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► **To cite this version:**

Roland Faure, Jean-François Flot, Dominique Lavenier. Hairsplitter: Separating noisy long reads into an unknown number of haplotypes. *Genome Informatics 2022*, Sep 2022, London / Virtual, United Kingdom. pp.1-1. hal-03817928

**HAL Id: hal-03817928**

**<https://hal.science/hal-03817928>**

Submitted on 17 Oct 2022

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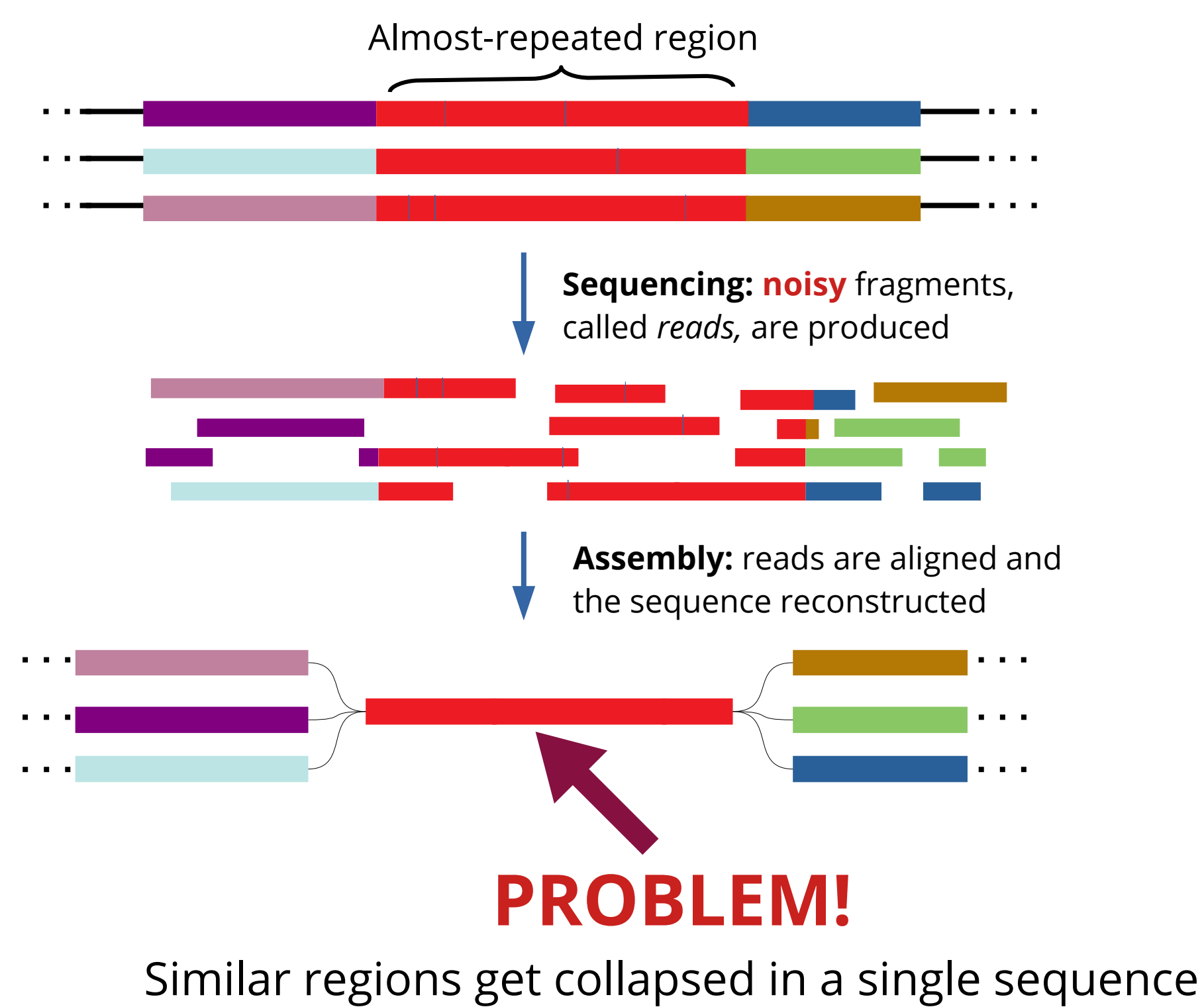


