Graph genome theory

Jordan Eizenga, Tobias Marschall, Erik Garrison

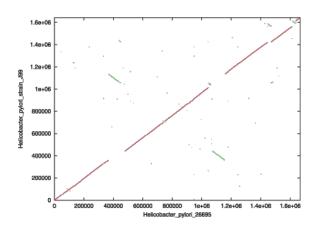
Adding variation

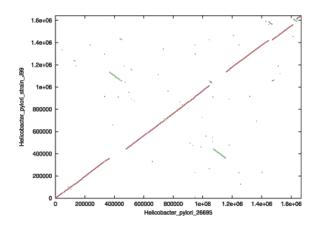
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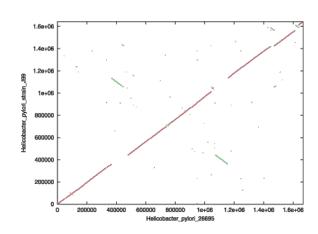
Adding variation

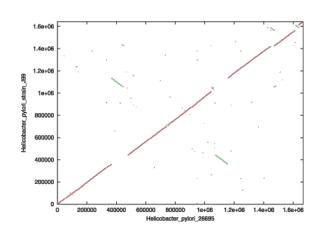
ATCC G ATACCAGATACCAT G TACCAGTACAG

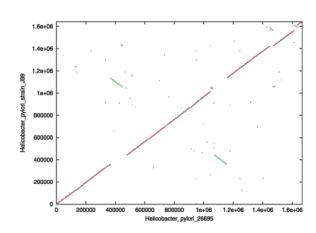
Adding variation

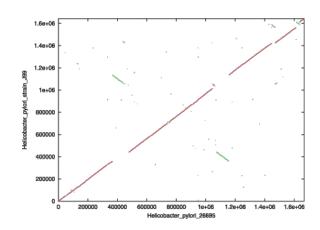


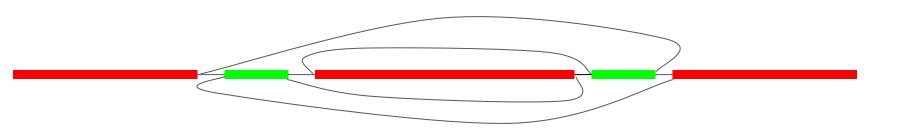


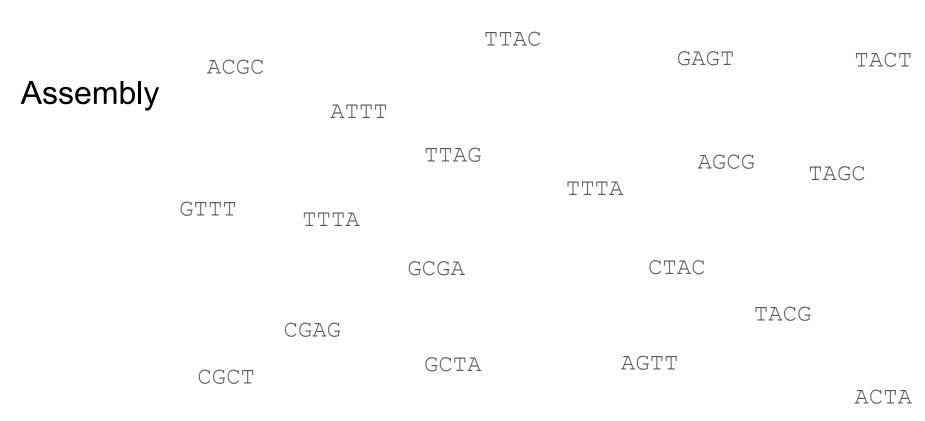


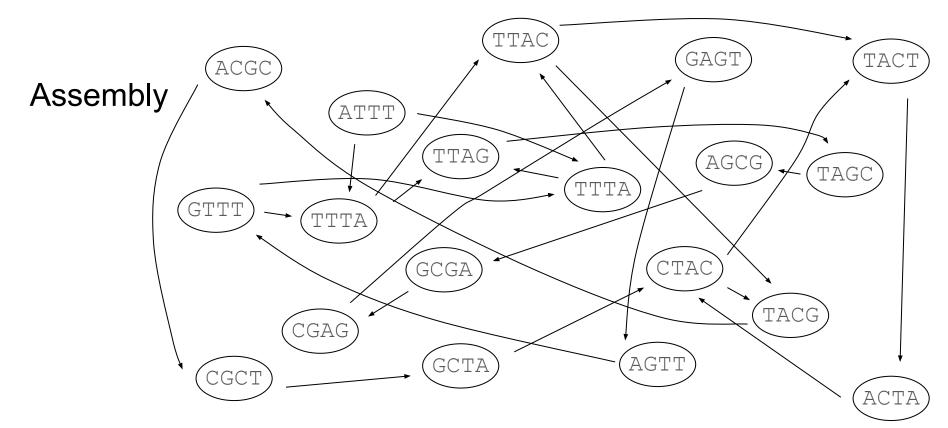




