

Assembly of long, error-prone reads using repeat graphs

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Long read assembly

- ▶ error rate long read \leftrightarrow short read

Long read assembly

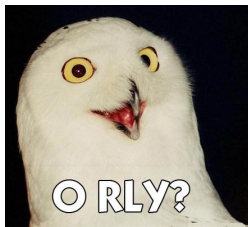
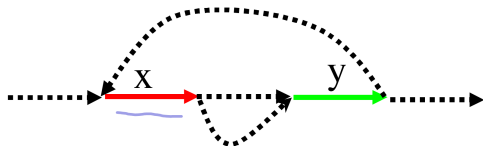
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Long read assembly

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

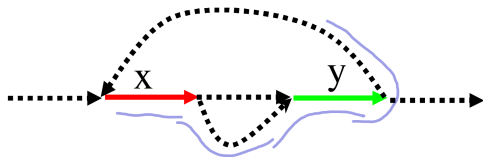
Disjointigs

- ▶ 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



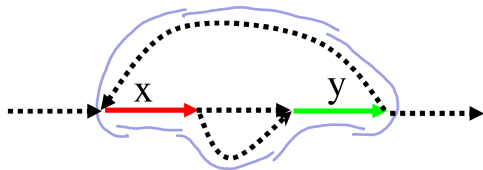
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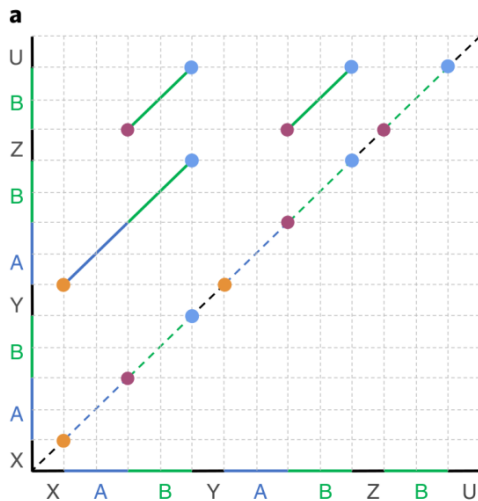


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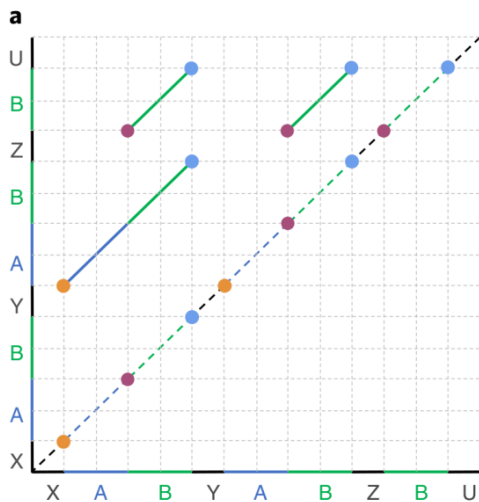
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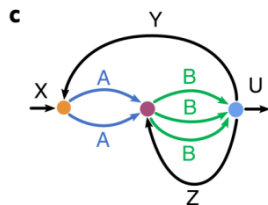
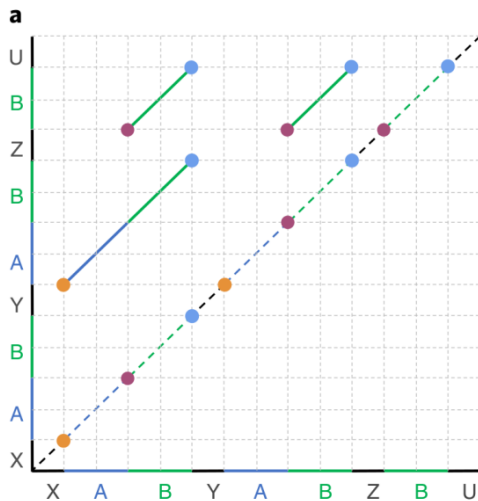
Repeat graph creation



