Assembly of long, error-pront reads using repeat graphs

Mikhail Kolmogorov, Jeffrey Yuan, Yu Lin, and Pavel A. Pevzner

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Long read assembly

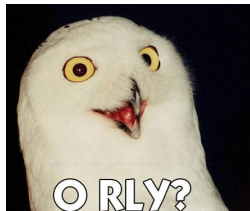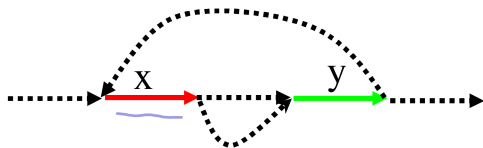▶ error rate long read <-> short read

Long read assembly

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Long read assembly

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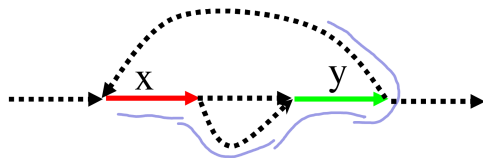- Flye shoult resolve these repeats correctly

Disjointigs

▶ current assemblers use much time on correct contig assembly

▶ Flye uses a different approach:

▶ generate paths from overlapping reads without checking for correct assembly -> disjointigs

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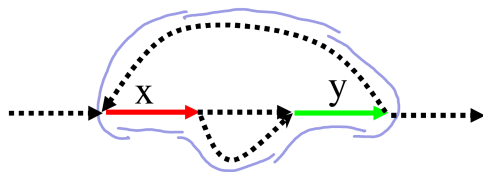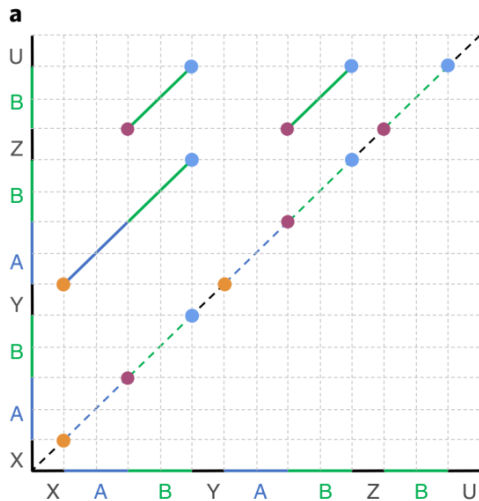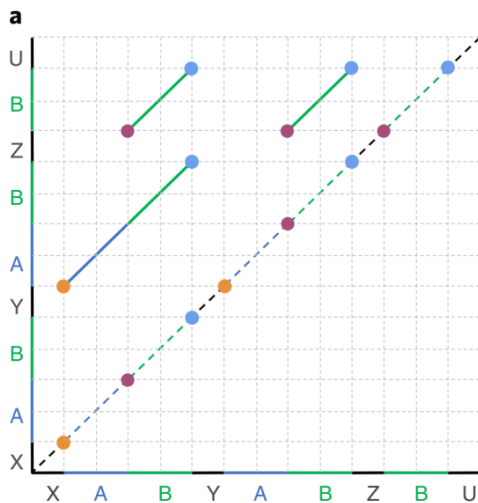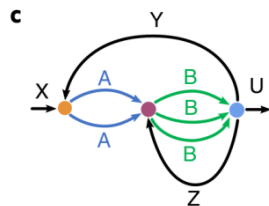▶ generate paths from overlapping reads without checking for correct assembly -> disjointigs
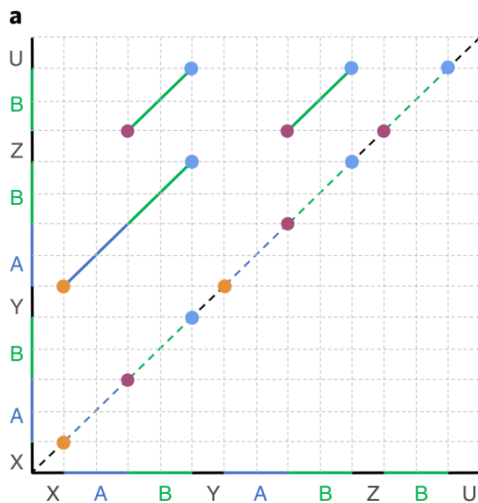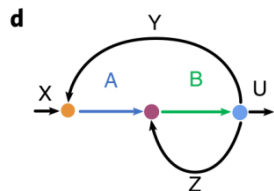
Repeat graph creation

a

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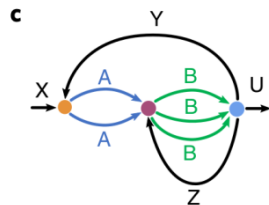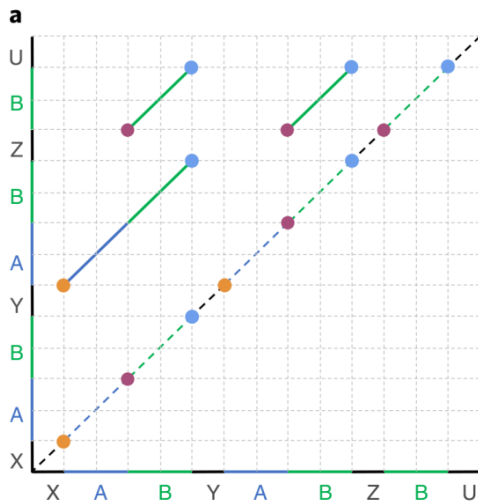
Repeat resolution