# Hairsplitter: Separating noisy long reads into an unknown number of haplotypes

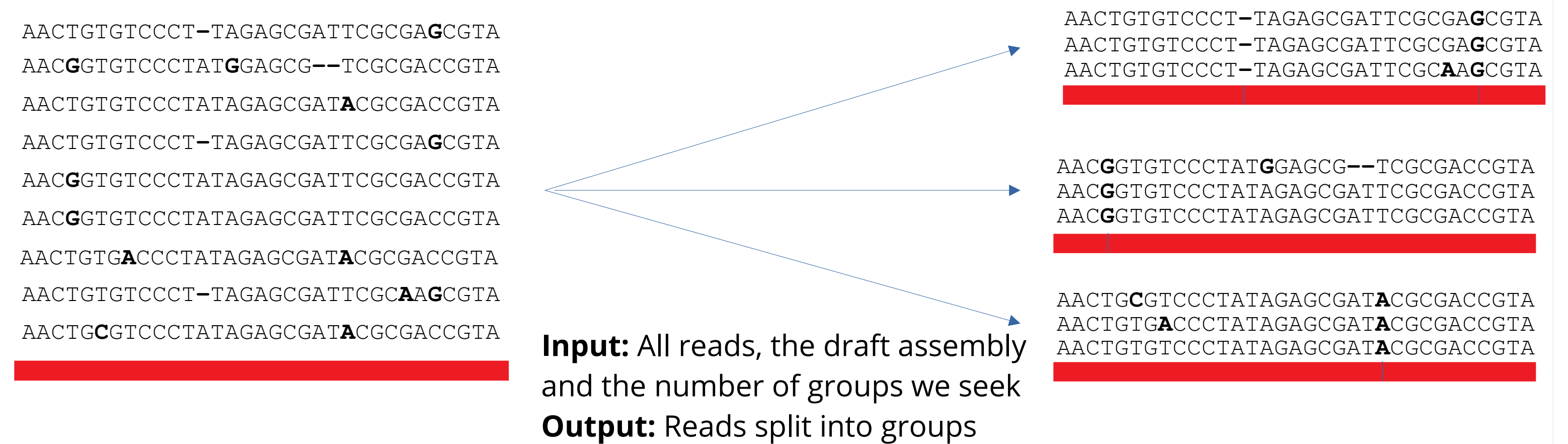
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## Problem: assembling similar sequences



## State of the art

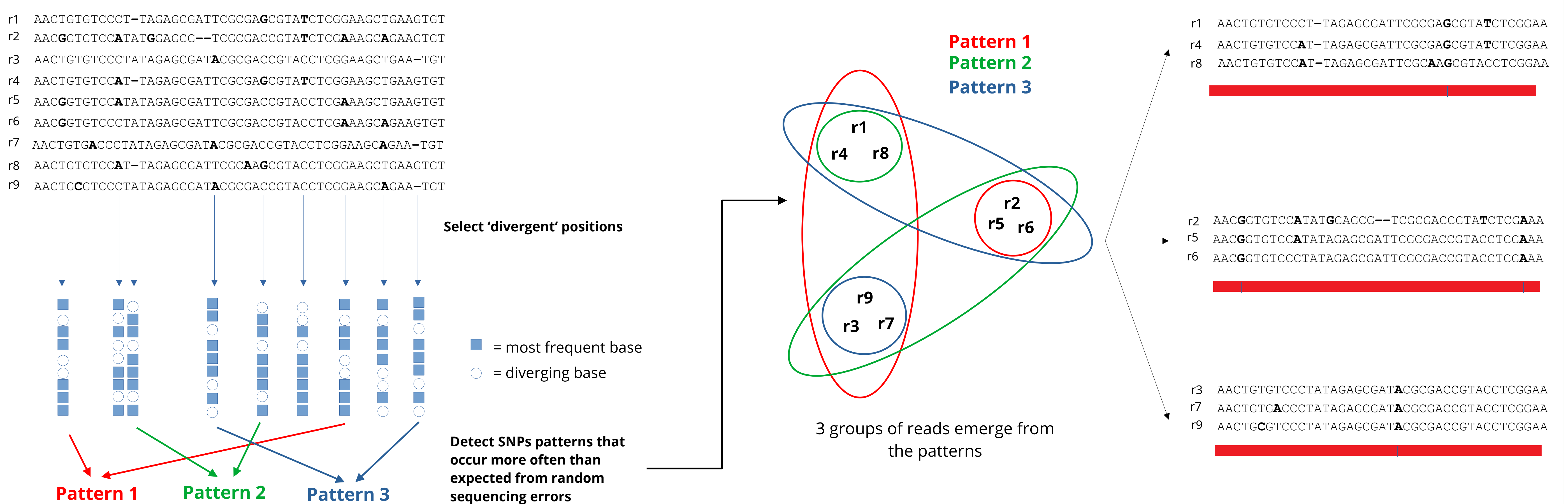


Existing software: WhatsHap (polyphase), Phasebook, Falcon-Unzip, HapCut, HapDup...

