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

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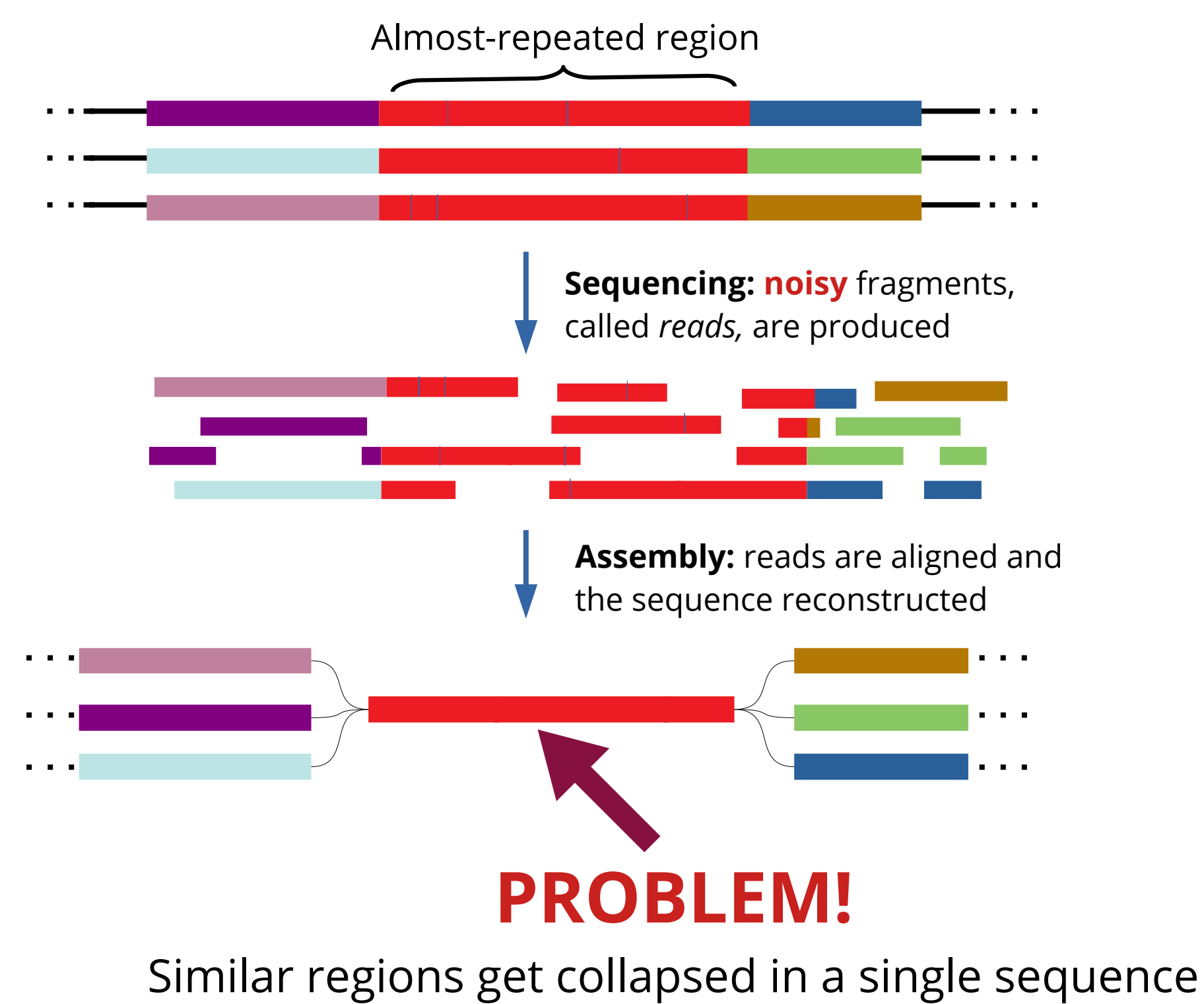
HAL Authorization

