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▶ To cite this version:

Lolita Lecompte, Camille Marchet, Pierre Morisse, Antoine Limasset, Pierre Peterlongo, et al.. ELECTOR: EvaLuation of Error Correction Tools for lOng Reads. JOBIM 2018 - Journées Ouvertes Biologie, Informatique et Mathématiques, Jul 2018, Marseille, France. pp.1-2. hal-01929900

HAL Id: hal-01929900

https://hal.science/hal-01929900

Submitted on 21 Nov 2018

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ELECTOR: Evaluation of Error Correction Tools for lOng Reads

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1. Introduction

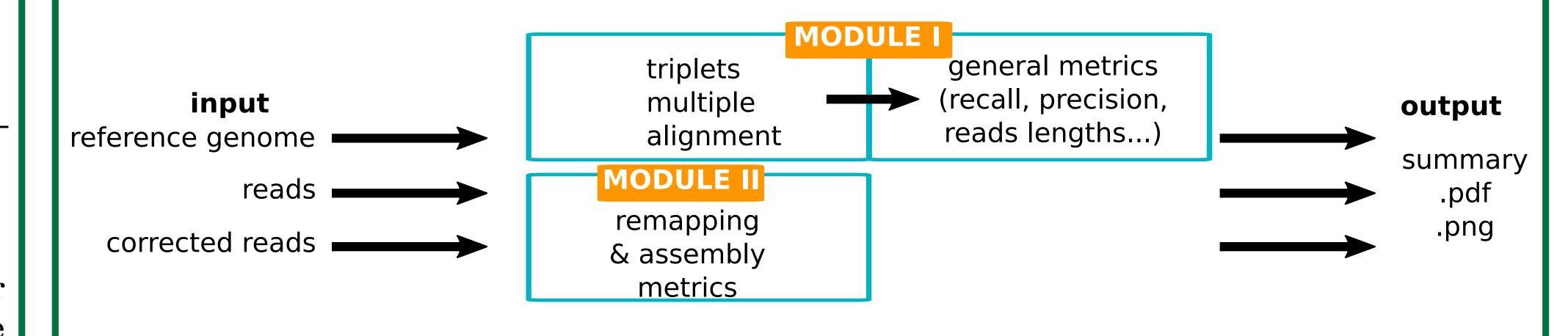
- ► Long read technologies, Pacific Biosciences and Oxford Nanopore, have **high error** rates (from 9% to 30%)
- ► Multiple error correction methods exist
- ► Important to assess the correction stage for downstream analyses
- ► Only one tool: LRCstats [1]
 - shows global correction gain
 - does not give access to correctors detailed behavior
 - high computation times

Developing methods allowing to evaluate error correction tools with precise and reliable statistics is therefore a crucial need.

2. Contribution

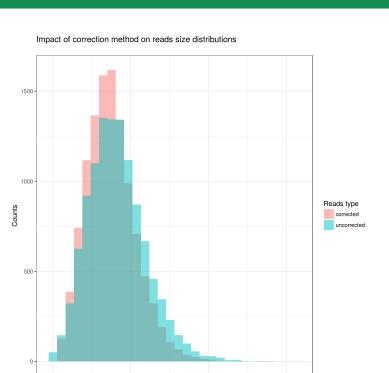
We propose **ELECTOR**, a novel tool that enables the evaluation of long read correction methods:

- ▶ provide more metrics than LRCstats on the correction quality
- ► scale to very long reads and large datasets
- ► compatible with a wide range of state-of-the-art error correction tools (hybrid/self)



3. Output statistics

- ► Recall
- **▶** Precision
- ► Overall correct bases rate
- ► GC content before and after correction
- ► Number of trimmed and/or split corrected reads
- ► Mean missing size in trimmed/split reads



