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

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Disjointigs

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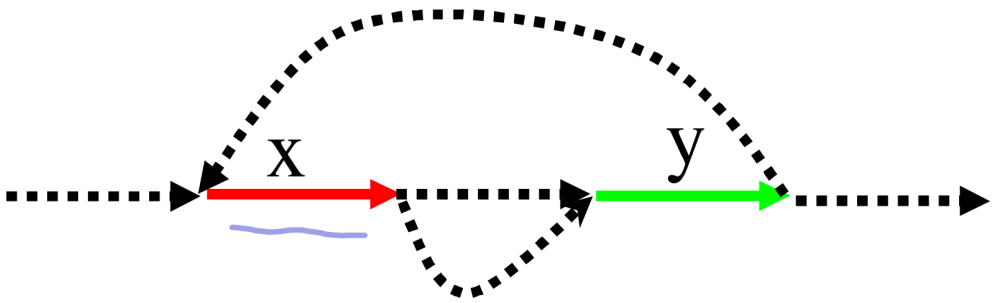

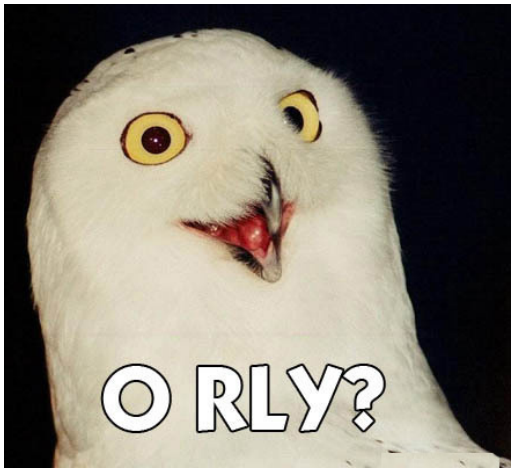

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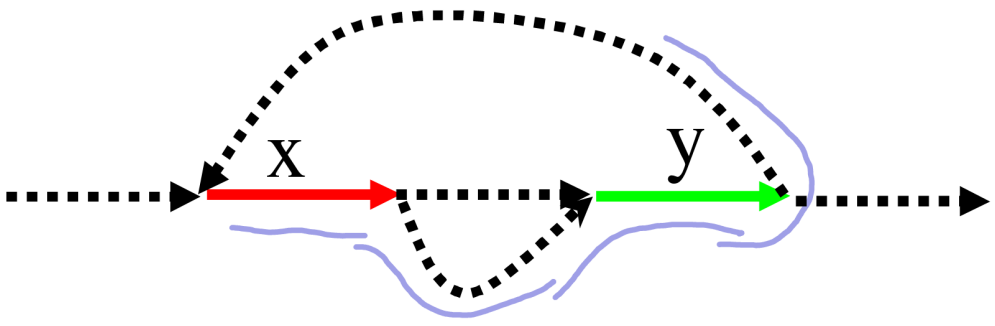

