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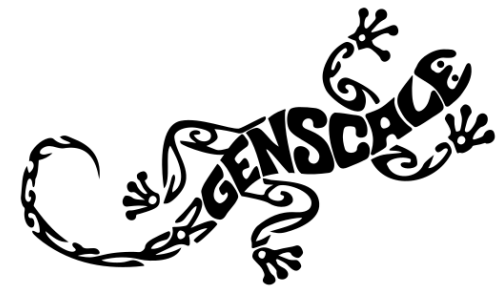
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# SVJedi : Structural variation genotyping using long reads

Lolita Lecompte<sup>1</sup>, Pierre Peterlongo<sup>1</sup>, Dominique Lavenier<sup>1</sup>, Claire Lemaitre<sup>1</sup>

<sup>1</sup>Univ Rennes, Inria, CNRS, IRISA, F-35000 Rennes, France



## 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.

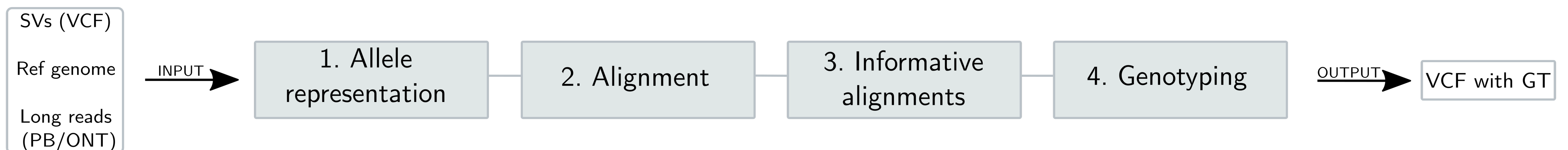
SVIM (2019), Sniffles (2018), pbsv (2018), NanoSV (2017)

### SV genotyping

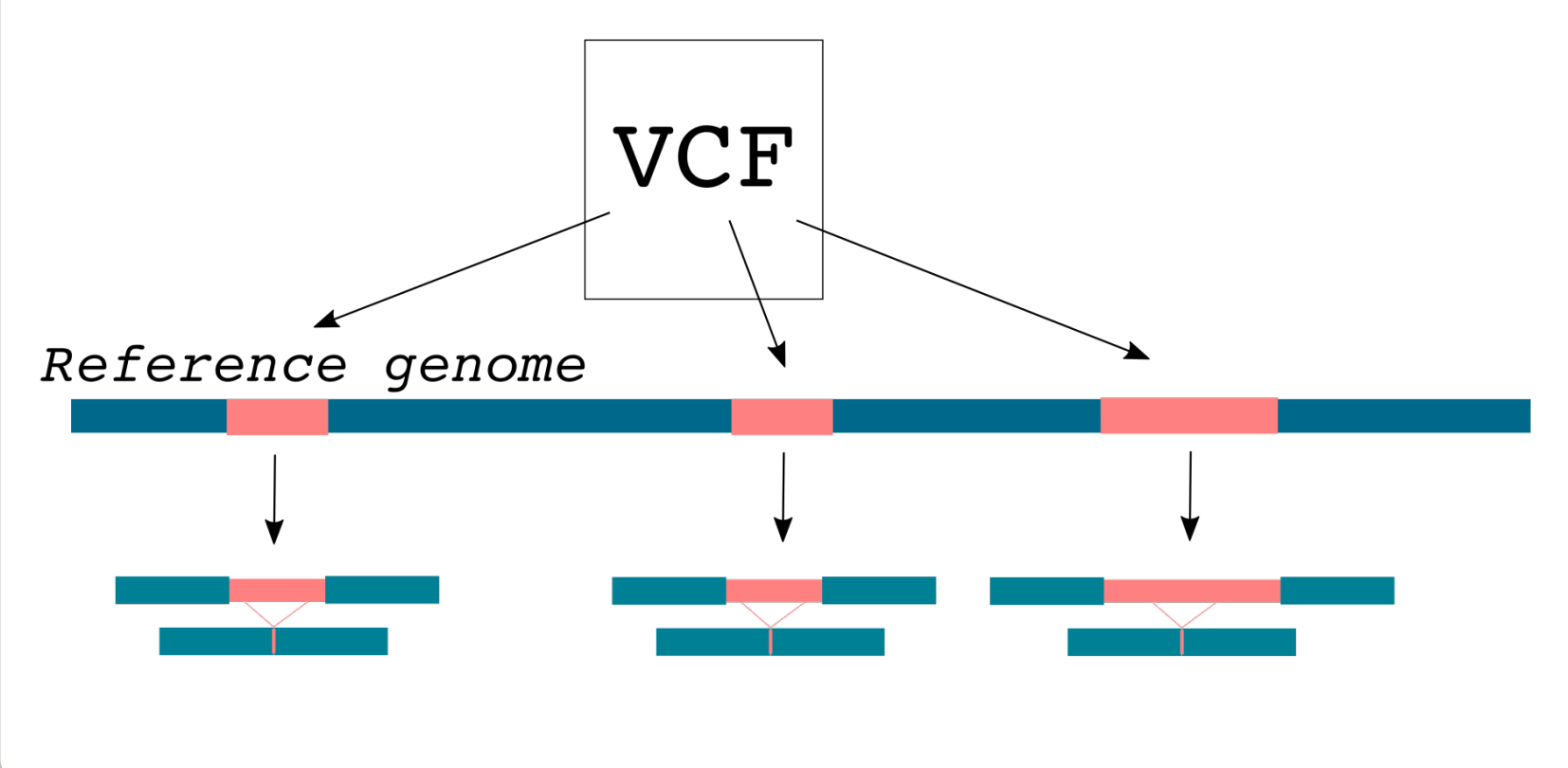
Given a set of already known variants for a species, **assess the presence or absence** of each variant in a given sequencing sample.