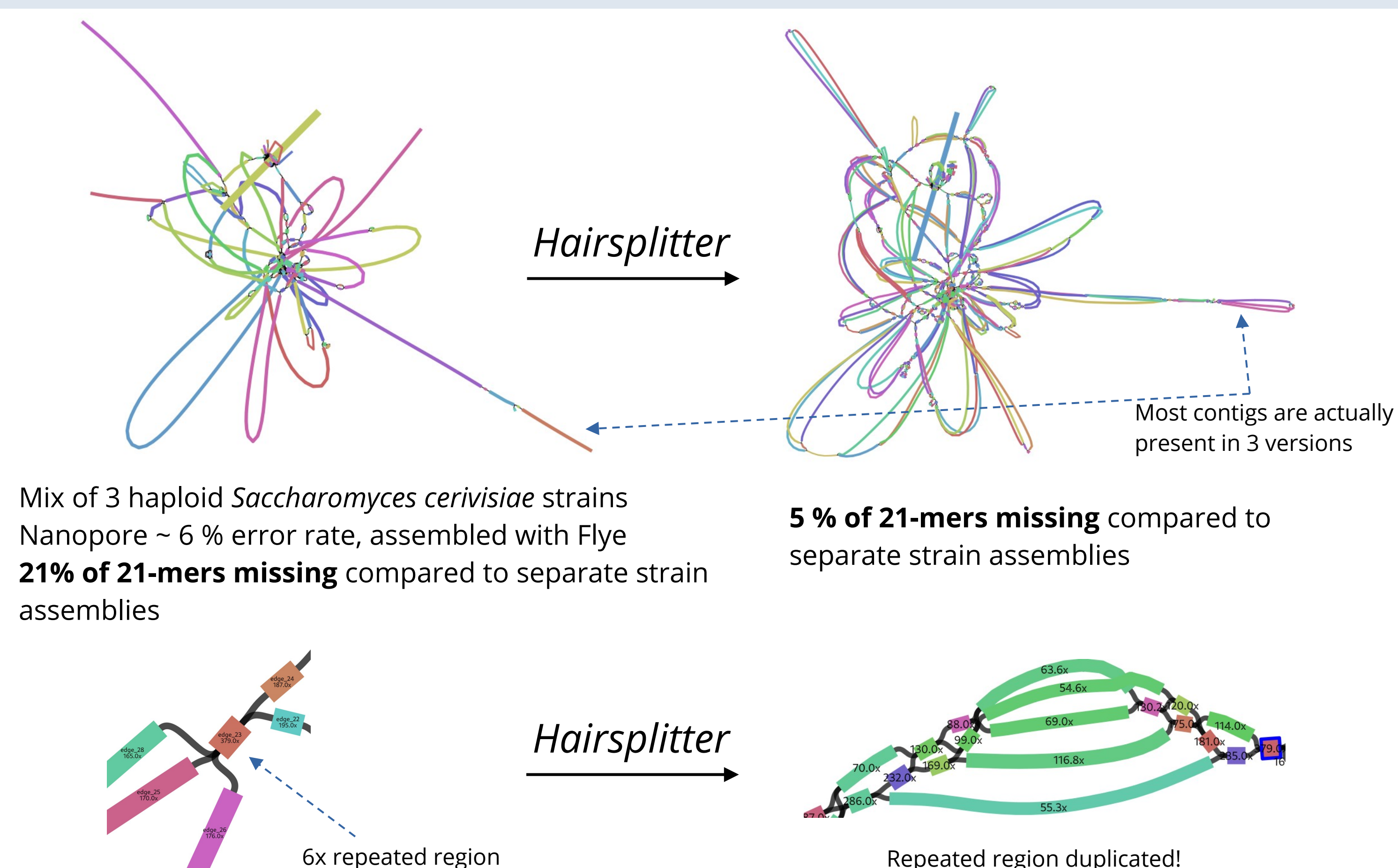
But: All software need to know the number of groups beforehand! We don't always know that → metagenomes, genomic repeats, insertions...

→ *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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