Assembly using *Miniasm*

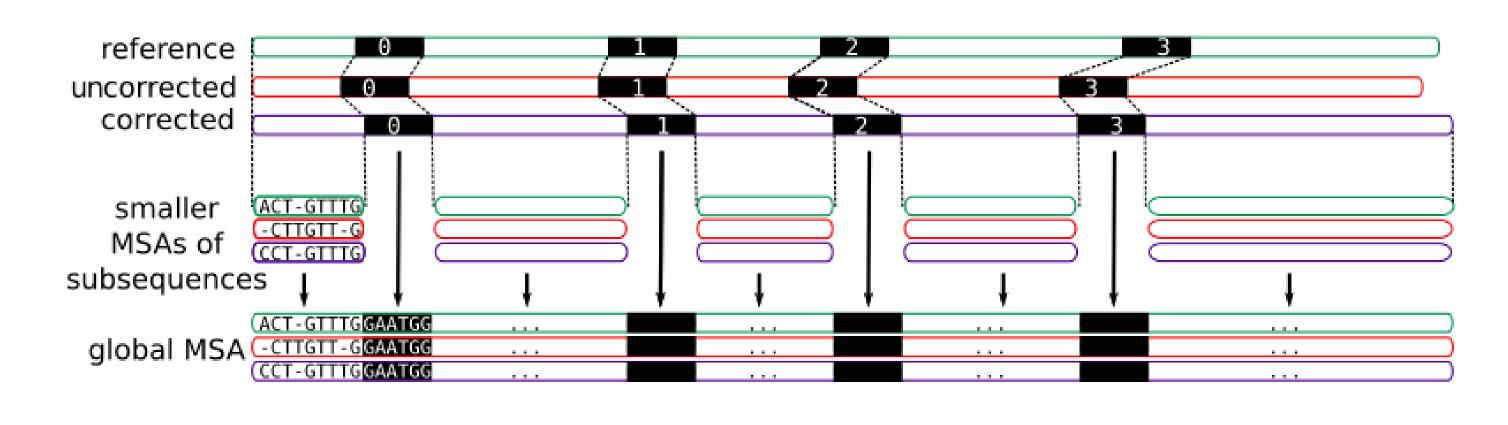
- ► Nb of contigs
- ► N50
- ► N75

If reference, remapping using BWA

- ► Average identity
- ► Genome coverage
- ► Nb of breakpoints
- ► NGA50
- ► NGA75

4. Methods

- 1. Multiple alignment of triplets: {reference read, uncorrected read, corrected read}
- 2. Seed-MSA strategy: multiple sequence alignment (MSA) using partial order graphs [2] coupled to a seed strategy comparable to MUMmer or Minimap.
 - ► Faster and scalable



5. Heuristic performances

Dataset from $E.\ coli,$ simulated with Sim-LoRD [3], and corrected with MECAT.

➤ Dataset: reads with a 10kb mean length, a 15% error rate, and a coverage of 100x.

Strategy	MSA	seed-MSA
Recall	84.505%	84.587%
Precision	88.347%	88.278%
Correct bases rate	95.290%	95.250%
Time	107h	42m

Similar results using both strategies.

A substantial **gain in time** is achieved using the seed-MSA strategy.

6. Results: ELECTOR vs. LRCstats

Dataset from *E. coli*, **simulated** with SimLoRD, composed of reads with a 8kb mean length, a 18% error rate, and a coverage of 20x.

Method	Original		Nanocorr		daccord	
	ELECTOR	LRCstats	ELECTOR	LRCstats	ELECTOR	LRCstats
Error rate	15.837	17.9267	0.339	0.3983	0.422	0.4498
\mathbf{Recall}	N/A	-	0.98503	-	0.98836	-
Precision	N/A	-	0.99424	-	0.98468	-
Deletions	$847,\!315$	$3,\!635,\!647$	$46,\!596$	56,708	$58,\!110$	$72,\!547$
Insertions	$10,\!393,\!229$	$13,\!038,\!057$	$237{,}798$	$279,\!970$	306,930	$336,\!686$
Substitutions	$5,\!611,\!023$	$671,\!040$	$143,\!605$	45,783	$72,\!265$	$25,\!643$
Trimmed / split reads	N/A	-	$1,\!612$	_	123	-
Mean missing size	N/A	-	341	_	$3,\!026$	-
$\%\mathbf{GC}$	50.7	-	50.8	_	50.8	-
${f Time}$	13min	3h53	13min	3h52	13min	3h50

Results of these experiments show that the metrics computed by ELECTOR are comparable to LRCstats outputs, but also highlight several novelties.

LRCstats, besides having low performance results, also fails to evaluate correction's detailed impact on big datasets and on very long reads.

7. Conclusion

- ► Novel and open-source method for fast long read correction assessment
- ► Compatible with hybrid and self correctors
- ► Numerous metrics for correction quality (recall/precision)
- ► Downstream analyses assessment (mapping/assembly)
- ► Time-saving, scaling computation

