Assembly of long, error-pront reads using repeat graphs

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Long read assembly

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- Flye shoult resolve these repeats correctly

Disjointigs

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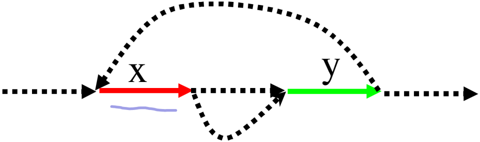
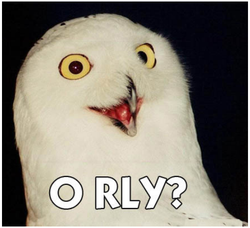
- Flye uses a different approach:
- generate paths from overlapping reads without checking for correct assembly -> disjointigs





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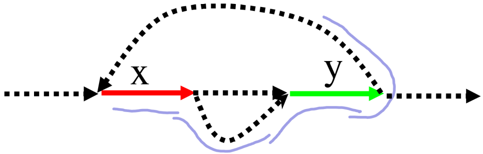

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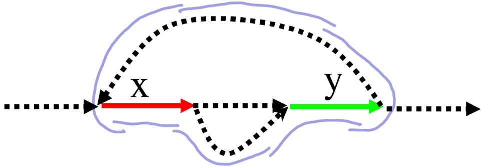
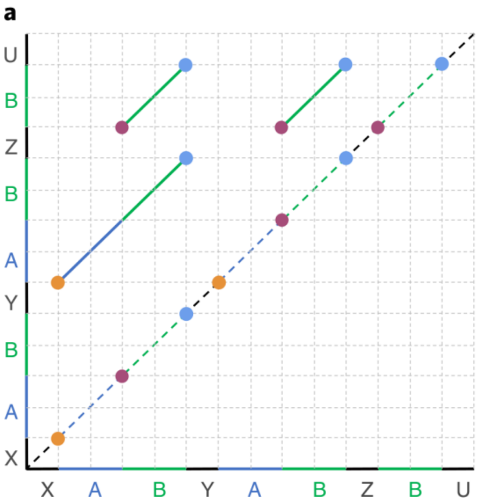


Repeat graph creation



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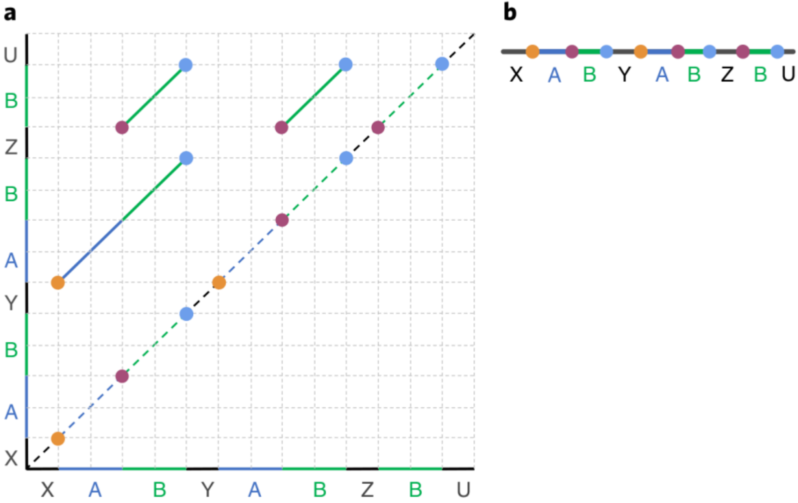