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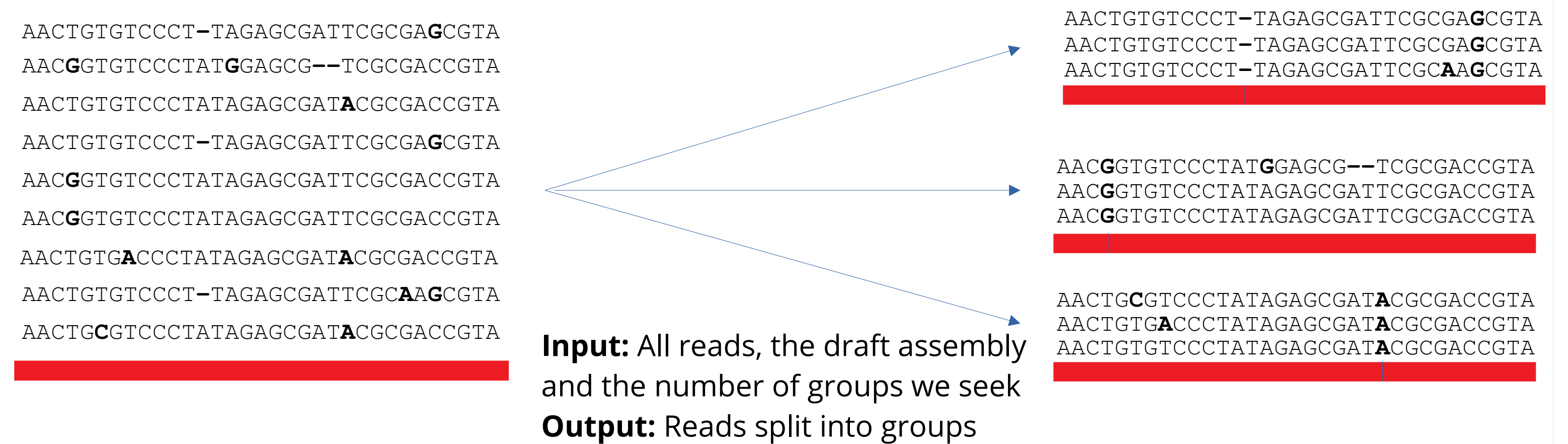
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Problem: assembling similar sequences



State of the art

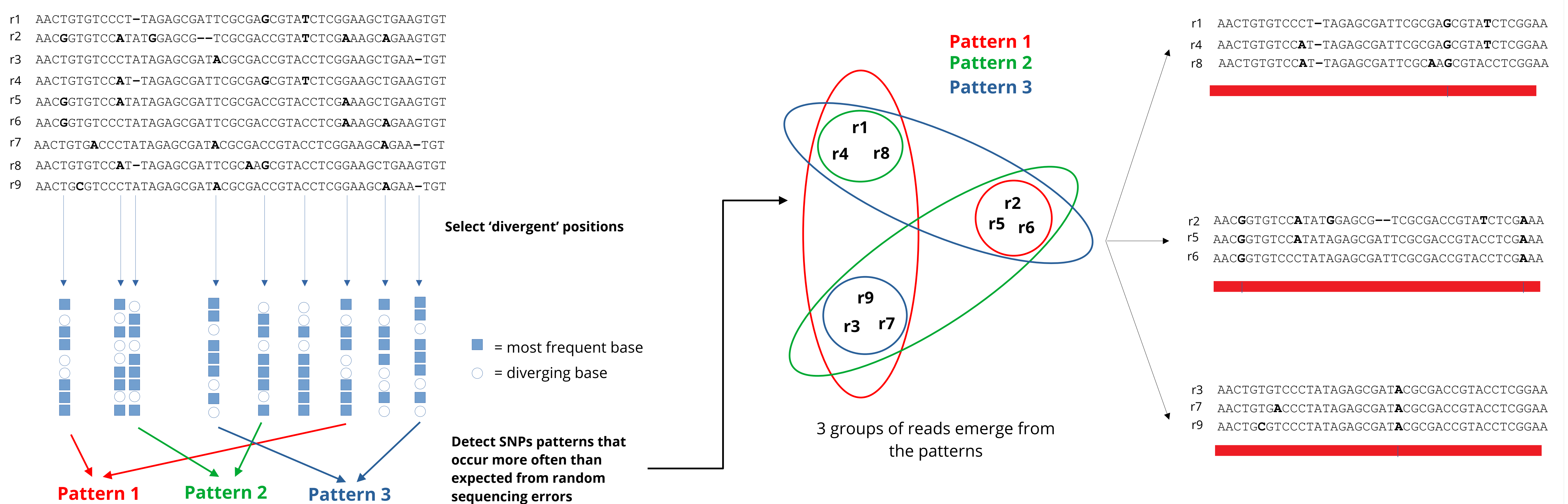


Existing software: WhatsHap (polyphase), Phasebook, Falcon-Unzip, HapCut, HapDup...