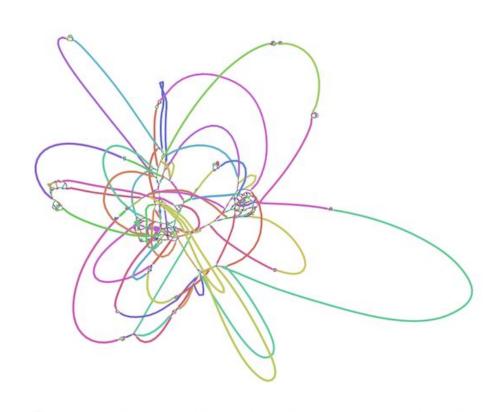


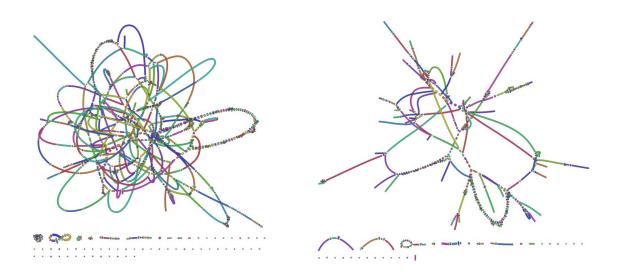




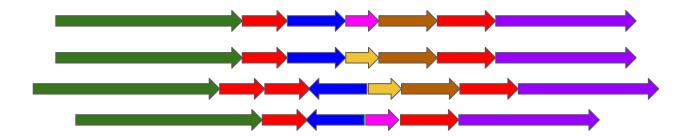


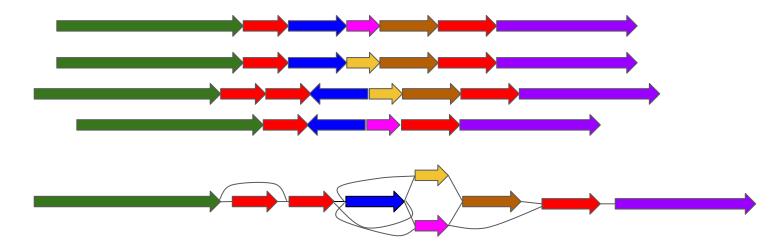
Assembly

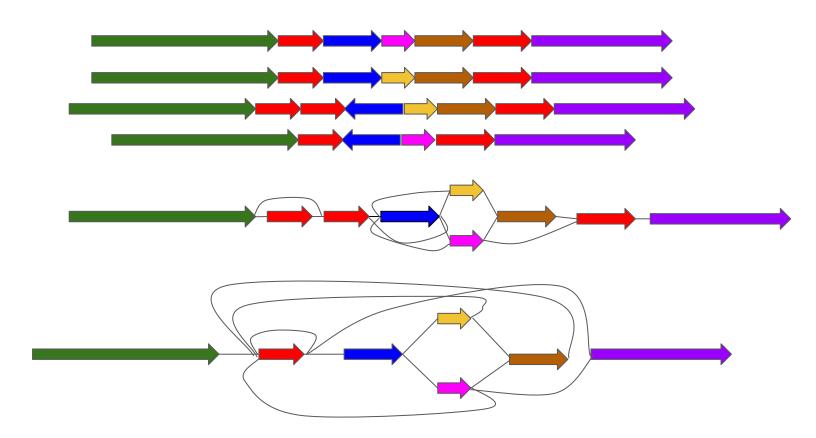


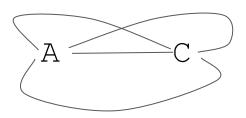


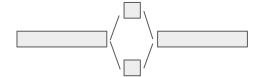
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25/1/2 2-11-1-1-11-11-11-11-11-11-11-11-11-11-1
XX111-1-111-1-1
V \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
U-1/2 Y U ~
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
V*^V



