HG-CoLoR: enHanced de bruijn Graph for the error COrrection of LOng Reads

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November 7, 2017

Plan

Third Generation Sequencing

- Recently, Third Generation Sequencing technologies started to develop
- Two main technologies: Pacific Biosciences and Oxford Nanopore
- Allow the sequencing of longer reads (several thousand of bases)
- Very useful to resolve assembly problems for large and complex genomes
- Much higher error rate, around 15% for Pacific Biosciences and up to 30% for Oxford Nanopore

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- Various methods already exist for the correction of short reads, but are not applicable to long reads
- Forces the development of new error correction methods
- Two main categories: self-correction and hybrid correction

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- NaS [Madoui et al., 2015]
- Yields highly contiguous assembly results
- Does not locally correct erroneous regions
- Uses long reads as templates to generate corrected long reads from assemblies of short reads
- Requires the mapping of the short reads both on the long reads and against each other

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NaS overview

NaS corrects a long read as follows:

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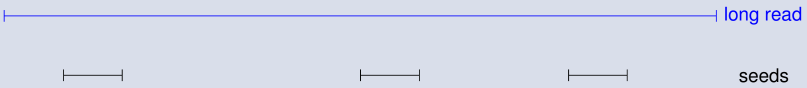
First step

Align the short reads to the long reads

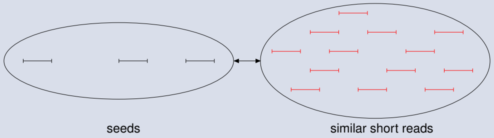


NaS overview

NaS corrects a long read as follows:

Second step

For each long read, recruit short reads that are similar to the seeds



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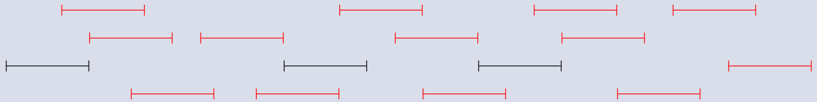
Third step

Assemble the obtained subset of short reads



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Fourth step

Use the obtain contig as the correction of the initial long read

Main idea

- Use long reads as templates
- Get rid of the time consuming step of aligning the short reads against each other
- Focus on a seed and extend approach
- Rely on an enhanced de Bruijn graph, built from the short reads

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Enhanced de Bruijn graph

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- de Bruijn graphs are widely used for correction and assembly...
- ...But face difficulties with locally insufficient coverage

Usual solutions

- Usually, multiple de Bruijn graphs of different orders are built
- Requires a different graph for each order
- Consumes large amounts of time and memory

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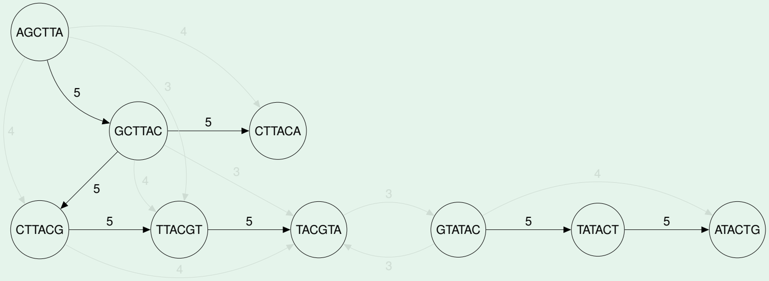
Idea

Enhance the de Bruijn graph with the capability of computing overlaps of variable lengths between the *k*-mers, in an overlap graph fashion, in order to avoid building multiple de Bruijn graphs of different orders.

Enhanced de Bruijn graph

Example

With the set of reads $S = \{\text{AGCTTACA, CTTACGTA, GTATACTG}\}$, we obtain the following enhanced de Bruijn graph of order 6:



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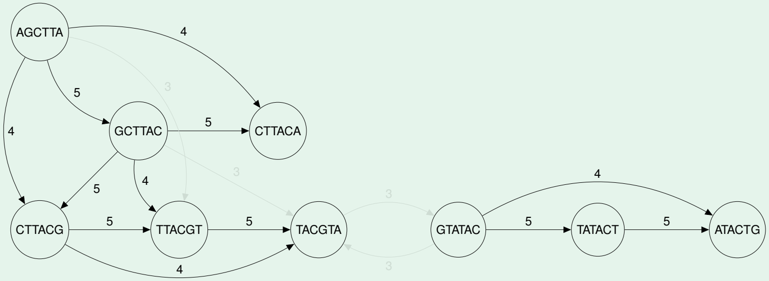

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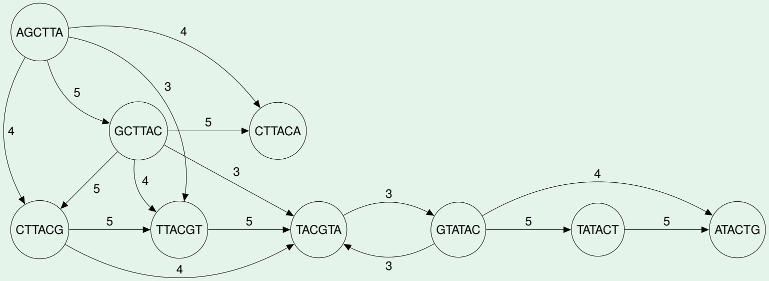