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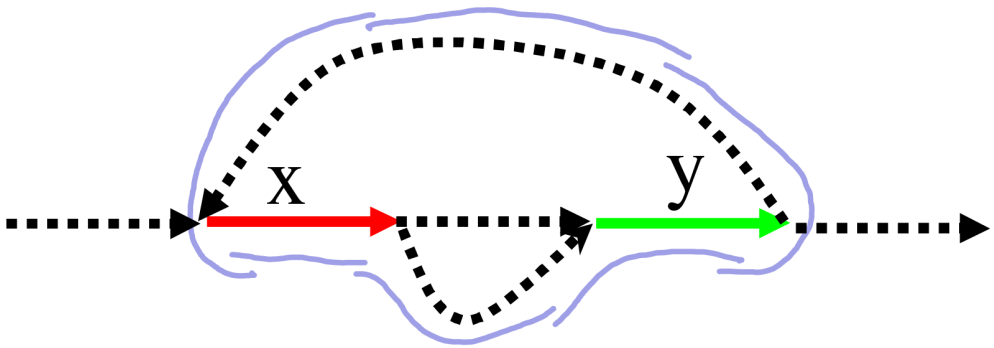
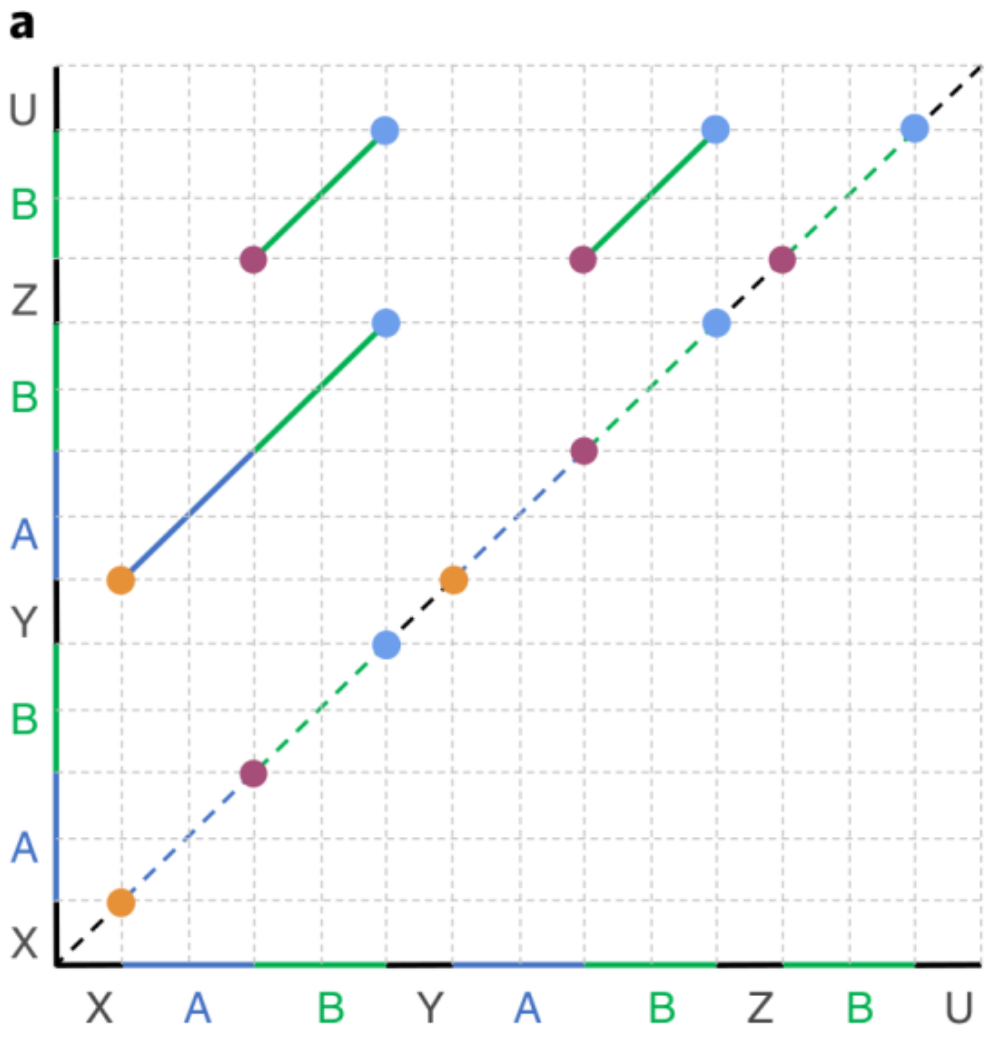