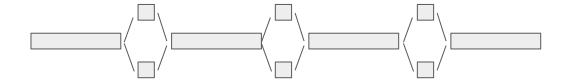




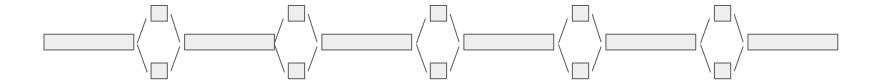




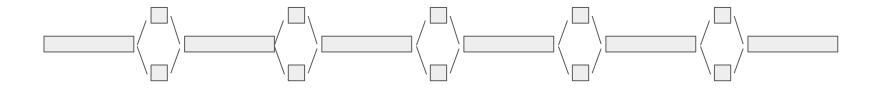




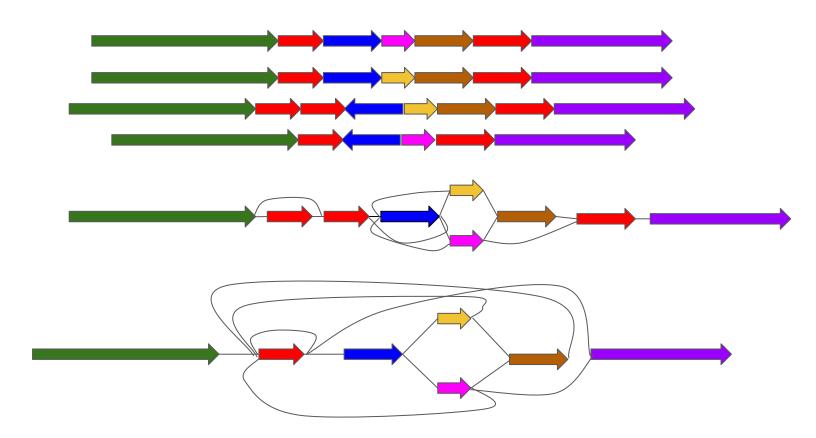




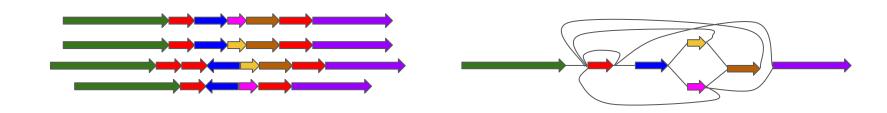
32 paths



With 40 SNPs >1,000,000,000,000 paths

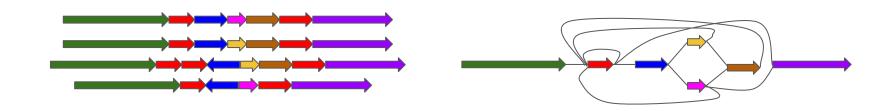


Fundamental tradeoff:



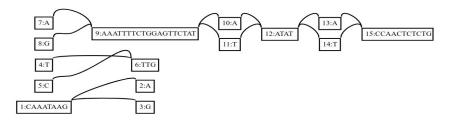
Fundamental tradeoff:

Homology ambiguity vs. Layout ambiguity

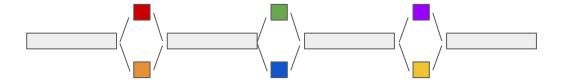


Pruning

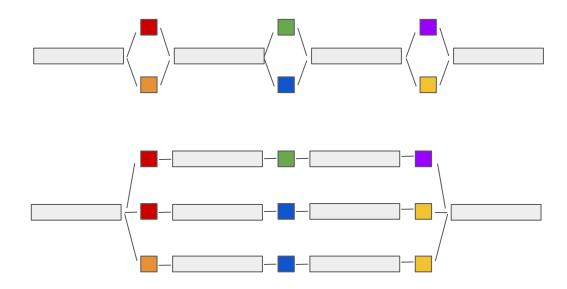




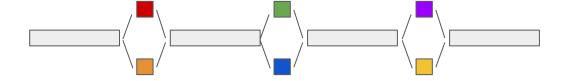
Combining and duplicating



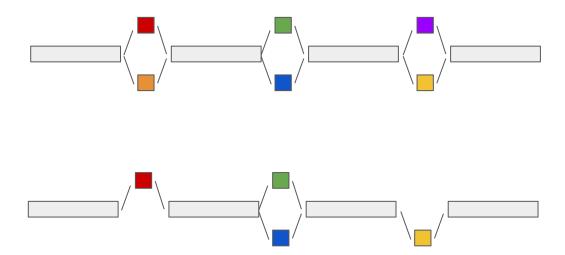
Combining and duplicating



Filtering



Filtering



Math sidebar?

Variants and loci

(go to PowerPoint)