Traversal

- The enhanced de Bruijn graph does not need to be explicitly built
- It can be traversed with the help of PgSA [Kowalski et al., 2015]:
  - The *k*-mers from the reads are stored in the index
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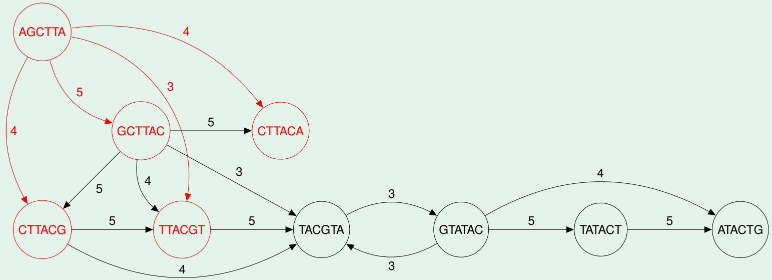
Traversing the previous enhanced de Bruijn graph:



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k-mers set

1: AGCTTA
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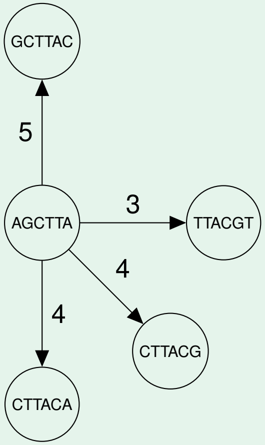
PgSA Index



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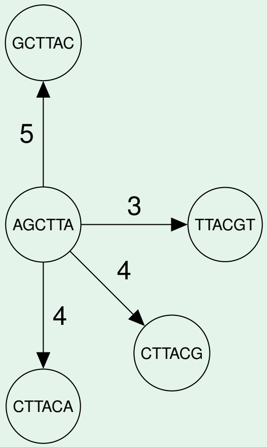

$$\begin{tikzcd}
 & \text{GCTTAC} & \\
 & \text{AGCTTA} \arrow[u, "5"] \arrow[r, "3"] \arrow[d, "4"] \arrow[dr, "4"] & \text{TTACGT} \\
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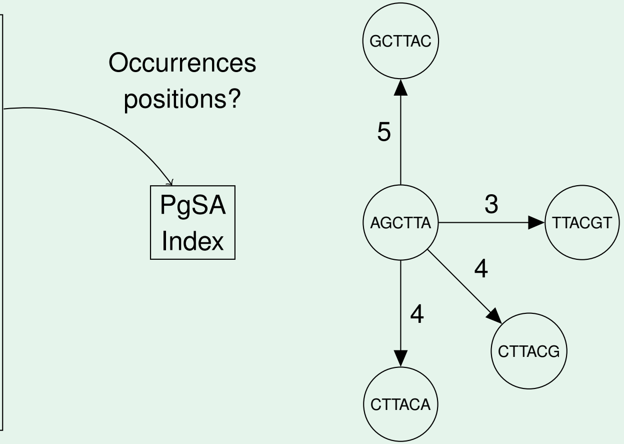

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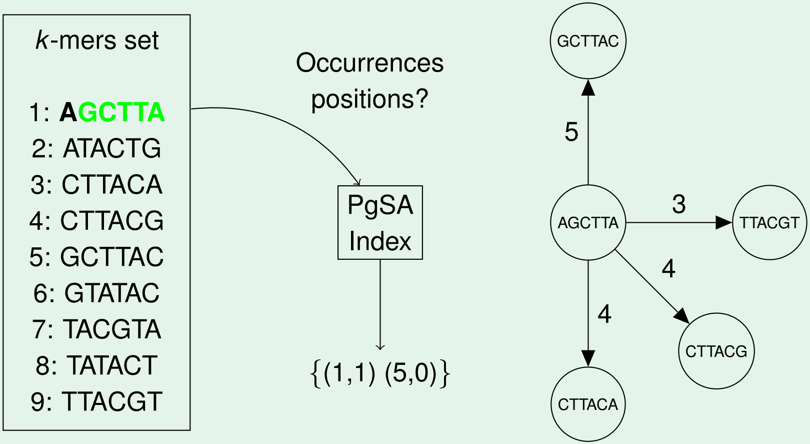

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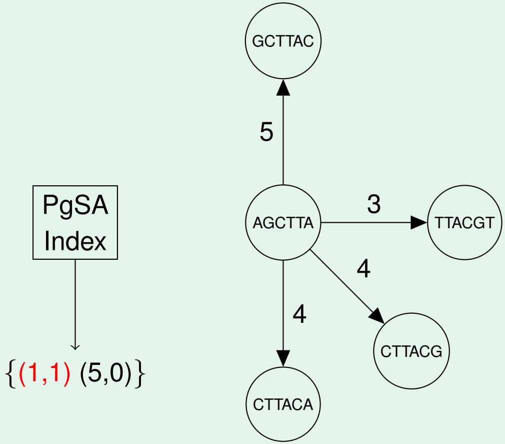

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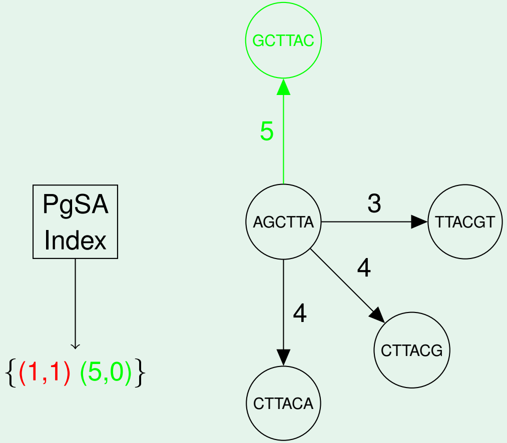

