

Assembly of long, error-prone reads using repeat graphs

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- repeats \rightarrow assembly fragmentation
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- Flye should resolve these repeats correctly

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- Flye uses a different approach [1]:
 - we don't care (at least at the initial stage)
 - correct assembly graph
- generate paths from overlapping reads without checking for correct assembly → disjointigs

Repeat Graph Creation

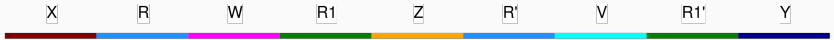


Figure 1: Example Genome

Repeat Graph Creation

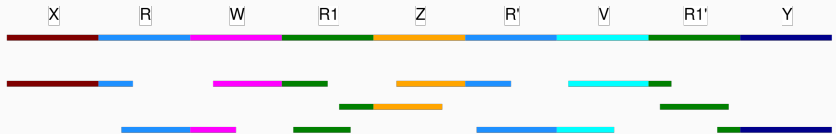


Figure 2: Example Genome and Reads

Repeat Graph Creation

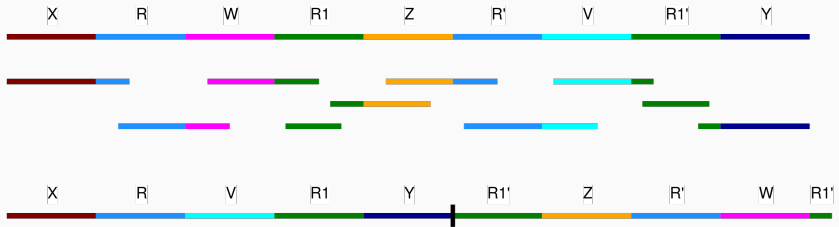


Figure 3: Example Genome, Reads and Disjointigs

Repeat Graph Creation

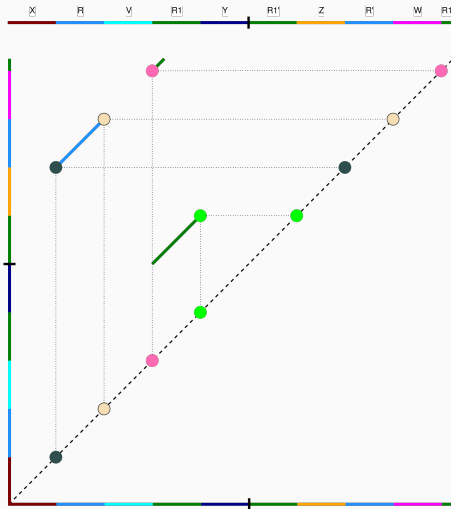


Figure 4: Breakpoint Graph

Repeat Graph Creation

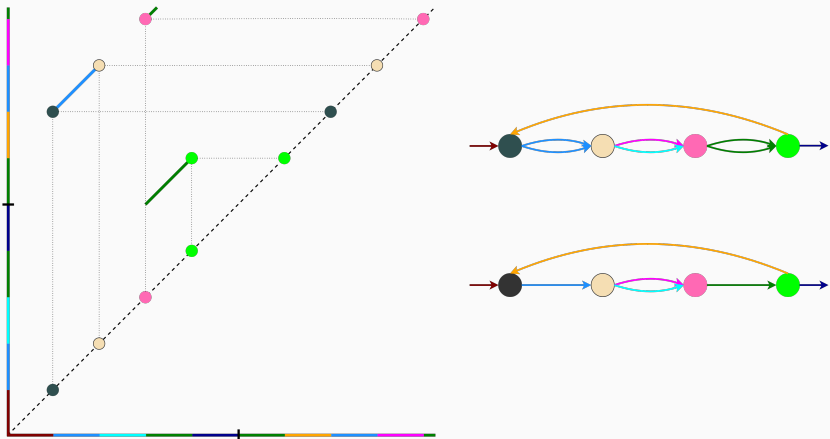


Figure 5: Repeat Graph

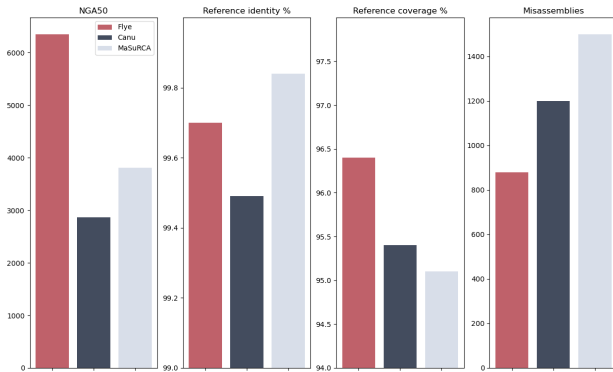


Figure 6: Results for HUMAN testset



M. Kolmogorov, J. Yuan, Y. Lin, and P. A. Pevzner.

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Nature Biotechnology, 37(5):540–546, May 2019.