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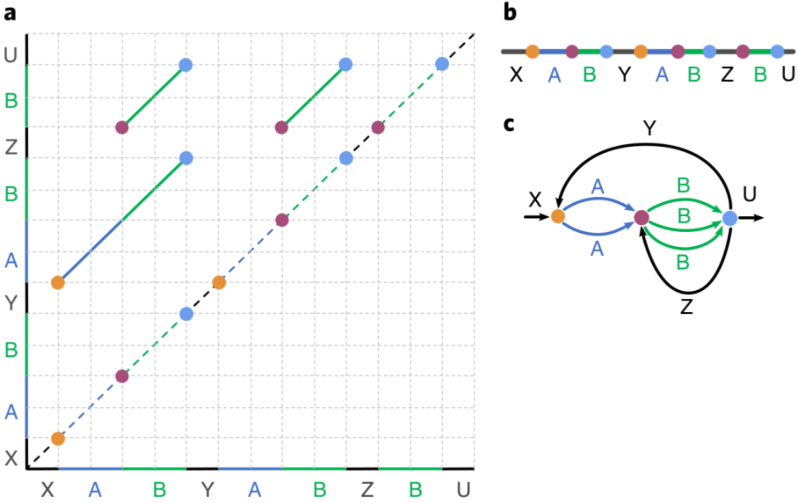

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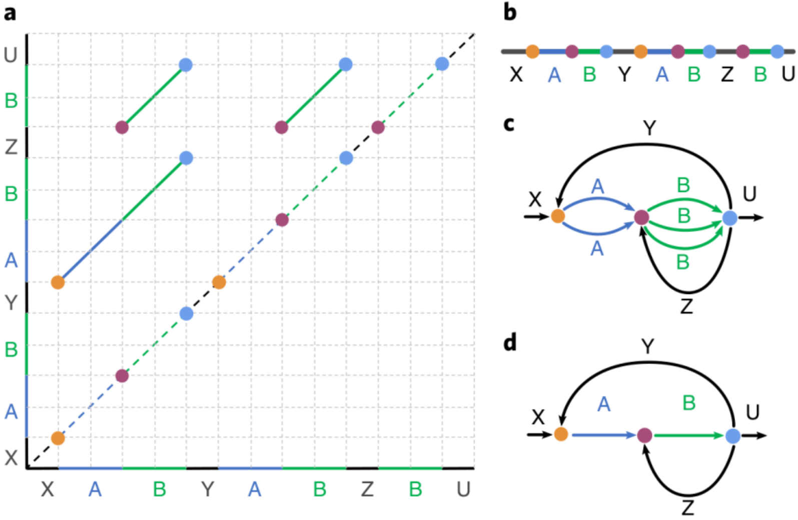
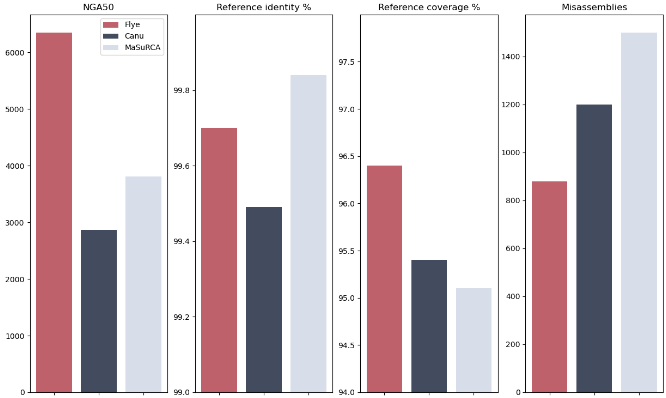


Repeat resolution

Results

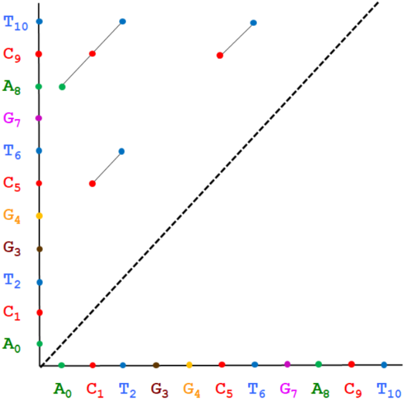

NGA50
Flye
Canu
MaSuRCA
0
1000
2000
3000
4000
5000
6000
Reference identity %
99.0
99.2
99.4
99.6
99.8
Reference coverage %
94.0
94.5
95.0
95.5
96.0
96.5
97.0
97.5
Misassemblies
0
200
400
600
800
1000
1200
1400

