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Roland Faure, Jean-François Flot, Dominique Lavenier

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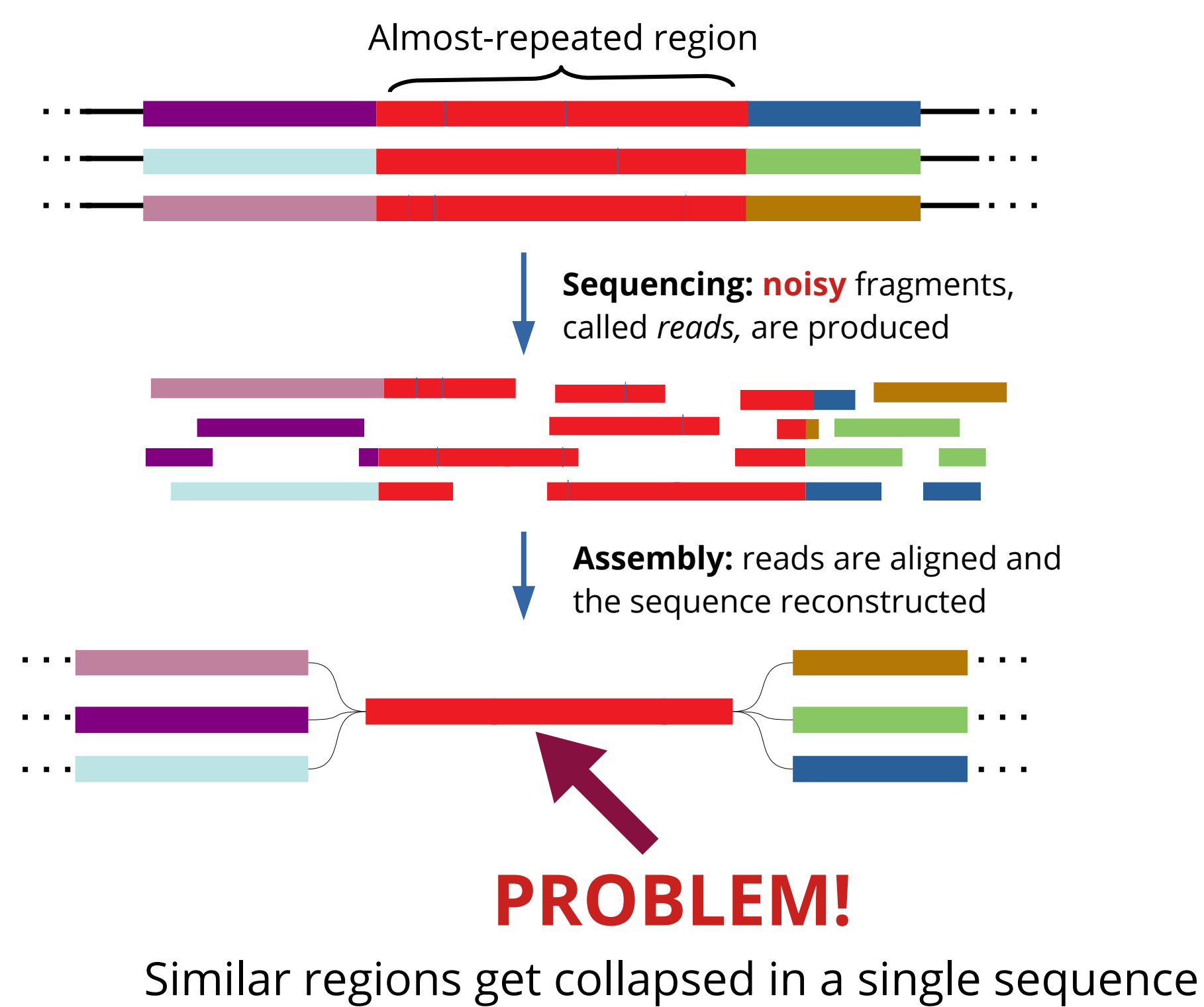
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# Hairsplitter: Separating noisy long reads into an unknown number of haplotypes