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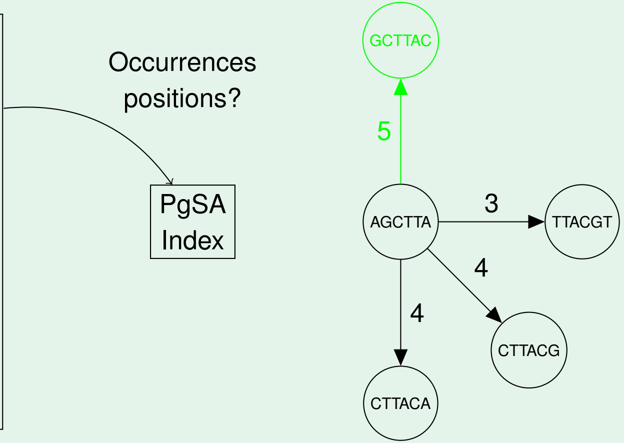

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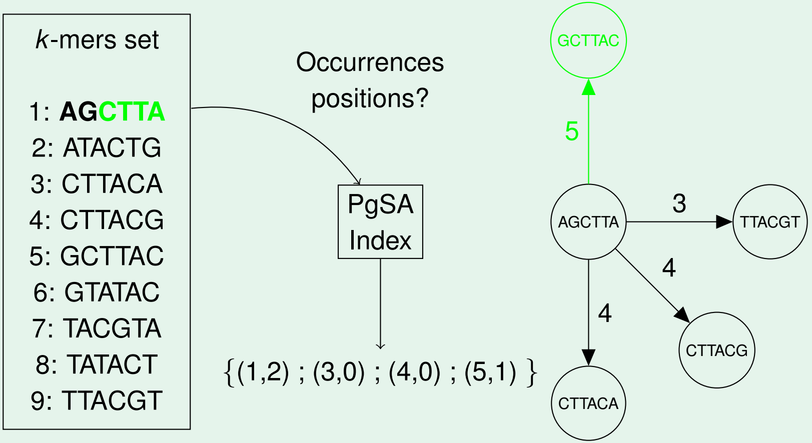

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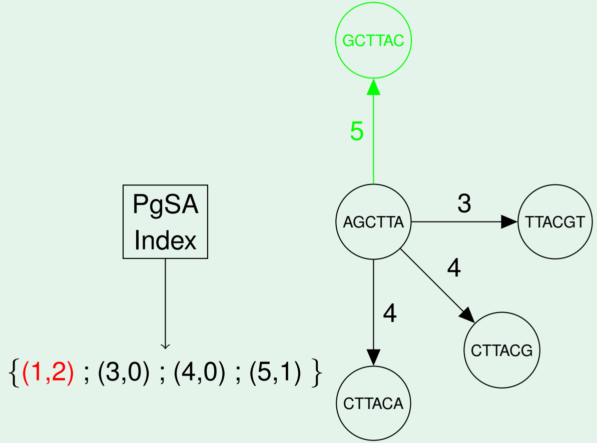

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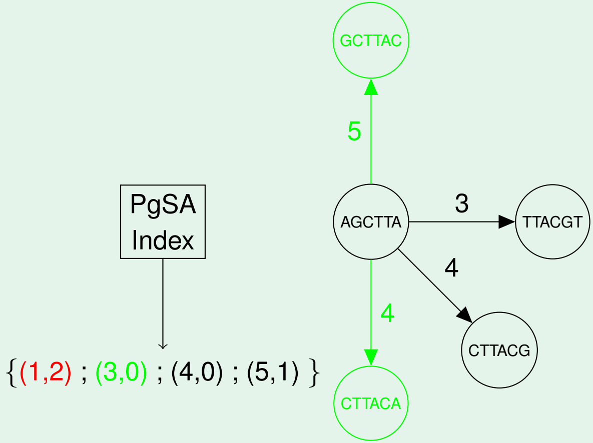

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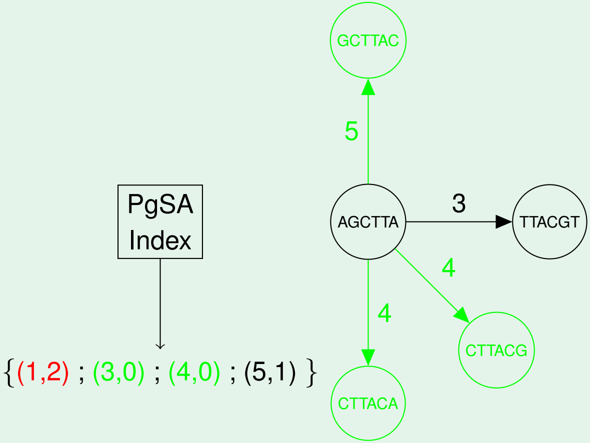

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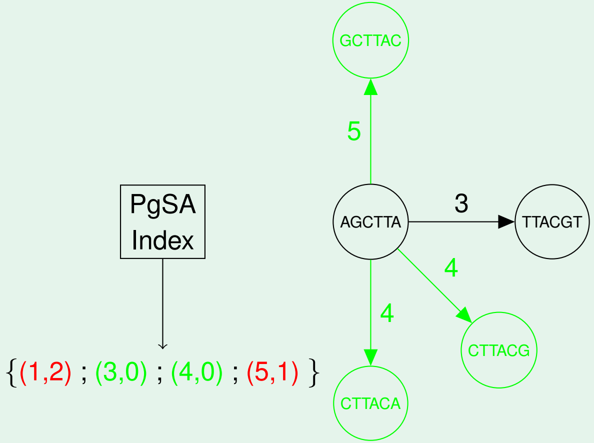

