SVJedi: Structural variation genotyping using long reads
Lolita Lecompte, Pierre Peterlongo, Dominique Lavenier, Claire Lemaitre

To cite this version:
Lolita Lecompte, Pierre Peterlongo, Dominique Lavenier, Claire Lemaitre. SVJedi: Structural variation genotyping using long reads. HiTSeq 2019 - Conference on High Throughput Sequencing, Jul 2019, Basel, Switzerland. hal-02290884

HAL Id: hal-02290884
https://inria.hal.science/hal-02290884
Submitted on 18 Sep 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
Introduction

Structural variations (SVs) are DNA segments that have been moved regarding another reference genome. The number of known SVs is increasing, especially with the development of third generation sequencing technologies, which produce long reads data.

Discovery vs. Genotyping

**SV discovery**

Given a reference genome, discover SVs between a sequencing sample and a reference genome.


**SV genotyping**

Given a set of already known variants for a species, assess the presence or absence of each variant in a given sequencing sample.

There is no known method for SV genotyping with long reads.

Method - SVJedi

1. Generating allele sequences
2. Alignment: Minimap2
3. Selection of informative alignments
   - Breakpoint overlap
   - Semi-global alignment
4. Genotype estimation

Results on a simulated dataset

Simulated dataset

- **1,000 deletions** selected on the human chromosome 1 from dbVar (50 bp - 10k bp)
- Equally distributed: 0/0, 0/1, 1/1
- Long reads simulated with SimLoRD [1]

16 % error rate, 20X sequence depth

<table>
<thead>
<tr>
<th>Truth</th>
<th>SVJedi</th>
<th>Sniffles [2]</th>
</tr>
</thead>
<tbody>
<tr>
<td>0/0</td>
<td>330 3 0 0</td>
<td>0/1 3 89 0</td>
</tr>
<tr>
<td>0/1</td>
<td>19 305 6 4</td>
<td>1/1 0 254 60</td>
</tr>
</tbody>
</table>
| 1/1   | 3 10 311 9 | 1/1 80.9 %

Precision: 95.85 %

Results on a real dataset

<table>
<thead>
<tr>
<th>Dataset</th>
<th>svclassify</th>
<th>SVJedi</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample: NA12878</td>
<td>0/0 1/1</td>
<td>0/0 1/1 1/1</td>
</tr>
<tr>
<td>Data: Nanopore WGS consortium (37X)</td>
<td>8 75 877 4</td>
<td>194 1,289 202 28</td>
</tr>
</tbody>
</table>

Identity: 81.89%

Predicted genotypes: 98.81%

Runtime: 2h35 (40 CPU)

Conclusion

- New method to genotype SVs using long reads data.
- Importance of dedicated genotyping methods.
- Currently only applied to deletions.
- Implementation: SVJedi

References