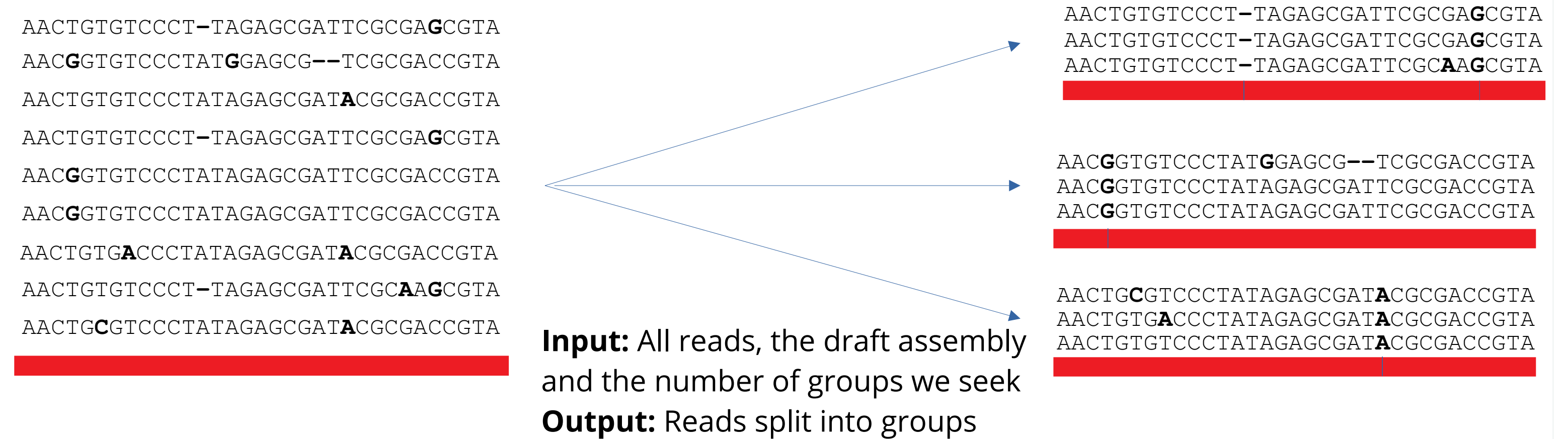
Roland Faure<sup>1,2</sup>, Jean-François Flot<sup>1</sup>, Dominique Lavenier<sup>2</sup>

1. Service Evolution Biologique et Ecologie, ULB, Brussels, Belgium 2. Univ. Rennes, Inria RBA, CNRS UMR 6074, Rennes, France

## Problem: assembling similar sequences



## State of the art

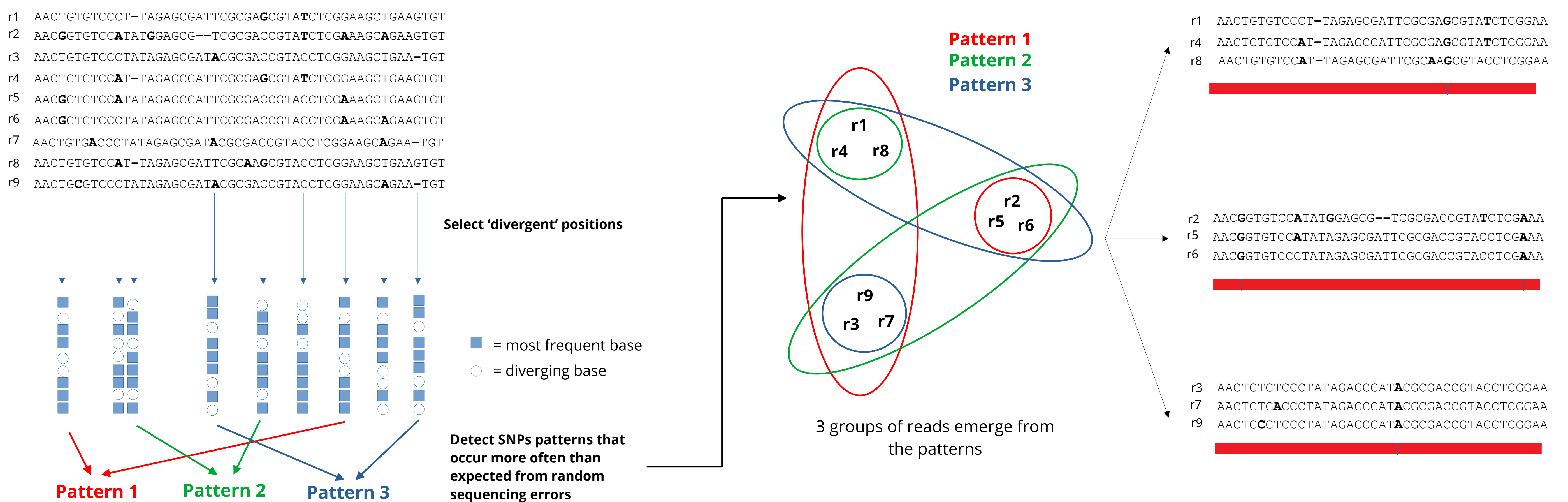


Existing software: WhatsHap (polyphase), Phasebook, Falcon-Unzip, HapCut, HapDup...

