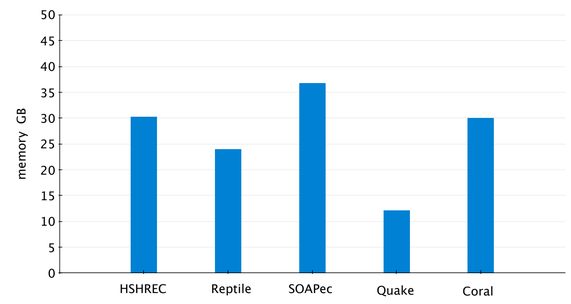
Next generation sequencing technologies generate a high amount of short DNA sequences, but may contain imperfections.

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 spetrum

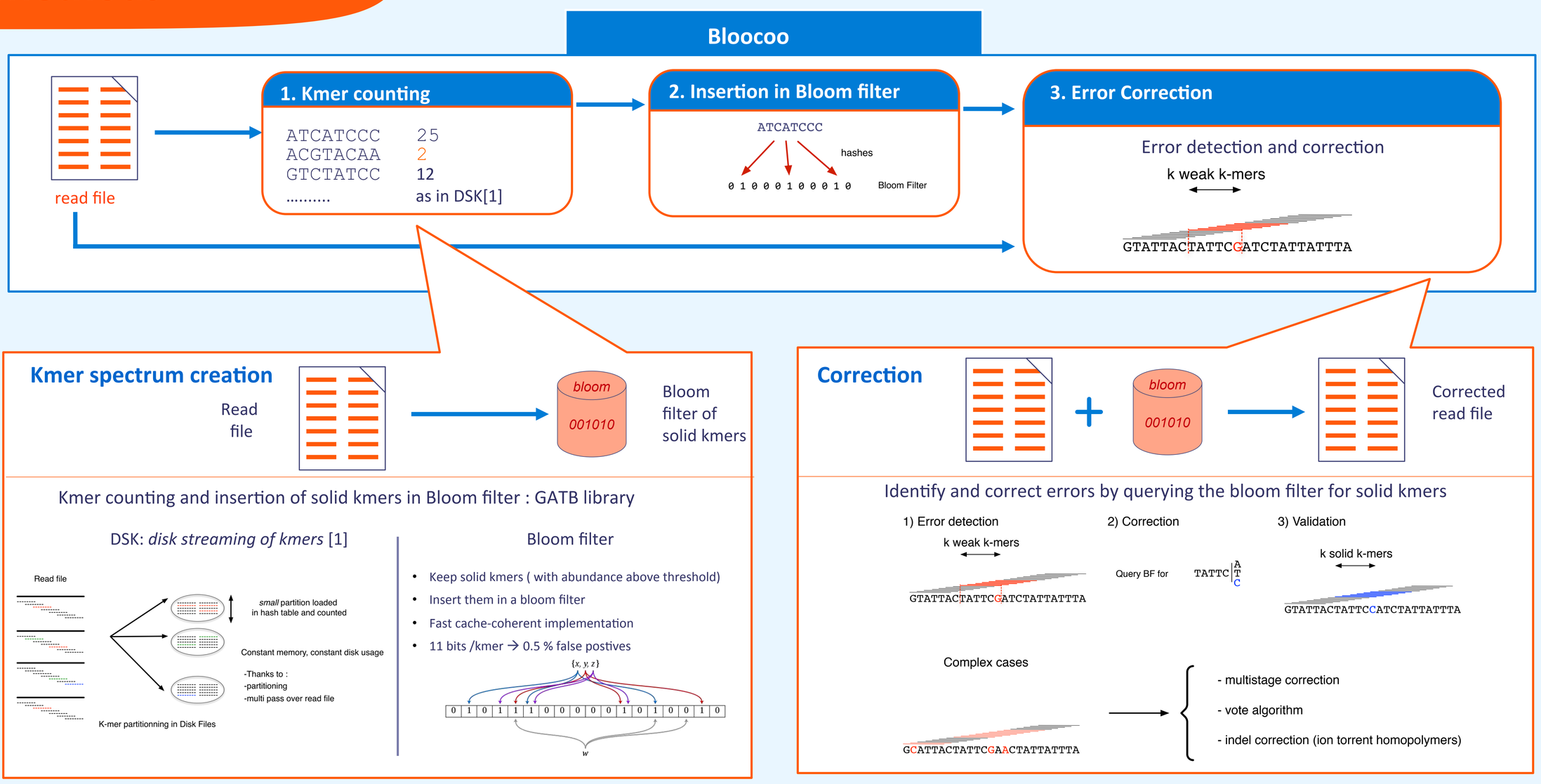
Most methods use large amount of memory
And therefore limited to small datasets



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



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]

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

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

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:

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Download and use Bloocoo

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

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

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