Results
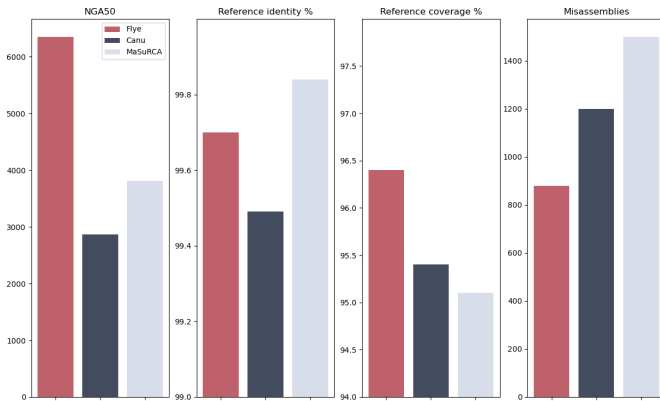
References

Appendix

Dot plot creation


```
-   9  10  -   -   9  10  -   -   5   6
8   5   6   -   -   1   2   -   0   1   2
0   1   2   3   4   5   6   7   8   9  10

A   C   T   G   G   C   T   G   A   C   T
```
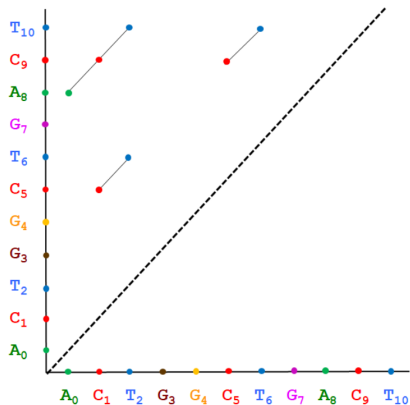
Repeat graphs

▶ generalization of de bruijn graphs

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- A-Bruijn graph (alignments) generalizes the de Bruijn graph

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▶ We thus argue that the time has come to explain that the breakpoint graphs and the de Bruijn graphs are two identical data structures (if one ignores a cosmetic difference between them) as they both represent specific instances of a general notion of the A-Bruijn graph introduced in [13]. The A-Bruijn graphs are based on representing genomes as sets of labeled paths and further gluing identically labeled edges (breakpoint graphs) or vertices (de Bruijn graphs) in the resulting paths.

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▶ de Bruijn graphs need correct bases

▶ otherwise tangled graph

Segmental duplications
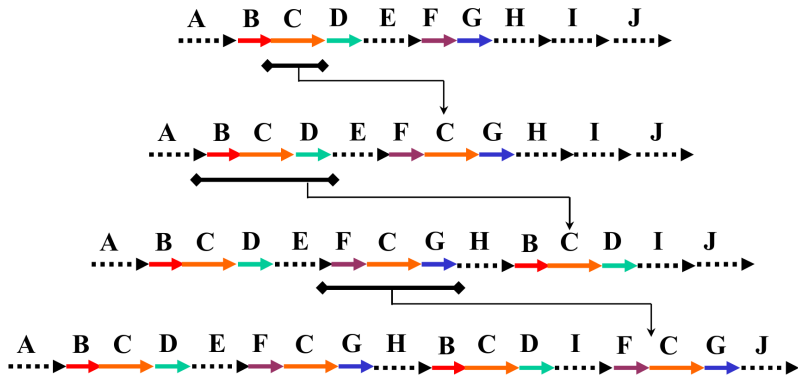
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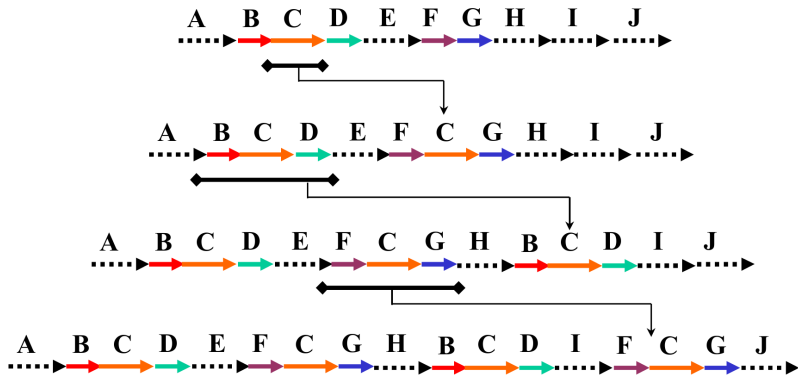
- Segmental duplications are duplicated blocks of genomic DNA typically ranging in size from 1-200 kb (IHGSC 2001)
- They often contain sequence features such as high-copy repeats and gene sequences with intron-exon structure

Contigity improvement
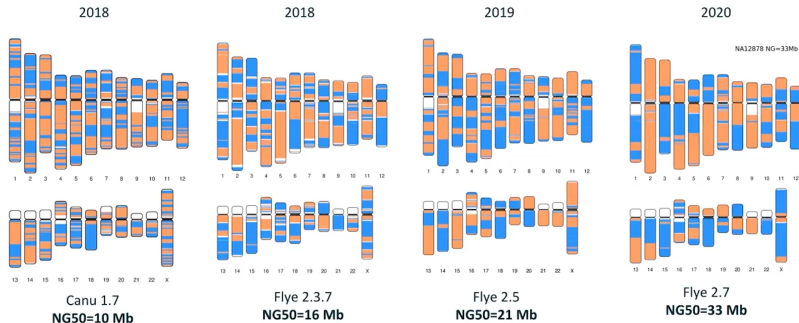
colors are contigs

color changes -> fragmented