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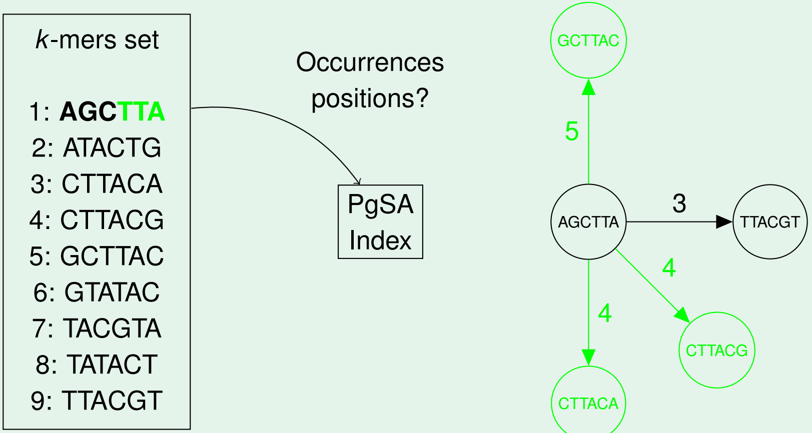

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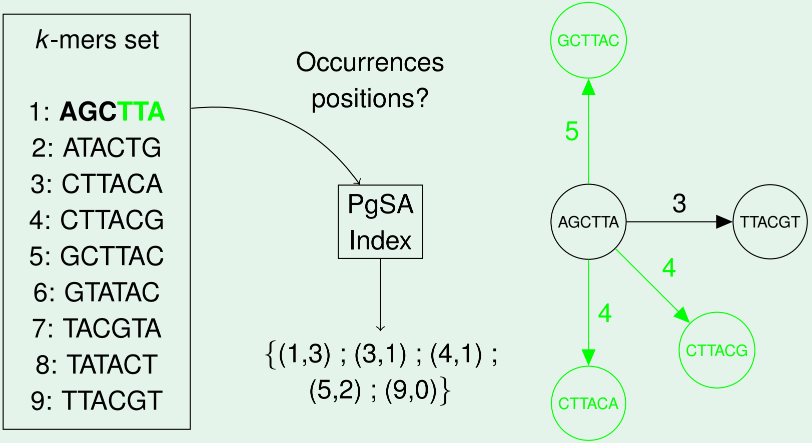

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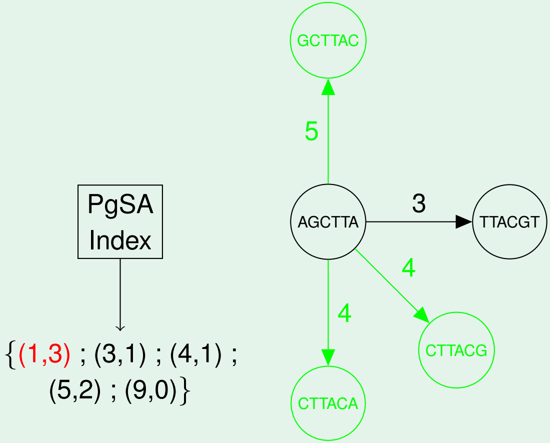

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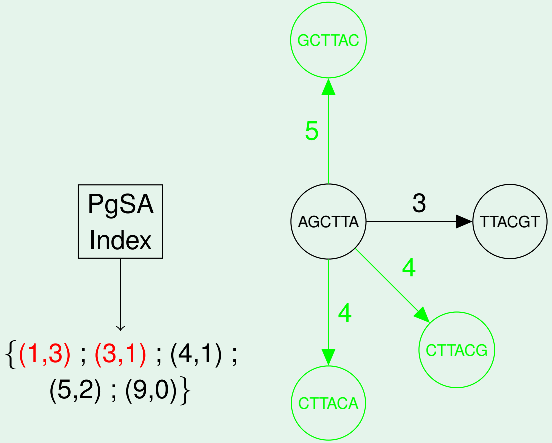

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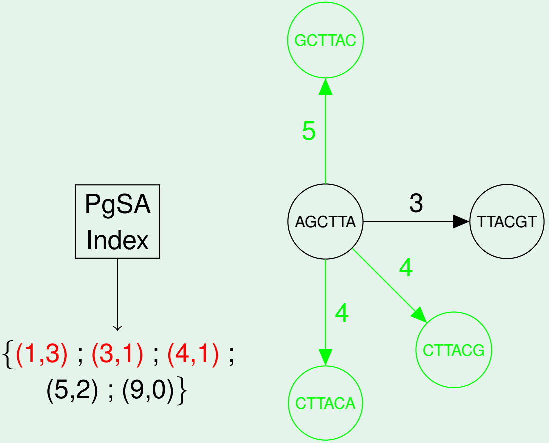

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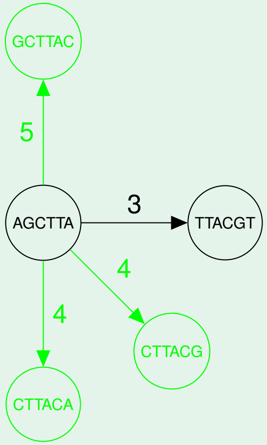

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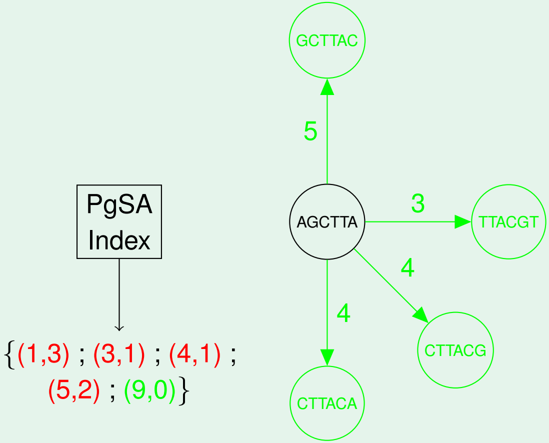

Workflow

5 steps:

