

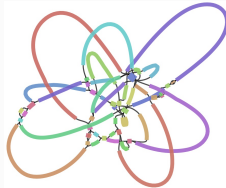
Assembly of long, error-prone reads using repeat graphs

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July 5, 2021

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Background

- Assembly: reconstruct target sequence from the reads
- Different assemblers, different graph structures
- Repeats → assembly fragmentation

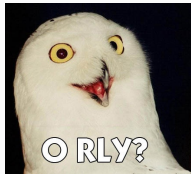


Tangled assembly graph of *E.coli* [2]

- Small differences between repeat copies → hard to resolve with error-prone reads

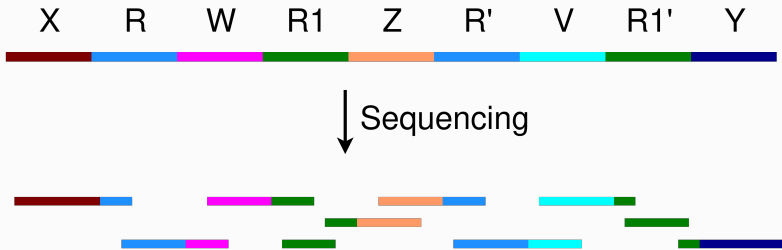
Disjointigs

- Most assemblers spend much time on correct contig assembly
- Flye uses a different approach:
 - we don't care about the correct contig assembly
 - at least at the initial stage

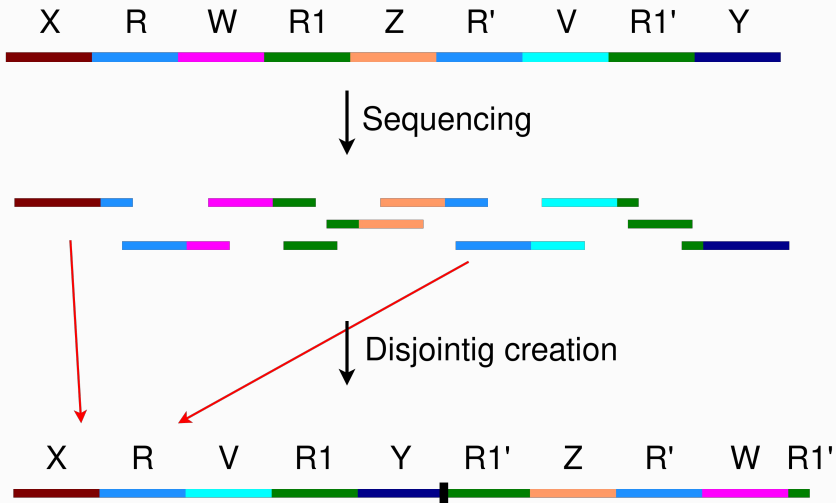


- Generate arbitrary paths from overlapping reads → Disjointigs

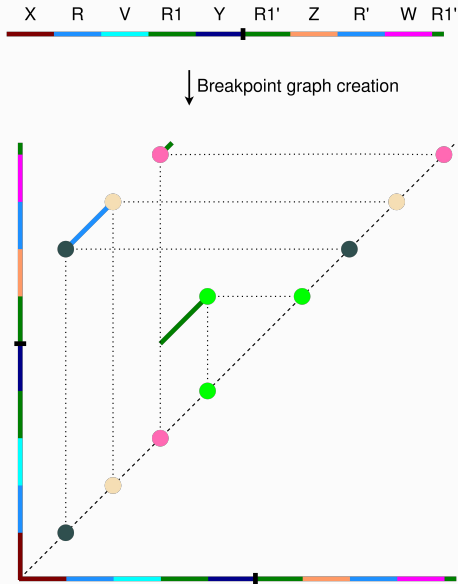
Repeat Graph Creation



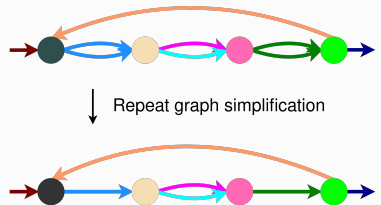
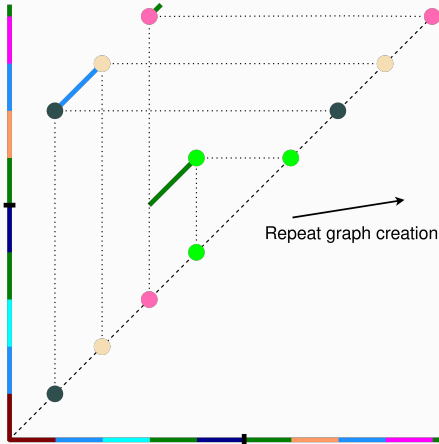
Repeat Graph Creation



Repeat Graph Creation



Repeat Graph Creation



Results

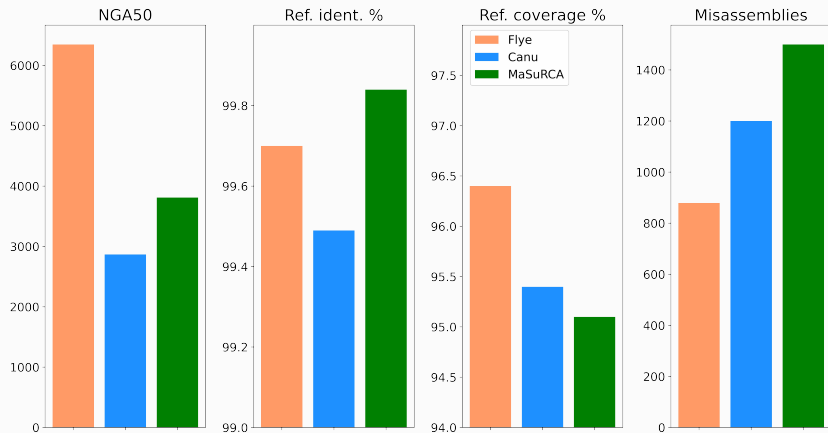


Figure 1: Results for HUMAN testset



<https://github.com/LKress/ASA>



A. Gurevich, V. Saveliev, N. Vyahhi, and G. Tesler.

QUAST: quality assessment tool for genome assemblies.

Bioinformatics (Oxford, England), 29(8):1072–1075, Apr. 2013.



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

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



Y. Lin, S. Nurk, and P. A. Pevzner.

What is the difference between the breakpoint graph and the de Bruijn graph?

BMC genomics, 15 Suppl 6:S6, 2014.



P. A. Pevzner, P. A. Pevzner, H. Tang, and G. Tesler.

De novo repeat classification and fragment assembly.

Genome Research, 14(9):1786–1796, Sept. 2004.



B. J. Walker, T. Abeel, T. Shea, M. Priest, A. Abouelliel, S. Sakthikumar, C. A. Cuomo, Q. Zeng, J. Wortman, S. K. Young, and A. M. Earl.

Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement.

PloS One, 9(11):e112963, 2014.



A. V. Zimin, G. Marçais, D. Puiu, M. Roberts, S. L. Salzberg, and J. A. Yorke.

The MaSuRCA genome assembler.

Bioinformatics, 29(21):2669–2677, Nov. 2013.