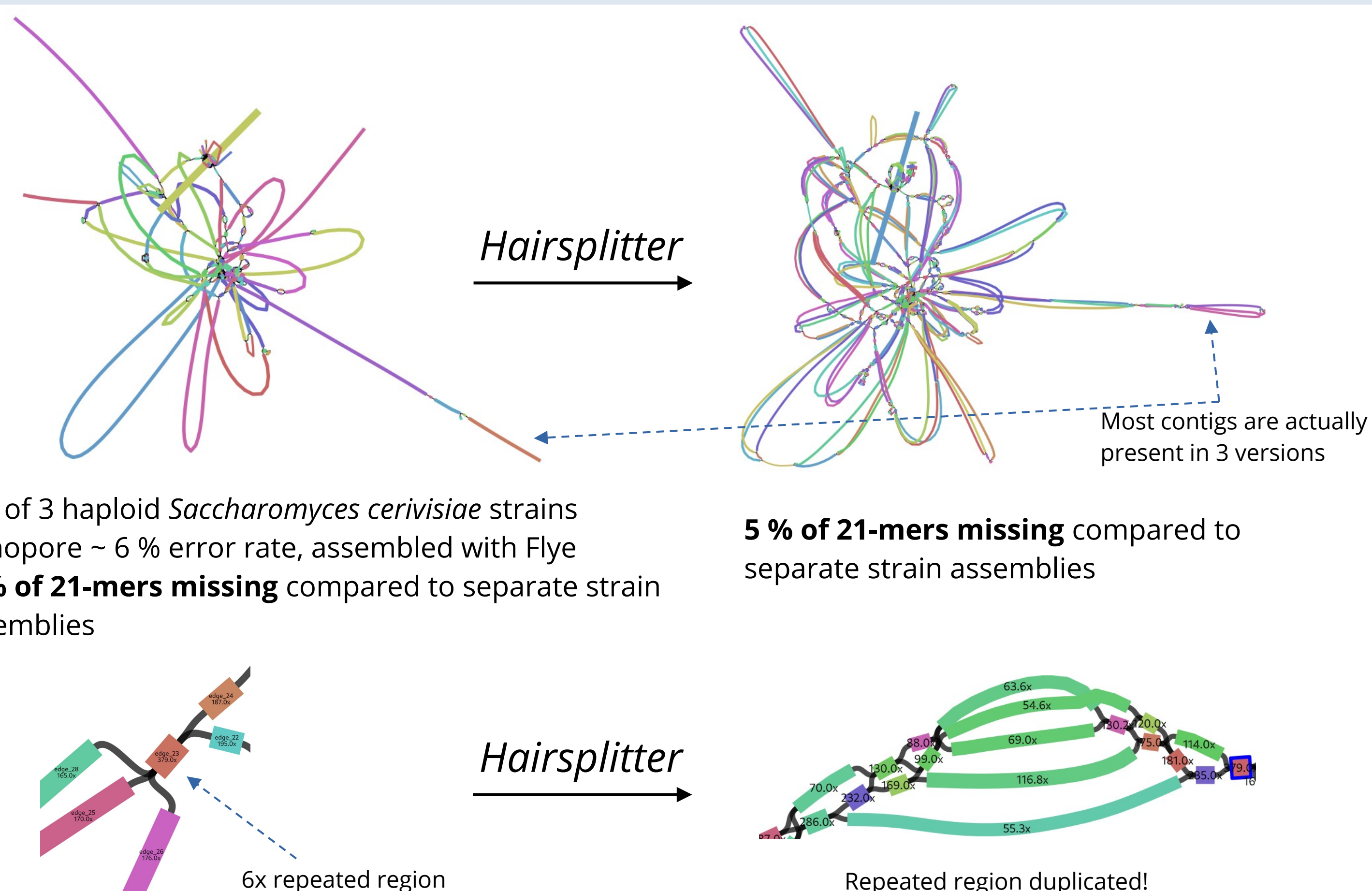
But: All software need to know the number of groups beforehand! We don't always know that → metagenomes, genomic repeats, insertions...

→ *HairSplitter* splits reads in an agnostic number of groups

## Algorithm



## Results



## Conclusion & Perspectives

- *Hairsplitter* splits a contig into an **agnostic number of groups**
- *Hairsplitter* can safely be **applied to all contigs** of the graph to split the contigs that need to be split
- *Hairsplitter* could be used to **improve the contiguity** of assemblies by overcoming almost-repeated regions

## References

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