1. Correct the short reads (with QuorUM [Marçais et al., 2015])
2. Filter out corrected short reads containing weak *k*-mers, and index solid *k*-mers with PgSA
3. Align the remaining short reads to the long reads, to find seeds (with BLASR [Chaisson and Tesler, 2012])
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  - Perfect overlap: merge
  - Otherwise: keep the best seed
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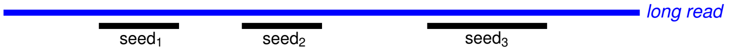

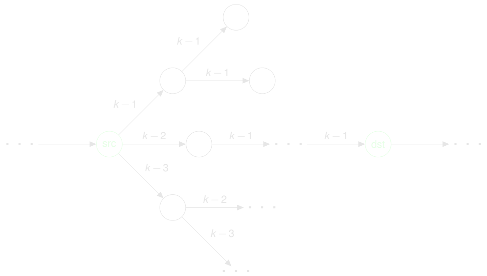

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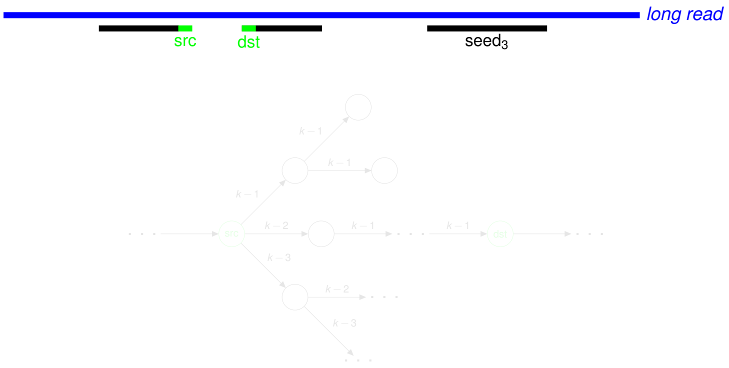

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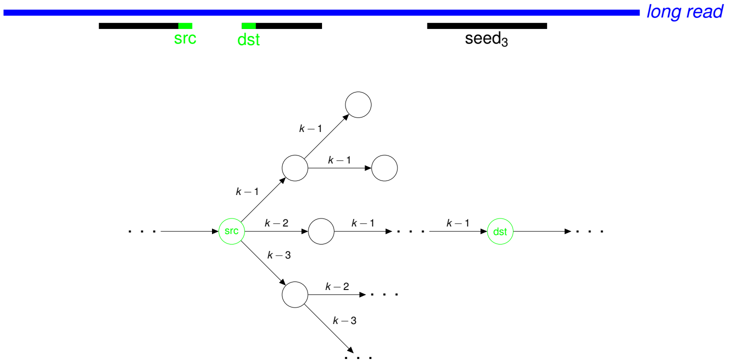

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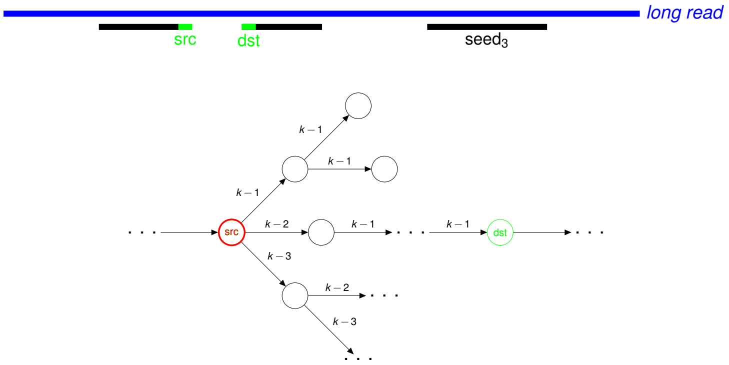

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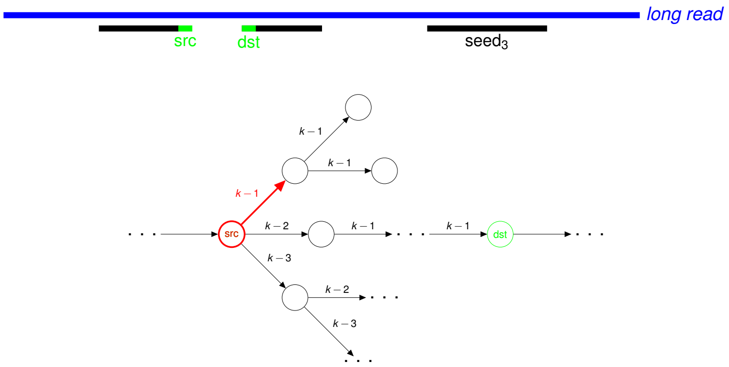

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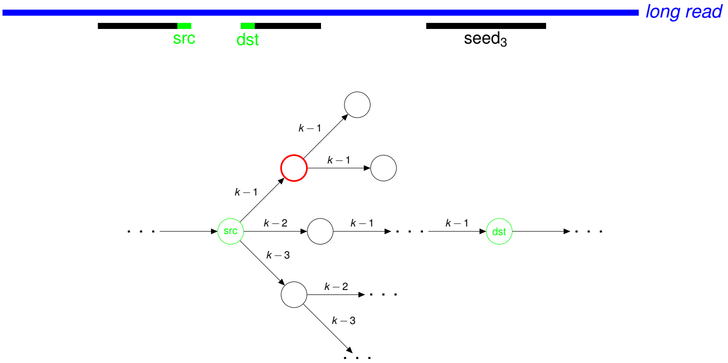