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

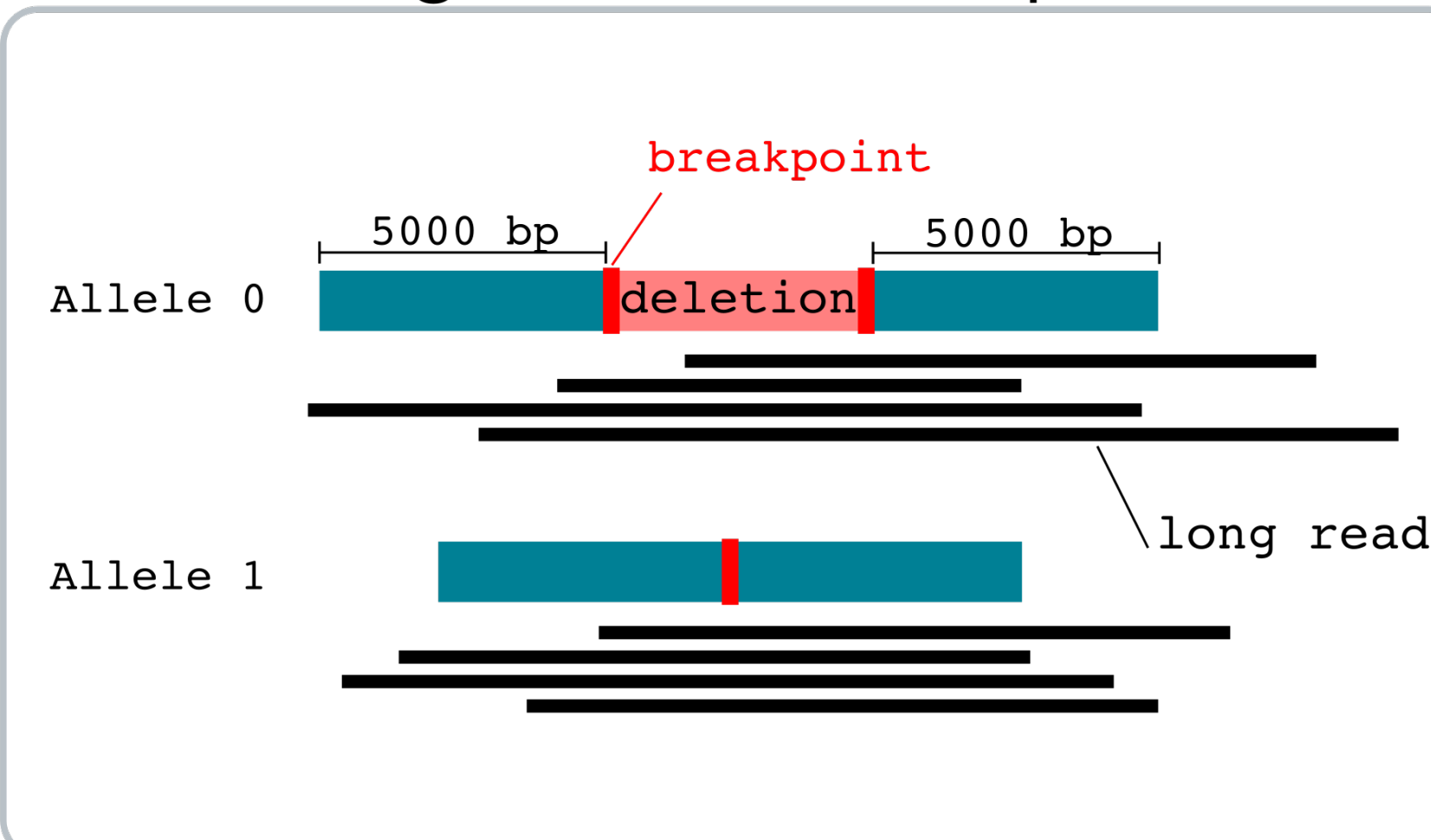
