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

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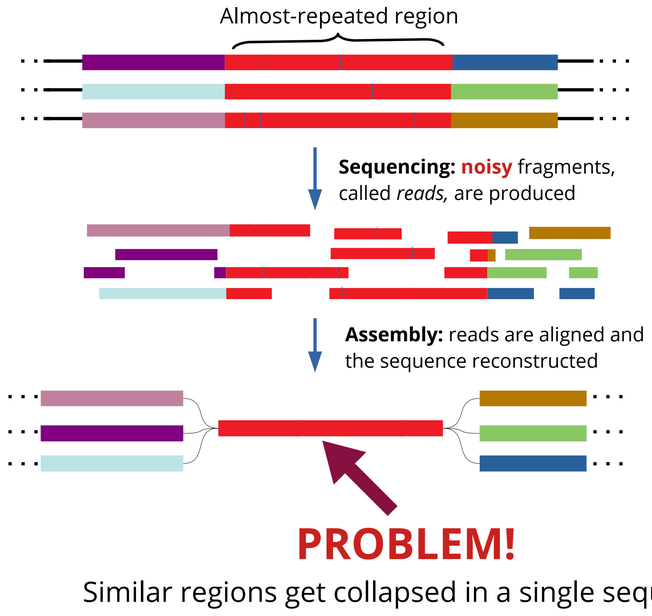
Roland Faure[1,2], Jean-François Flot[1], Dominique Lavenier[2]

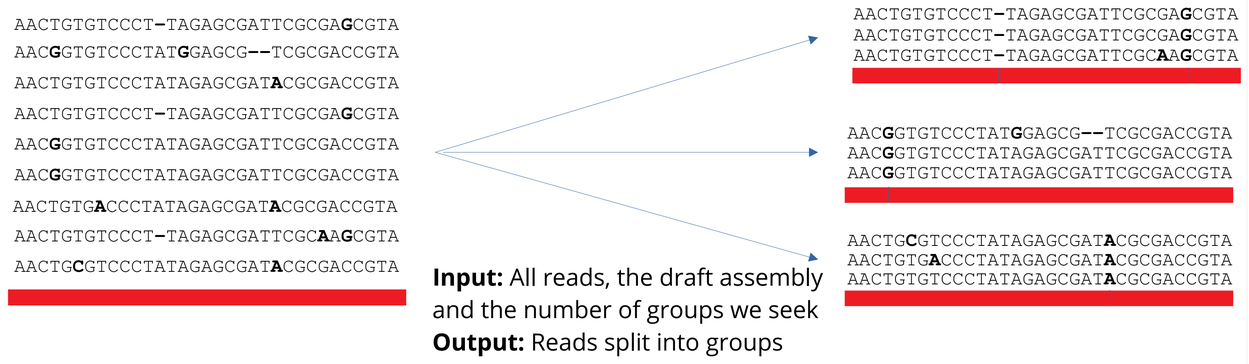
1. Service Evolution Biologique et Ecologie, ULB, Brussels, Belgium 2. Univ. Rennes, Inria RBA, CNRS UMR 6074, Rennes, France