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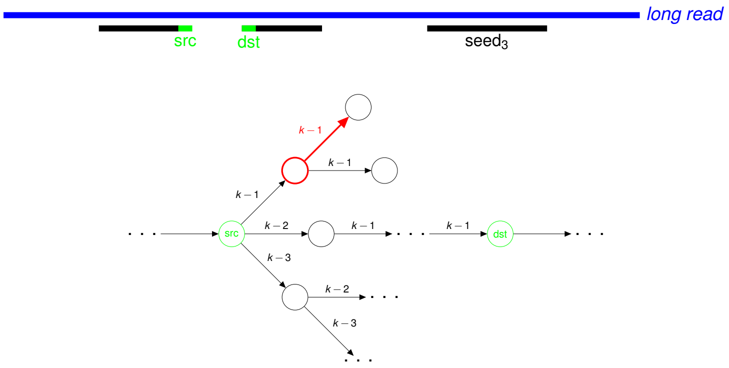

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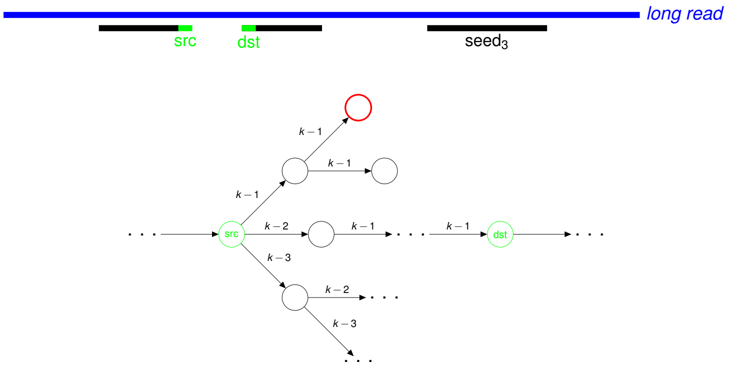

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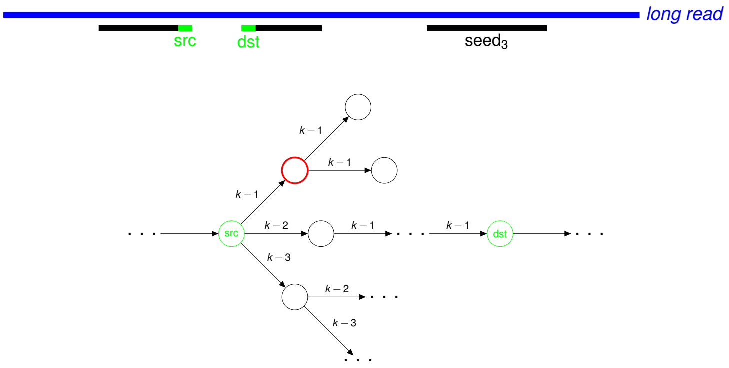

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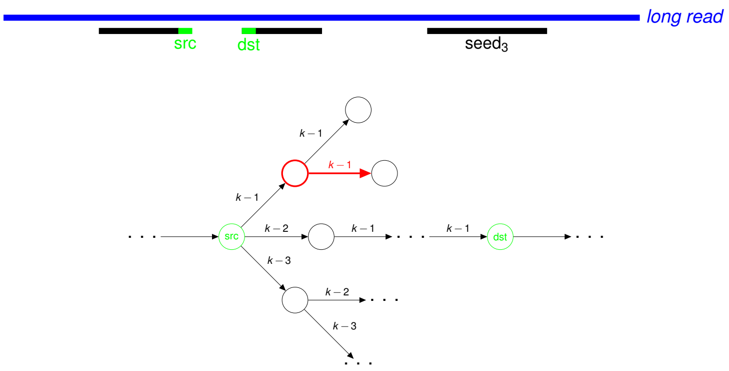

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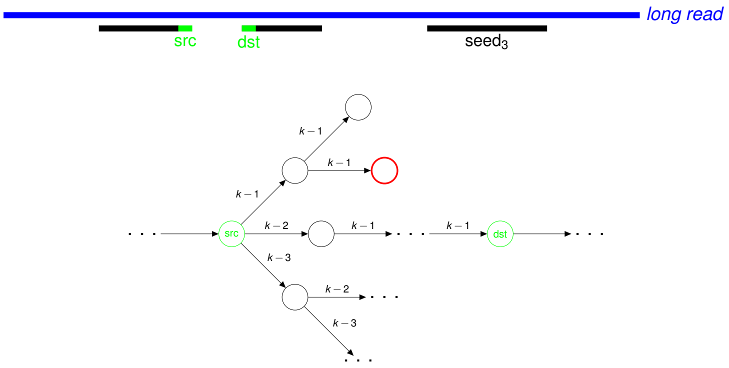

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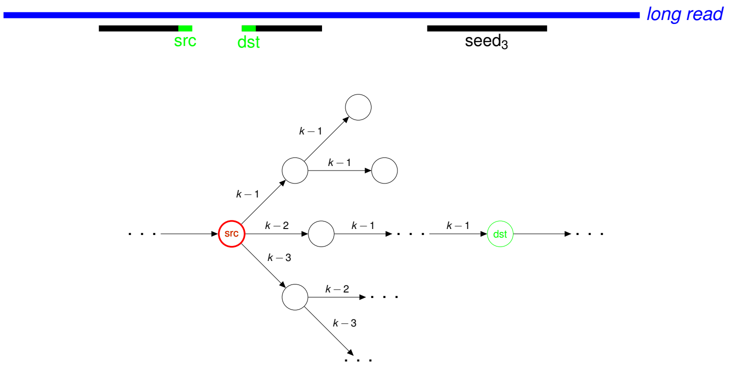

