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 correction details
  - 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 base 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

**5. Heuristic performances**

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.

<table>
<thead>
<tr>
<th>Strategy</th>
<th>MSA seed-MSA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Recall</td>
<td>84.505% 84.587%</td>
</tr>
<tr>
<td>Precision</td>
<td>88.347% 88.278%</td>
</tr>
<tr>
<td>correct bases rate</td>
<td>95.290% 95.250%</td>
</tr>
<tr>
<td>Time</td>
<td>107h 42m</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>Original</th>
<th>LRCstats</th>
<th>ELECTOR</th>
<th>Accord</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error rate</td>
<td>15.837</td>
<td>17.9267</td>
<td>0.339</td>
<td>0.422</td>
</tr>
<tr>
<td>Precision</td>
<td>N/A</td>
<td>-</td>
<td>0.96303</td>
<td>0.98436</td>
</tr>
<tr>
<td>Deletions</td>
<td>847.315</td>
<td>3,635.647</td>
<td>46.506</td>
<td>56.709</td>
</tr>
<tr>
<td>Insertions</td>
<td>13,035.229</td>
<td>13,038.027</td>
<td>217,798</td>
<td>279,970</td>
</tr>
<tr>
<td>Substitutions</td>
<td>5,611.023</td>
<td>671.040</td>
<td>143,605</td>
<td>45,783</td>
</tr>
<tr>
<td>Trimmed / split reads</td>
<td>N/A</td>
<td>-</td>
<td>1.612</td>
<td>-</td>
</tr>
<tr>
<td>Mean missing size</td>
<td>N/A</td>
<td>-</td>
<td>341</td>
<td>-</td>
</tr>
<tr>
<td>%GC</td>
<td>5.7</td>
<td>-</td>
<td>56.8</td>
<td>-</td>
</tr>
<tr>
<td>Time</td>
<td>13min</td>
<td>30min</td>
<td>13min</td>
<td>38.52min</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