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)

![MODULE I]

**ELECTOR**

**LRCstats**

![MODULE II]

**input**

- Reference genome
- Reads
- Corrected reads

**output**

- Summary
- .pdf
- .png

**general metrics**

- Recall
- Precision
- Coverage
- Time

**numerical metrics**

- Error rate
- Precision
- Recall
- Deletions
- Insertions
- Substitutions
- Trimmed / split reads
- Mean missing size
- %GC

**triple alignment**

- Mean missing size
- %GC

**remapping & assembly metrics**

- Nb of breakpoints
- Genome coverage
- NGA50
- NGA75

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**

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

![Reference reads]

**Assembly using** Miniasm

- Nb of contigs
- N50
- N75

**If reference, remapping using** BWA

- Average identity
- Genome coverage

Dataset from E. coli, simulated with SimLoRD [3], and corrected with MECAT.

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

5. Heuristic performances

<table>
<thead>
<tr>
<th>Strategy</th>
<th>MSA seed-MSA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Recall</td>
<td>84.505%</td>
</tr>
<tr>
<td>Precision</td>
<td>88.347%</td>
</tr>
<tr>
<td>Correct bases rate</td>
<td>95.290%</td>
</tr>
<tr>
<td>Time</td>
<td>107h</td>
</tr>
</tbody>
</table>

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.

<table>
<thead>
<tr>
<th>Method</th>
<th>ELECTOR</th>
<th>LRCstats</th>
<th>ELECTOR</th>
<th>LRCstats</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Error rate</strong></td>
<td>0.98503</td>
<td>0.98836</td>
<td>0.97803</td>
<td>0.98203</td>
</tr>
<tr>
<td><strong>Precision</strong></td>
<td>0.94044</td>
<td>0.94044</td>
<td>0.94044</td>
<td>0.94044</td>
</tr>
<tr>
<td><strong>Deletions</strong></td>
<td>46,506</td>
<td>56,708</td>
<td>58,110</td>
<td>72,547</td>
</tr>
<tr>
<td><strong>Insertions</strong></td>
<td>217,798</td>
<td>279,970</td>
<td>306,930</td>
<td>336,686</td>
</tr>
<tr>
<td><strong>Substitutions</strong></td>
<td>143,605</td>
<td>45,783</td>
<td>72,265</td>
<td>25,643</td>
</tr>
<tr>
<td><strong>Trimmed / split reads</strong></td>
<td>13min</td>
<td>36m52</td>
<td>13min</td>
<td>36m52</td>
</tr>
<tr>
<td><strong>Mean missing size</strong></td>
<td>341</td>
<td>3,626</td>
<td>341</td>
<td>3,626</td>
</tr>
<tr>
<td><strong>%GC</strong></td>
<td>50.7</td>
<td>50.7</td>
<td>50.7</td>
<td>50.7</td>
</tr>
</tbody>
</table>

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