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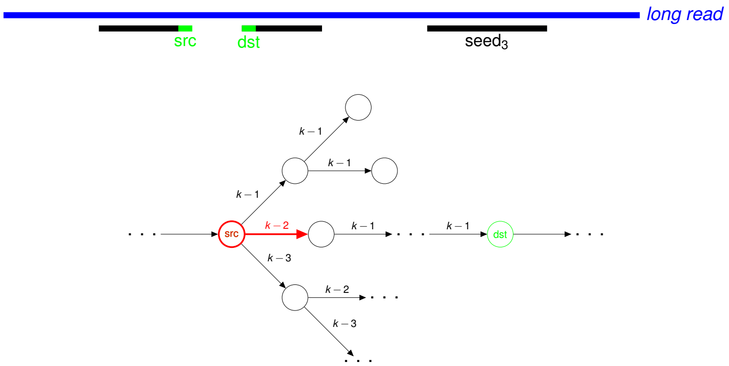

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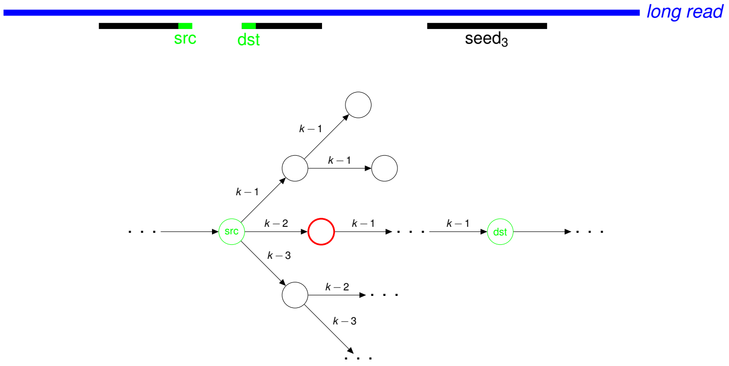

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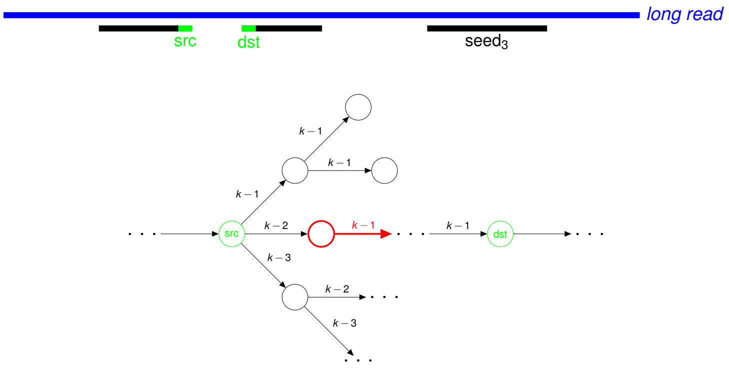

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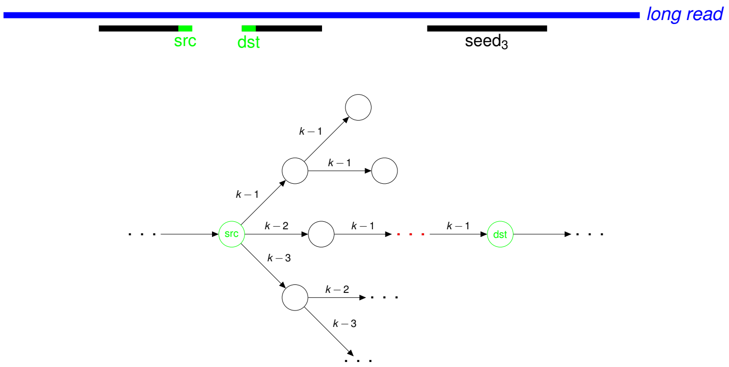

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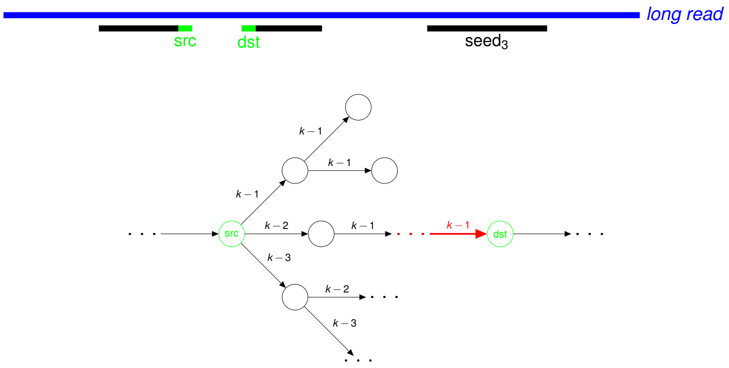

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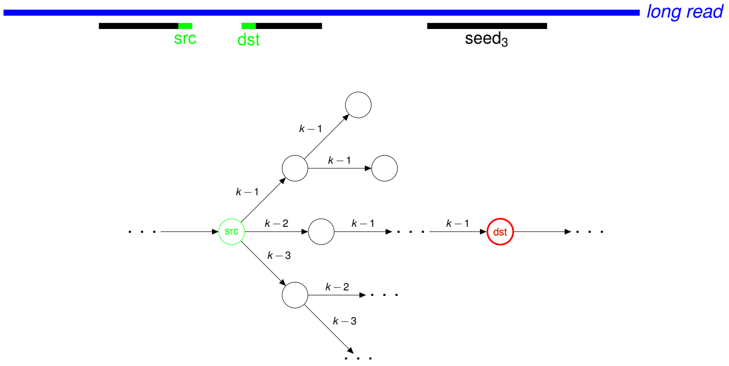