## Method - SVJedi



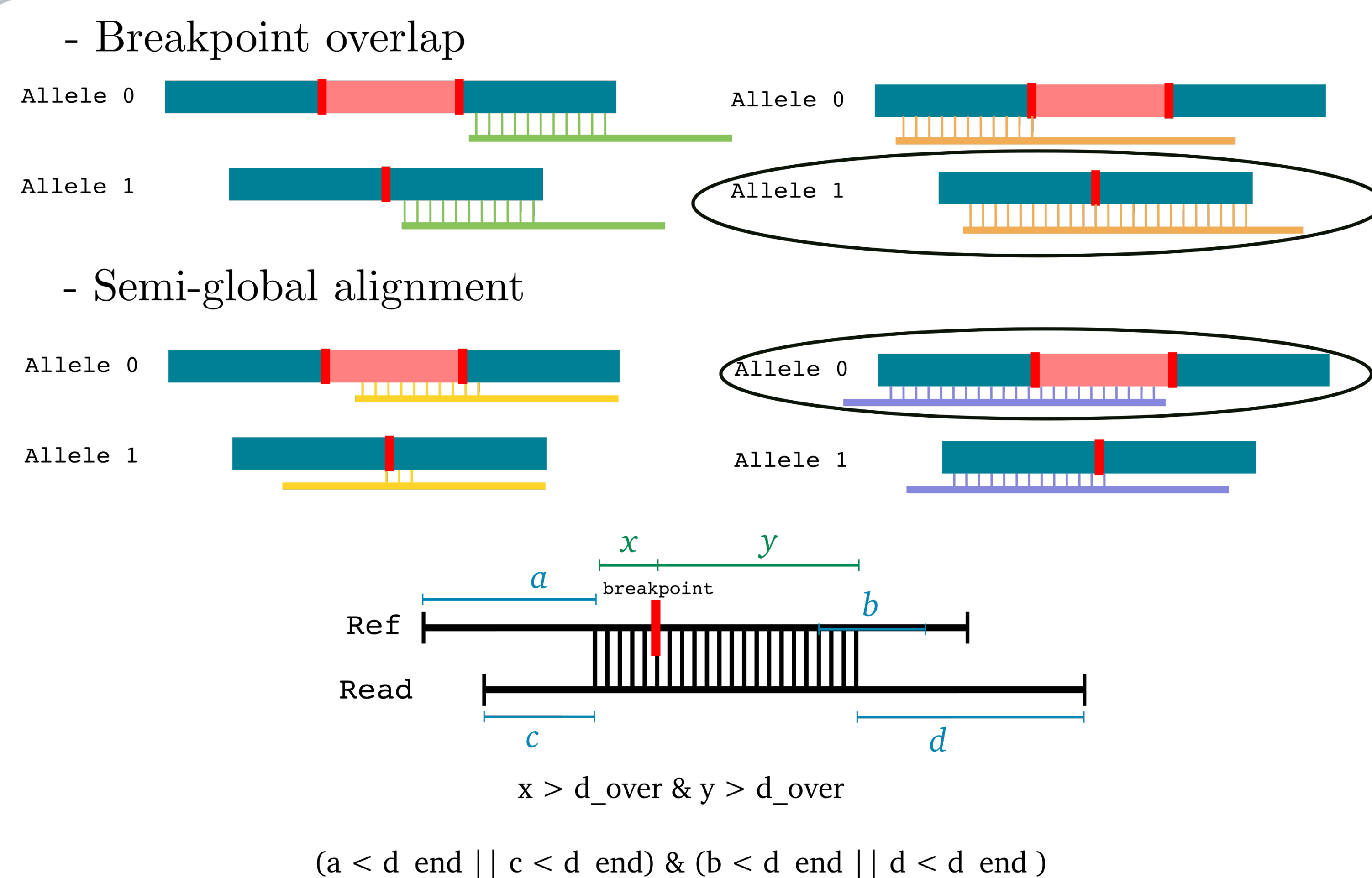
### 1. Generating allele sequences



### 2. Alignment : Minimap2



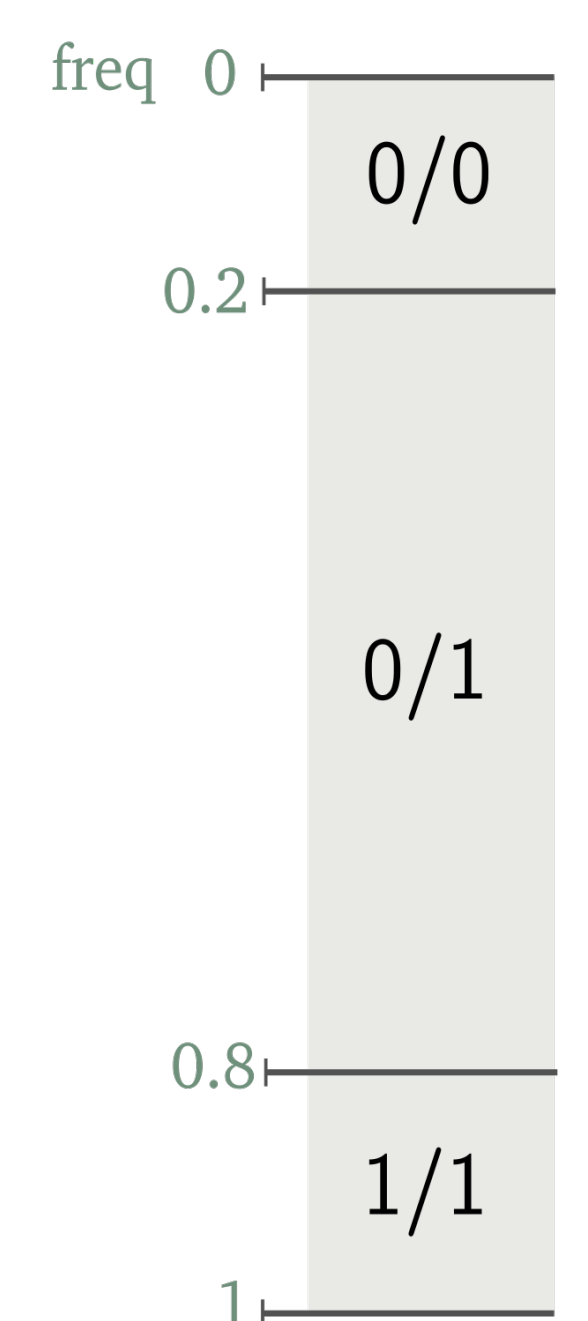
### 3. Selection of informative alignments