Repeat graph creation



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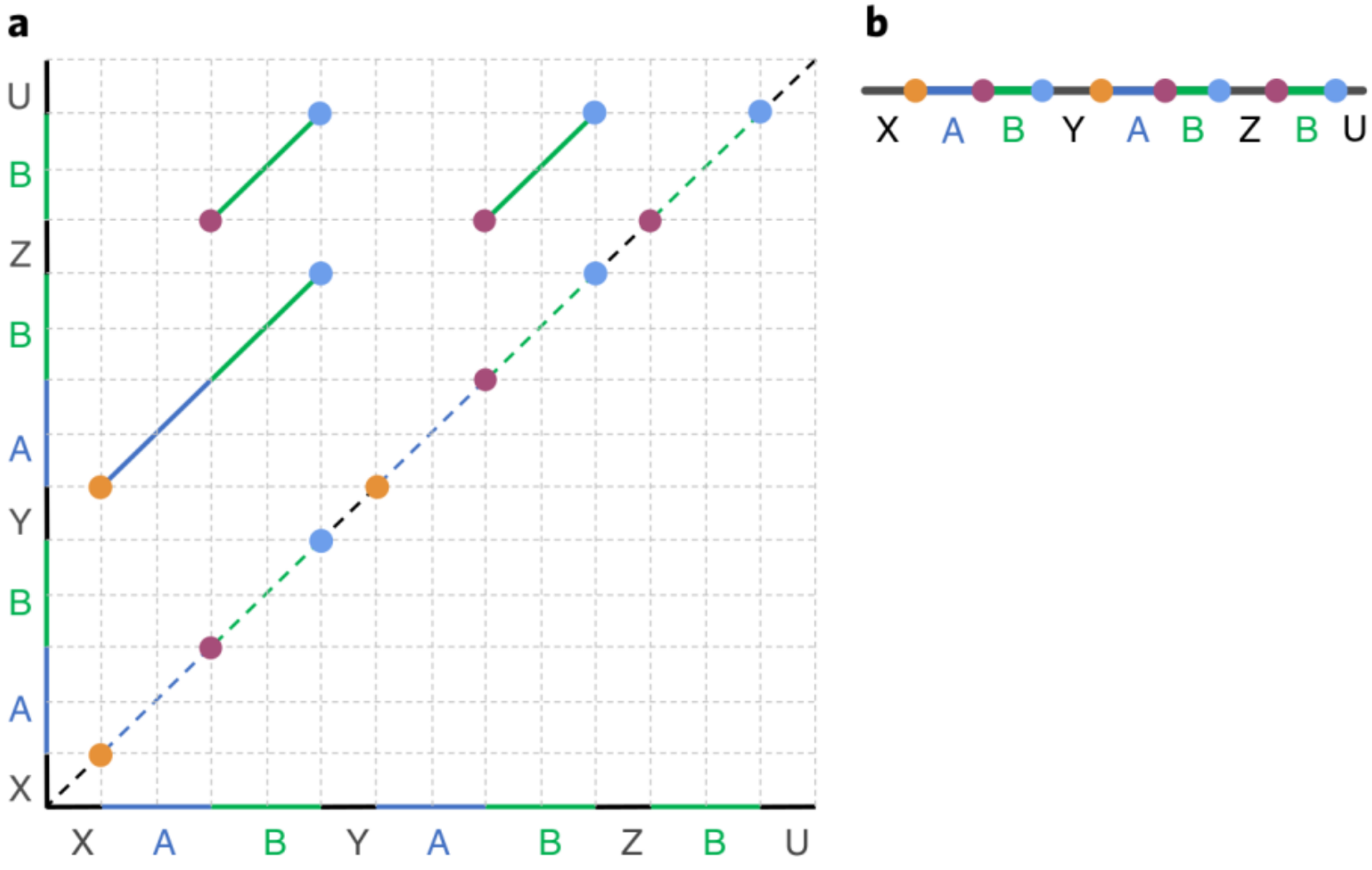
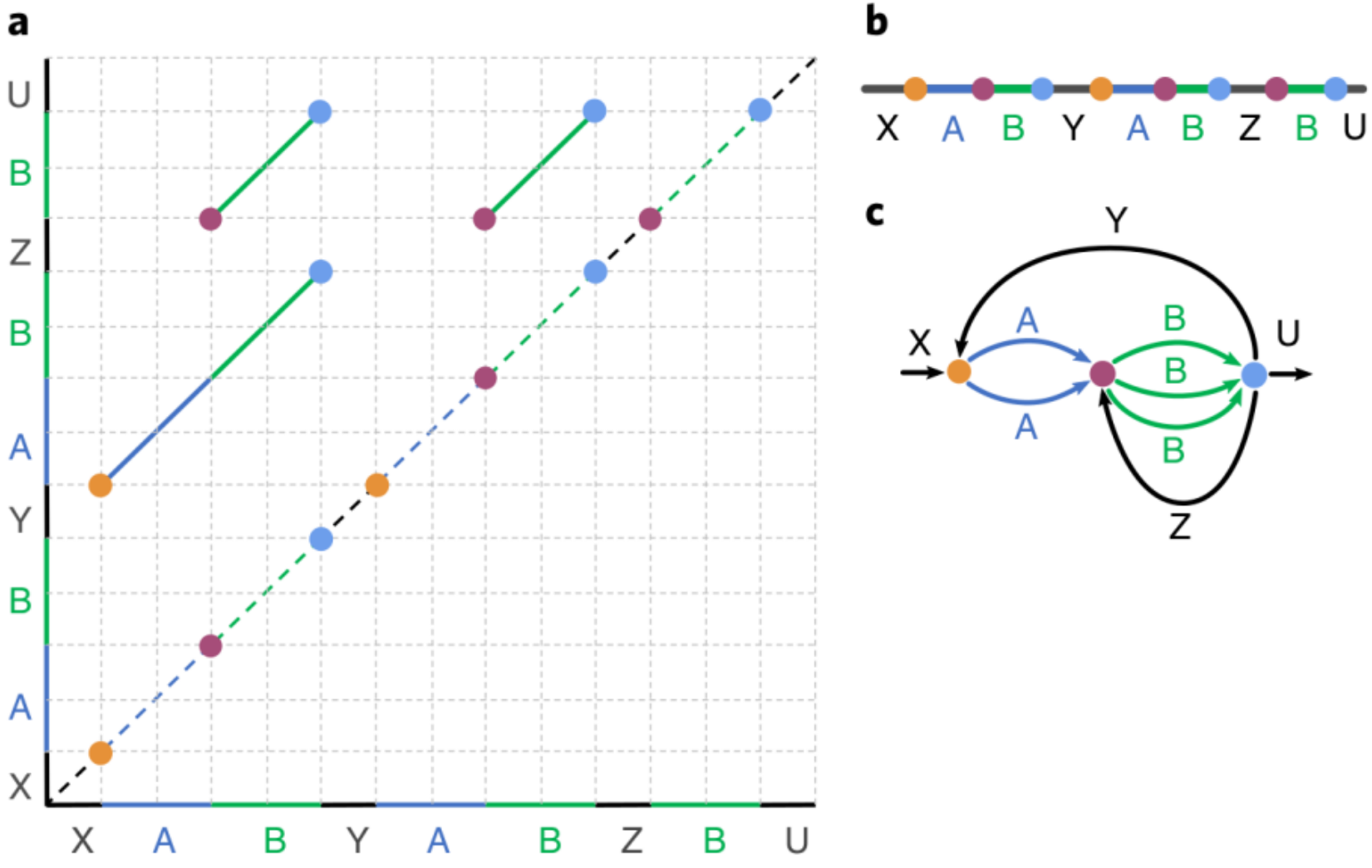