Problem: assembling similar sequences



Similar regions get collapsed in a single sequence

State of the art

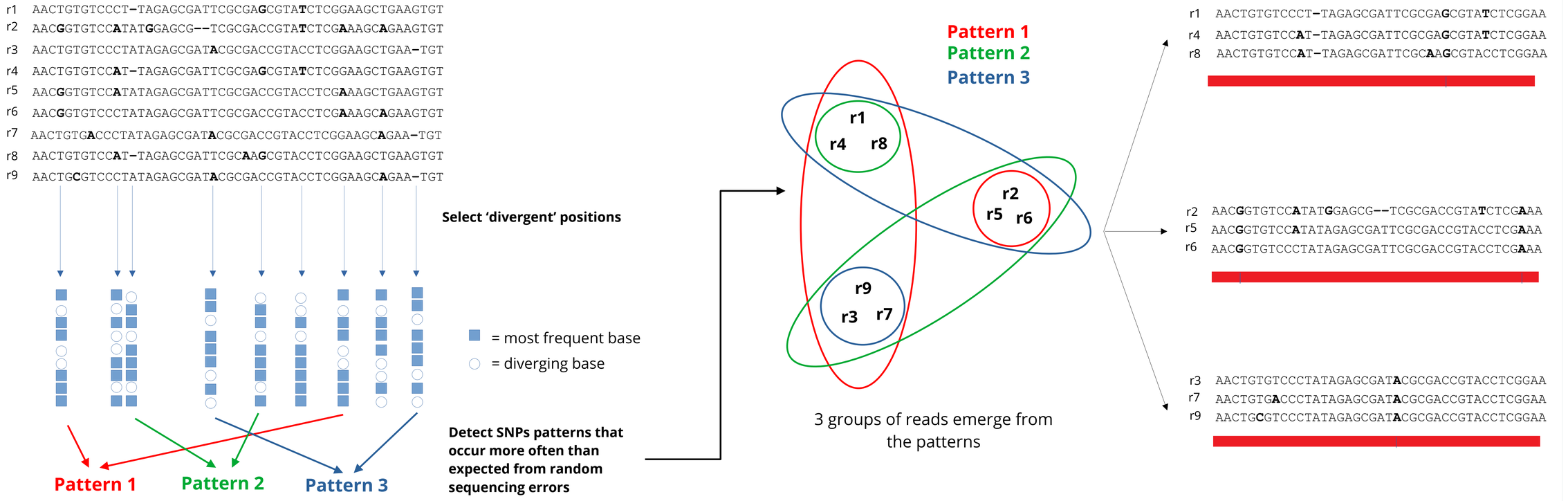


Existing software: WhatsHap (polyphase), Phasebook, Falcon-Unzip, HapCut, HapDup…

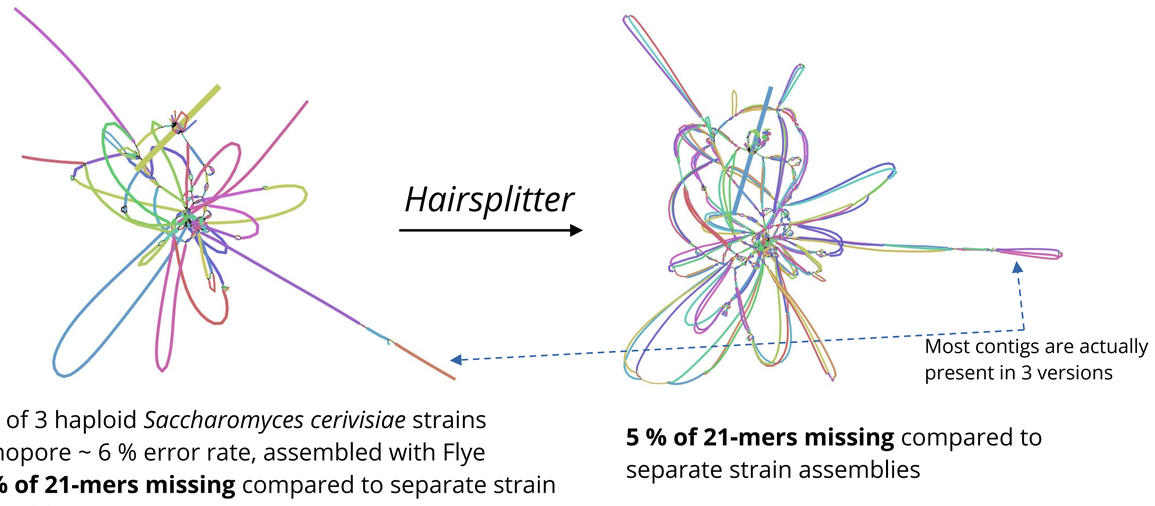
But: All software need to know the number of groups beforehand! We don't always know that
→ metagenomes, genomic repeats, insertions…

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

Algorithm

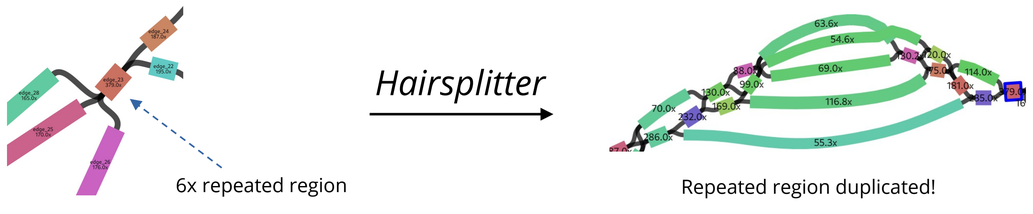


Results



Mix of 3 haploid *Saccharomyces cerivisiae* strains
Nanopore ~ 6 % error rate, assembled with Flye
21% of 21-mers missing compared to separate strain assemblies

5 % of 21-mers missing compared to separate strain assemblies



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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