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


T_{10}
C_9
A_8
G_7
T_6
C_5
G_4
G_3
T_2
C_1
A_0
A_0 C_1 T_2 G_3 G_4 C_5 T_6 G_7 A_8 C_9 T_{10}

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- generalization of de bruijn graphs

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>- means the repeat graph hasn't to be known
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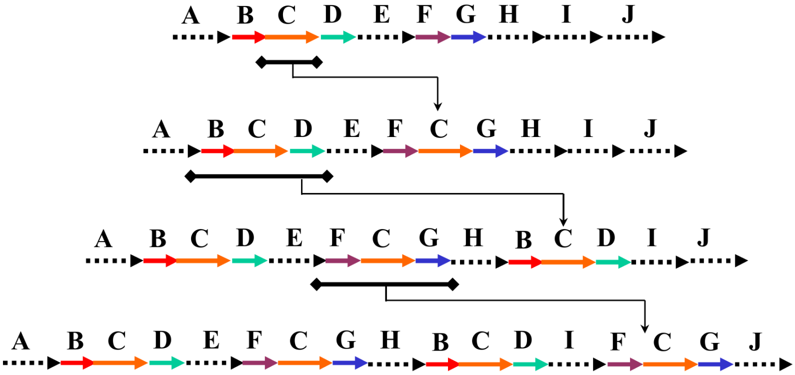
- de Bruijn graphs need correct bases
- otherwise tangled graph

Segmental duplications



A B C D E F G H I J
A B C D E F C G H I J
A B C D E F C G H B C D I J
A B C D E F C G H B C D I F C G J

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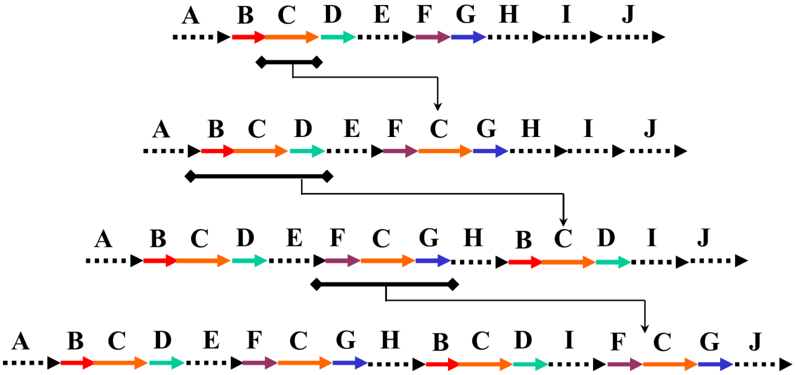
A B C D E F G H I J
A B C D E F C G H I J
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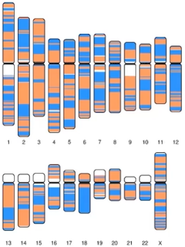
A B C D E F C G H B C D I F C G J

- 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.

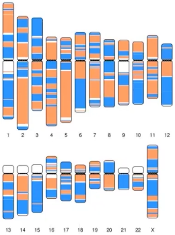
Contigity improvement

2018



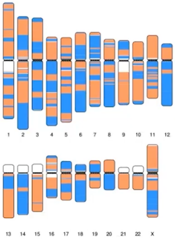
Canu 1.7
NG50=10 Mb

2018



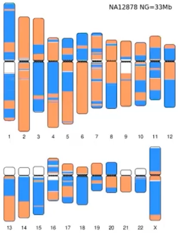
Flye 2.3.7
NG50=16 Mb

2019



Flye 2.5
NG50=21 Mb

2020



Flye 2.7
NG50=33 Mb

- colors are contigs
- color changes -> fragmented