Repeat graph creation



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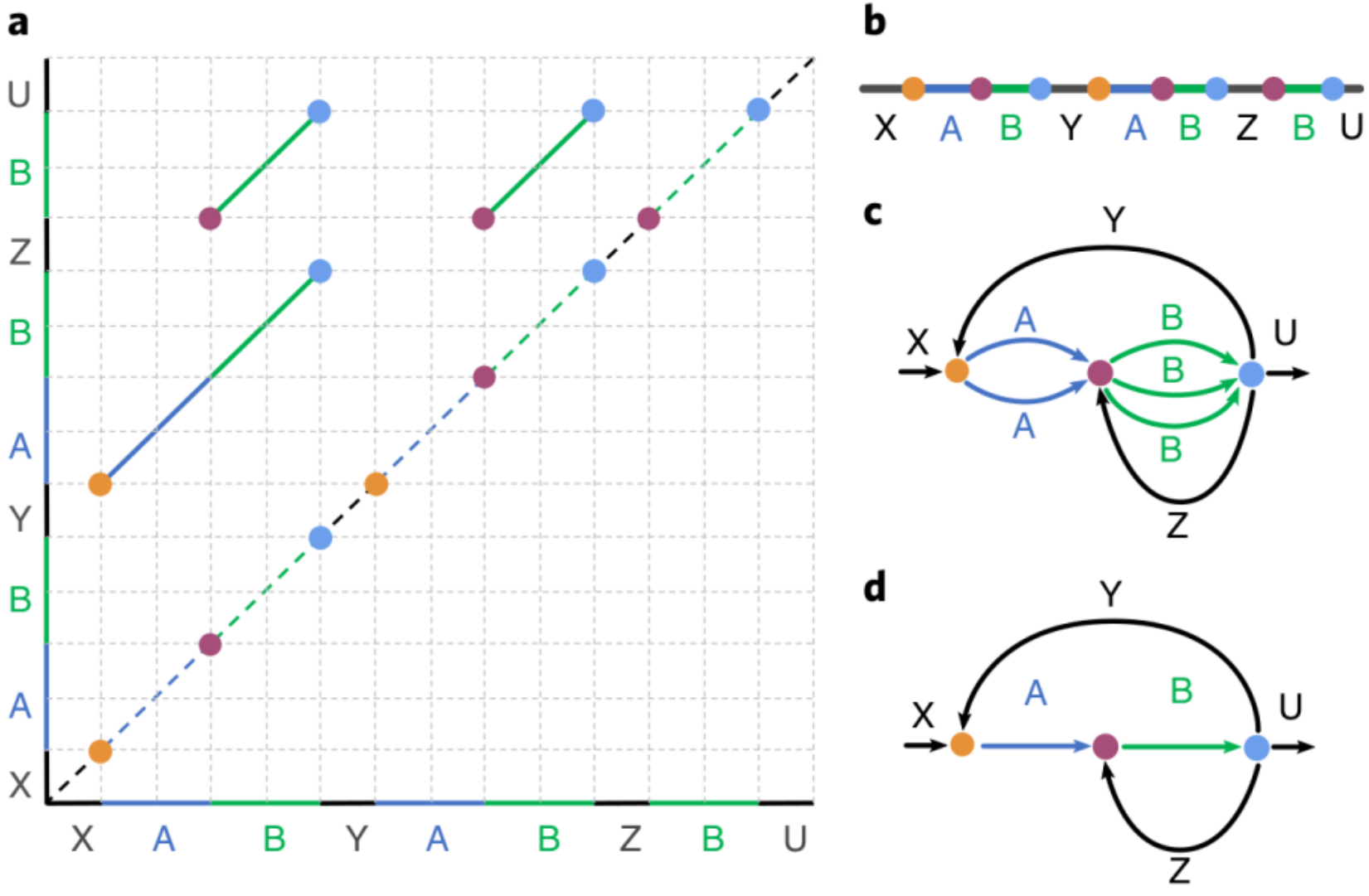
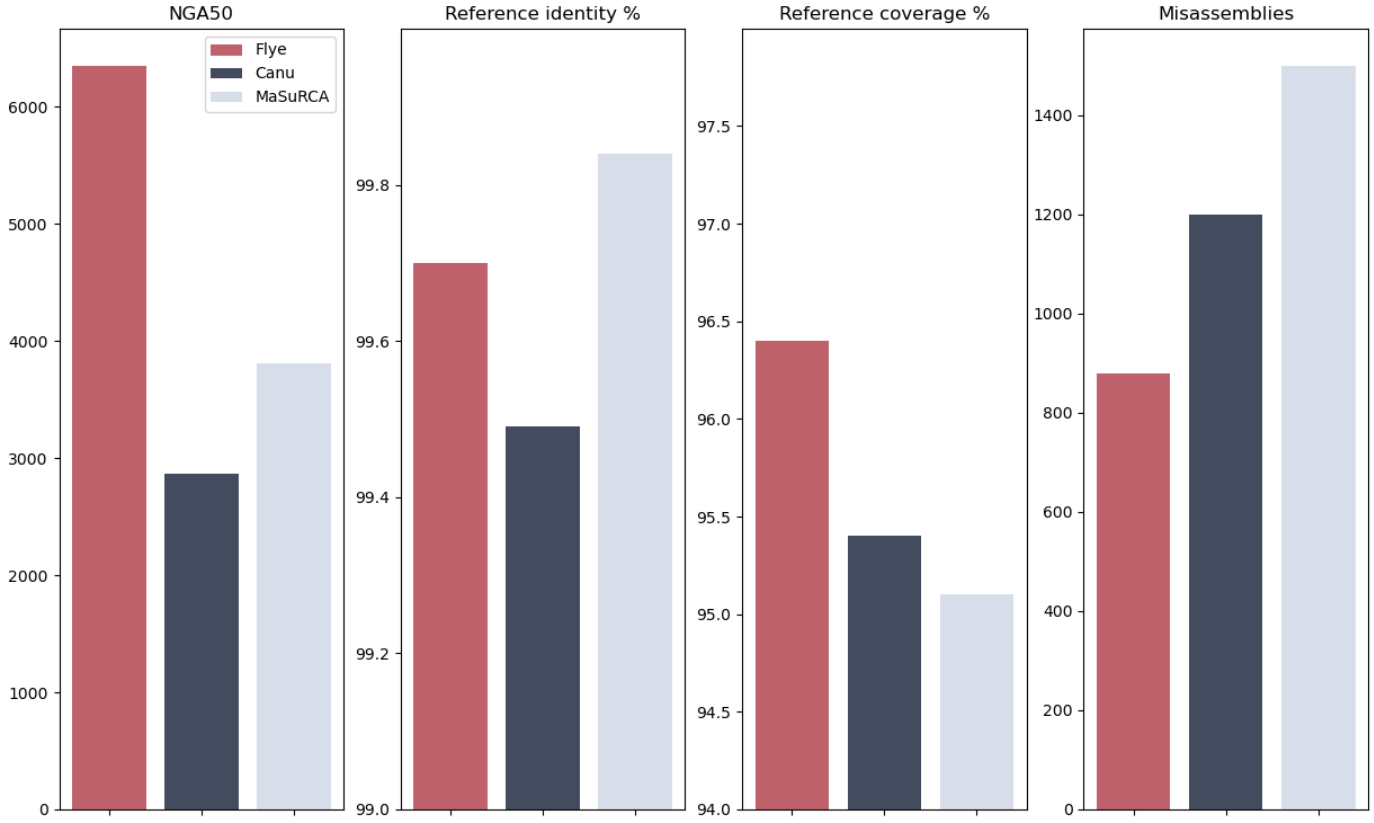