Git (presentation)



Figure 7: Link to our git repo

Appendix

Dot plot creation

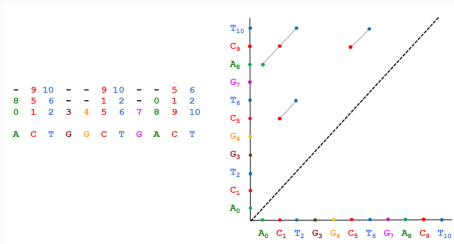


Figure 8: Dot plot creation

Repeat graphs

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 - from disjointigs = random walk of reads on the repeat graph
 - means the repeat graph hasn't to be known

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- de Bruijn graphs need correct bases
- otherwise tangled graph

Segmental duplications

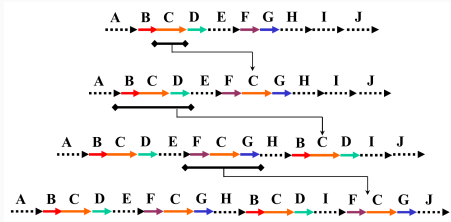


Figure 9: Segmental Duplications

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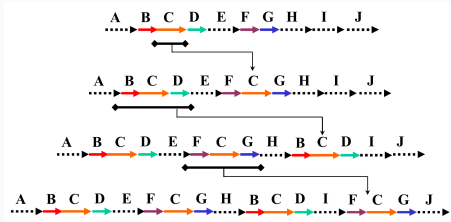


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- They often contain sequence features such as high-copy repeats and gene sequences with intron-exon structure.

Contigty improvement

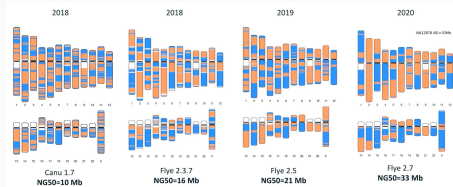


Figure 10: Contigty improvements

- colors are contigs

Contigty improvement

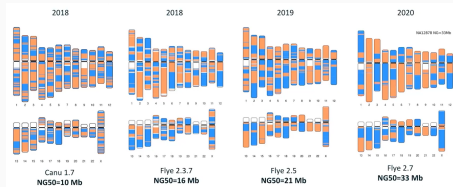


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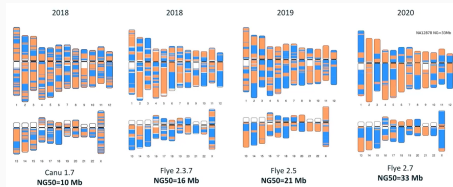


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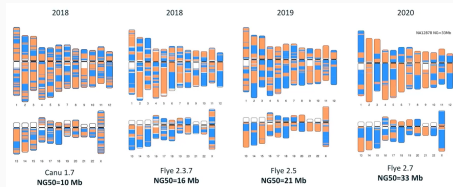


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