### 4. Genotype estimation

$$\text{freq} = \frac{\text{allele 0}}{\text{allele 0} + \text{allele 1}}$$

- Normalization
- Minimum read number filter
- 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

		SVJedi			
		0/0	0/1	1/1	./.
Truth	0/0	330	3	0	0
	0/1	19	305	6	4
	1/1	3	10	311	9
	./.				

Precision : 95.85 %

Does SV discovery tools correctly estimate genotypes?

		Sniffles [2]		
		0/0	0/1	1/1
Truth	0/1	3	89	0
	1/1	0	254	60
	./.			

Recall : 60.87 %  
Precision : 36.70 %

80.9 % of 1/1 deletions are wrongly genotyped as 0/1

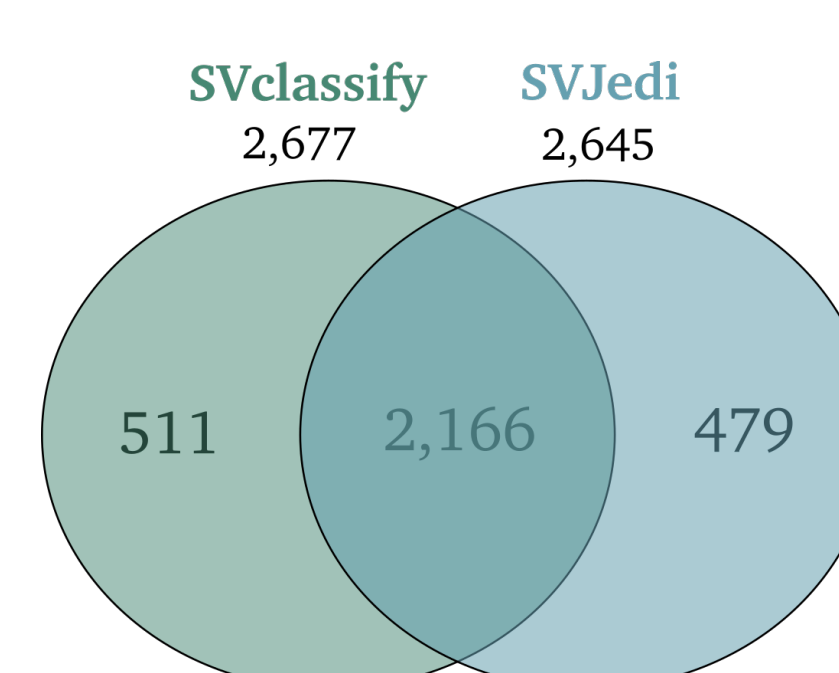
## Results on a real dataset

### Dataset

- Sample: NA12878
- Data: Nanopore WGS consortium (37X)
- svclassify [3]: **2,677** high confidence deletions

		SVJedi			
		0/0	0/1	1/1	./.
svclassify	0/1	194	1,289	202	28
	1/1	8	75	877	4
	./.				

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

- [1] Bianca K Stöcker, Johannes Köster, and Sven Rahmann. Simlord: simulation of long read data. *Bioinformatics*, 32(17):2704–2706, 2016.
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- [3] Hemang Parikh, Marghoob Mohiyuddin, Hugo YK Lam, Hariharan Iyer, Desu Chen, Mark Pratt, Gabor Bartha, Noah Spies, Wolfgang Losert, Justin M Zook, et al. svclassify: a method to establish benchmark structural variant calls. *BMC genomics*, 17(1):64, 2016.

<https://github.com/llecompte/SVJedi>  
Contact: [lolita.lecompte@inria.fr](mailto:lolita.lecompte@inria.fr)