Repeat resolution

Results

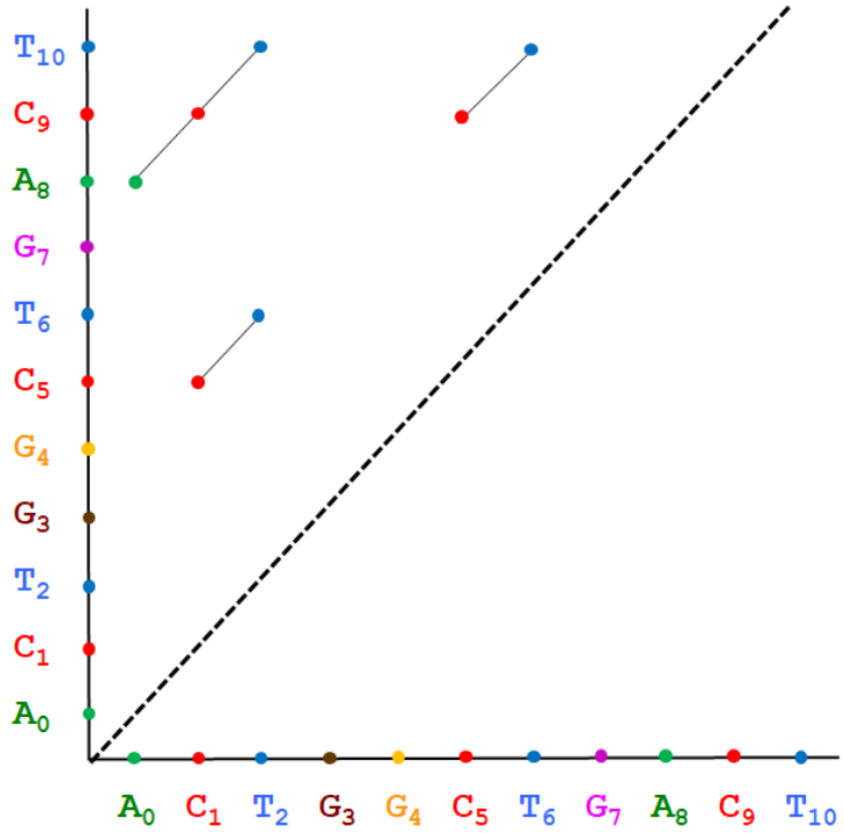

NGA50
Reference identity %
Reference coverage %
Misassemblies
Flye
Canu
MaSuRCA
6000
5000
4000
3000
2000
1000
0
99.8
99.6
99.4
99.2
99.0
97.5
97.0
96.5
96.0
95.5
95.0
94.5
94.0
1400
1200
1000
800
600
400
200
0