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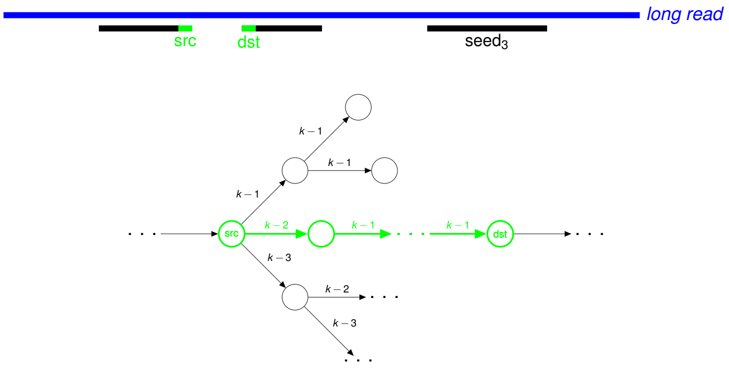

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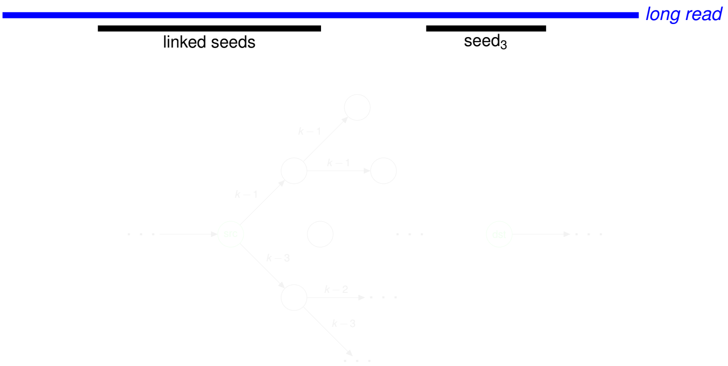

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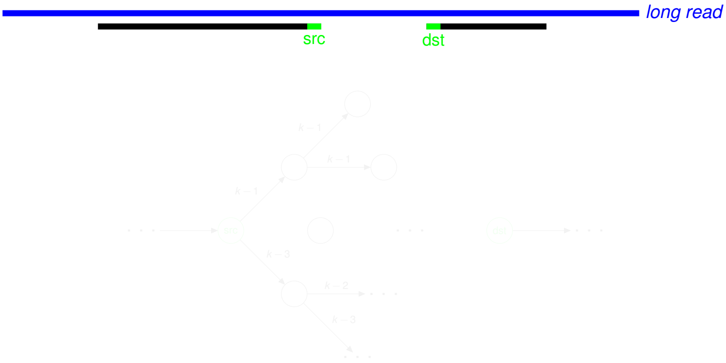

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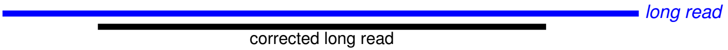

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- Seeds don’t always map right at the beginning or until the end of the long read
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Datasets

HG-CoLoR was compared to NaS, and two other state-of-the-art long read hybrid correction methods: CoLoRMap [Haghshenas et al., 2016] and Jabba [Miclotte et al., 2016]

The different tools were compared on the following datasets:

Dataset	Reference genome			Oxford Nanopore data			Illumina data		
	Strain	Reference sequence	Genome size	# Reads	Average length	Coverage	# Reads	Read length	Coverage
A. baylyi	ADP1	CR543861	3.6 Mbp	89,011	4,284	106x	900,000	250	50x
E. coli	K-12 substr. MG1655	NC_000913	4.6 Mbp	22,270	5,999	29x	775,500	300	50x
S. cerevisae	S288C	NC_001133-001148	12.2 Mbp	205,923	5,698	96x	2,500,000	250	50x

Alignment-based comparison

Dataset	Method	# Reads	Average length	Average identity	Genome coverage	Runtime
A. baylyi	Original	89,011	4,284	70.09%	100%	N/A
	CoLoRMap	89,011	4,355	67.93%	100%	14h33min
	Jabba	17,476	10,260	99.40%	99.80%	12min30
	NaS	28,492	9,530	99.83%	100%	128h55min
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E. coli	Original	22,270	5,999	79.46%	100%	N/A
	CoLoRMap	22,270	6,219	89.02%	100%	8h26min
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S. cerevisae	Original	205,923	5,698	55.49%	99.90%	N/A
	CoLoRMap	205,923	5,737	39.93%	99.40%	37h36min
	Jabba	36,958	6,613	99.55%	93.21%	44min05
	NaS	85,432	6,770	99.16%	99.37%	$>$ 16 days
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Chaisson, M. J. and Tesler, G. (2012).
Mapping single molecule sequencing reads using basic local alignment with successive refinement (BLASR): application and theory.
BMC bioinformatics, 13(1):238.

Haghshenas, E., Hach, F., Sahinalp, S. C., and Chauve, C. (2016).
CoLoRMap: Correcting Long Reads by Mapping short reads.
Bioinformatics, 32(17):i545–i551.

Kowalski, T., Grabowski, S., and Deorowicz, S. (2015).
Indexing arbitrary-length k-mers in sequencing reads.
PLoS ONE, 10(7):1–14.

References II

Madoui, M.-A., Engelen, S., Cruaud, C., Belser, C., Bertrand, L., Alberti, A., Lemainque, A., Wincker, P., and Aury, J.-M. (2015).
Genome assembly using Nanopore-guided long and error-free DNA reads.
BMC Genomics, 16:327.

Marçais, G., Yorke, J. A., and Zimin, A. (2015).
QuorUM: An Error Corrector for Illumina Reads.
PLOS ONE, 10(6):1–13.

Miclotte, G., Heydari, M., Demeester, P., Rombauts, S., Van de Peer, Y., Audenaert, P., and Fostier, J. (2016).
Jabba: hybrid error correction for long sequencing reads.
Algorithms Mol Biol, 11:10.

Thanks for your attention.