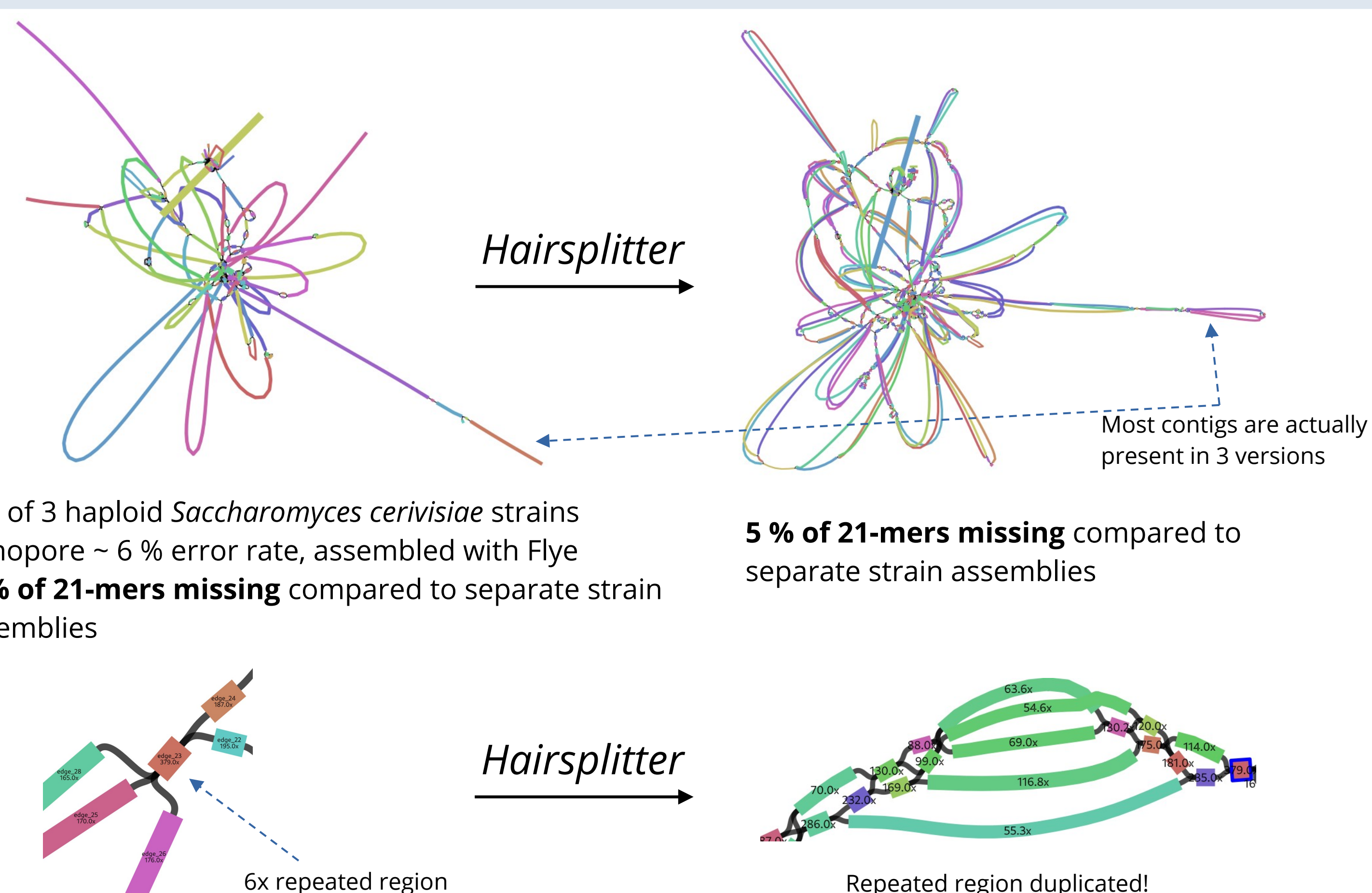
But: All software need to know the number of groups beforehand! We don't always know that → metagenomes, genomic repeats, insertions...

→ *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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