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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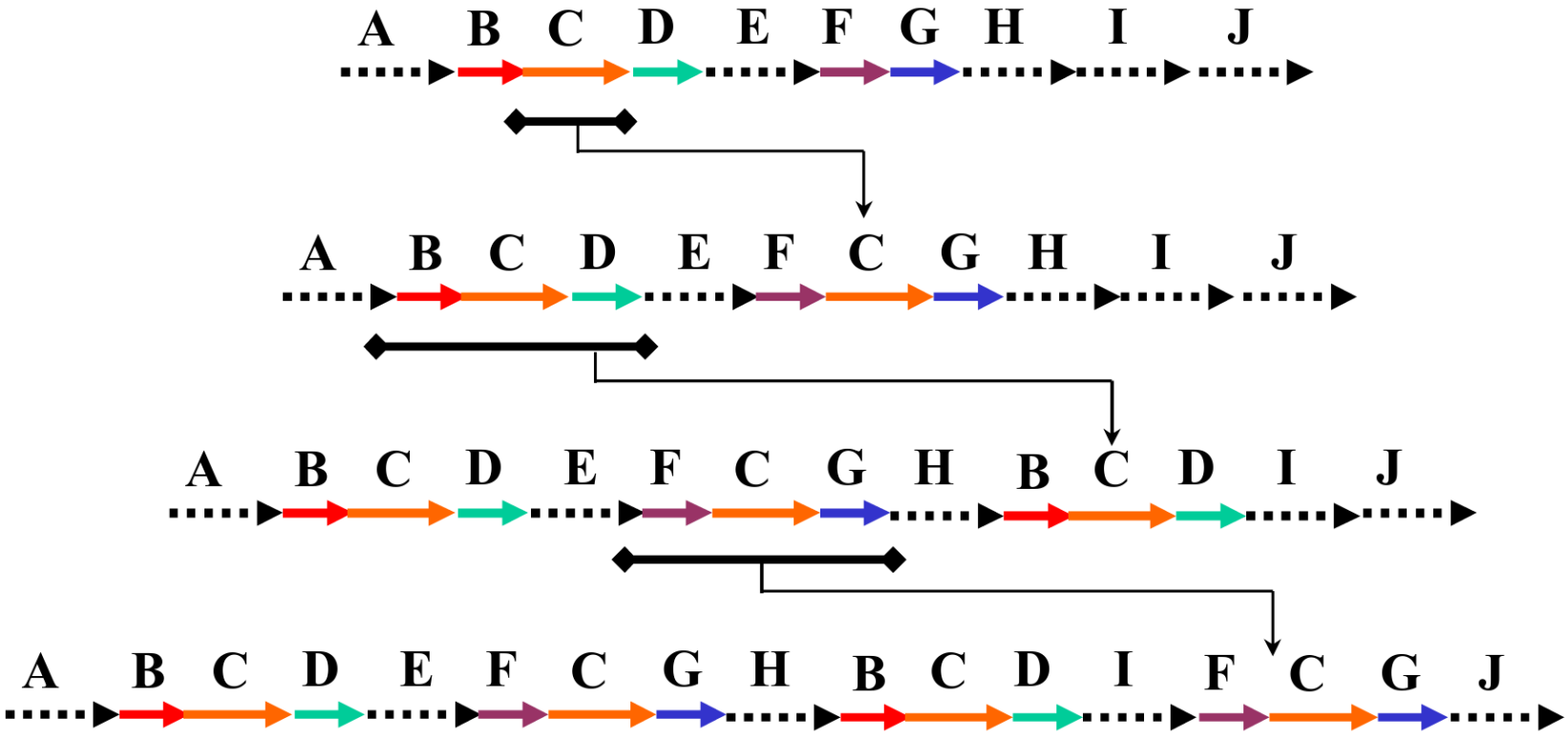
- de Bruijn graphs need correct bases
- otherwise tangled graph