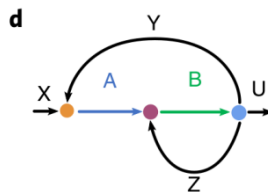
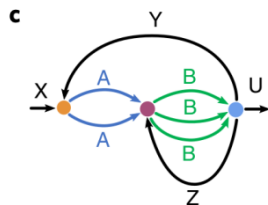
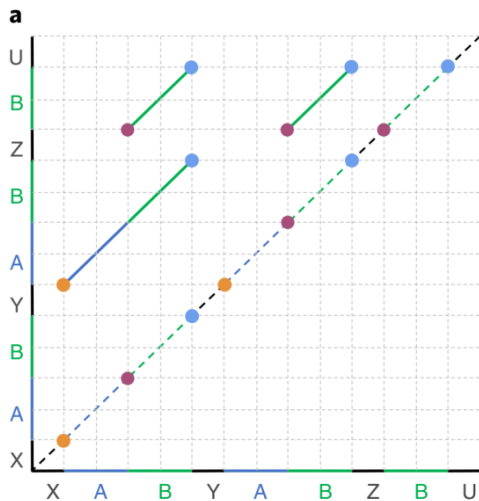
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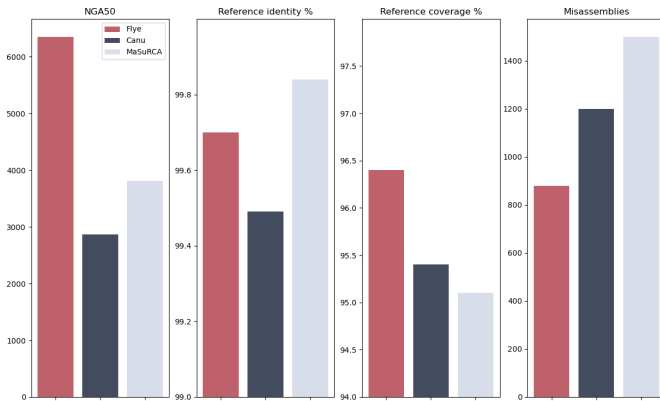


Repeat graph creation



Repeat resolution

Results

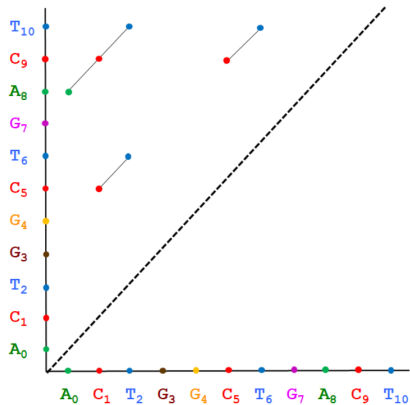


References

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



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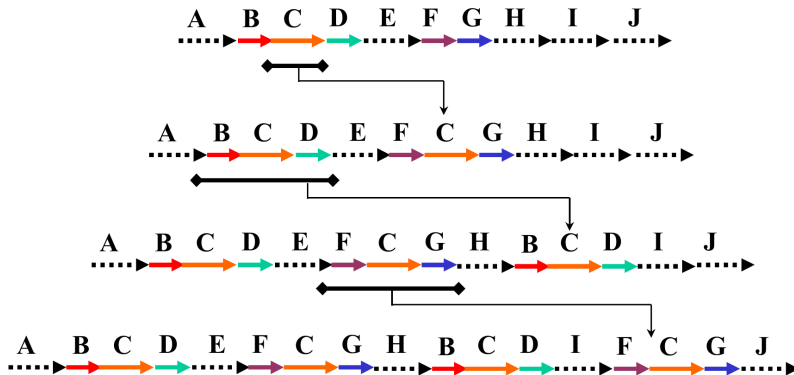
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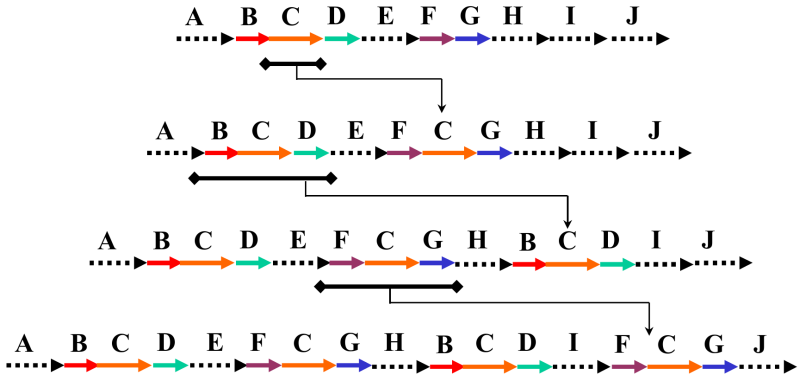
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- ▶ de Bruijn graphs need correct bases
- ▶ otherwise tangled graph

Segmental duplications



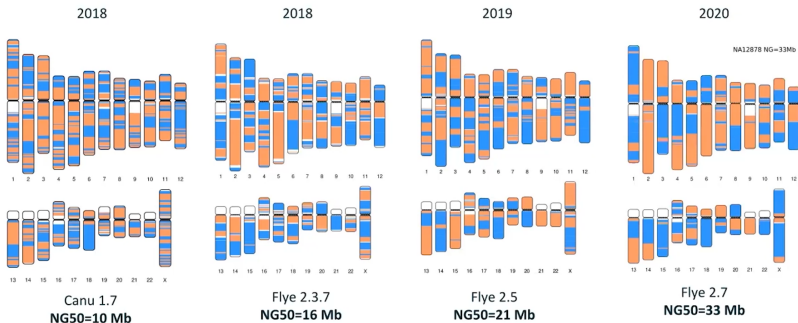
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- ▶ They often contain sequence features such as high-copy repeats and gene sequences with intron-exon structure.

Contigity improvement



- ▶ colors are contigs
- ▶ color changes -> fragmented