Segmental duplications



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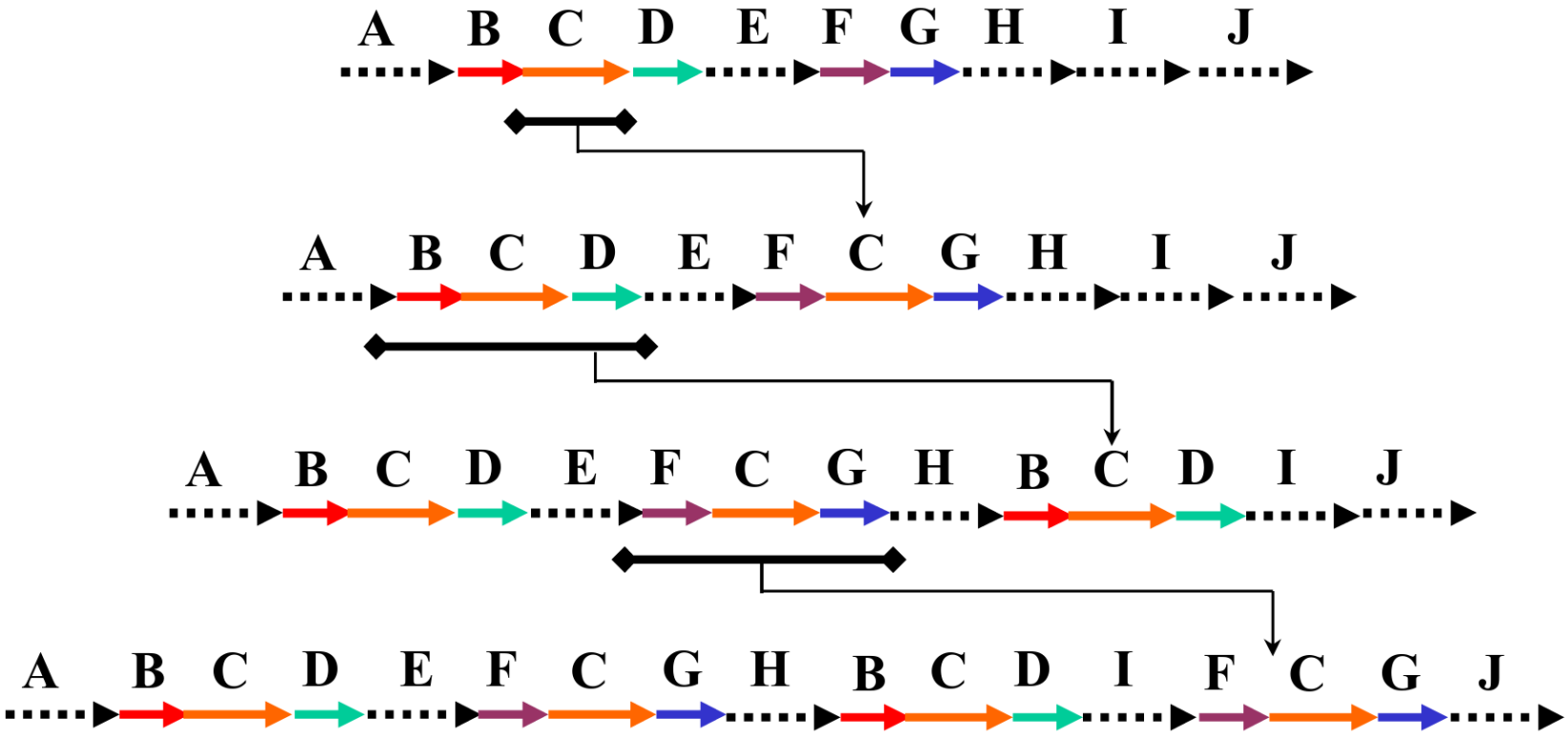

- Segmental duplications are duplicated blocks of genomic DNA typically ranging in size from 1-200 kb (IHGSC 2001)
- They often contain sequence features such as high-copy repeats and gene sequences with intron-exon structure.