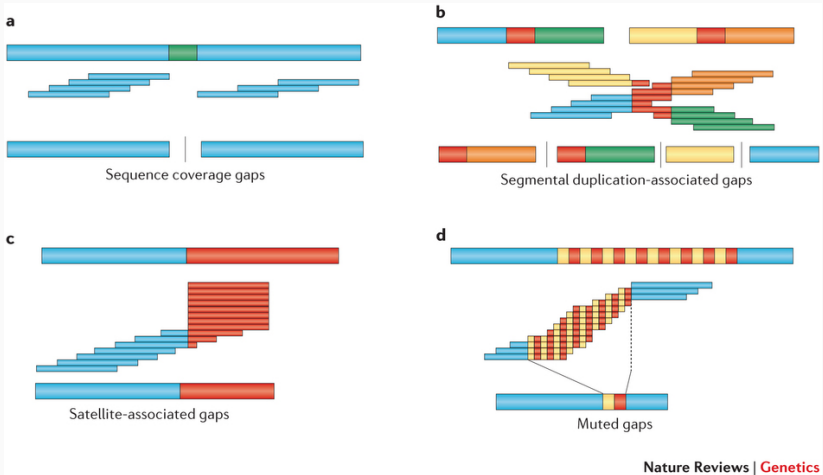


SHORT READY ASSEMBLY



Source[Chaisson et al, 2015]



1. Within a taxonomic group, GC content is largely conserved.
2. Within a taxonomic group, genome size is largely conserved.
3. Bacterial genomes are dense.
4. Nucleotide order is not random.

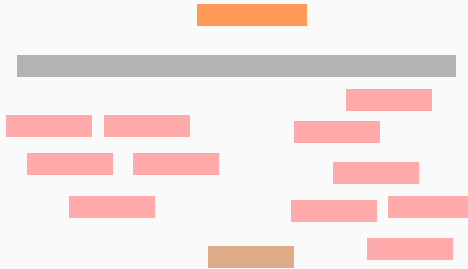


Figure: Bridge Reconstruction. Pink fragments are reads. Grey shows the gene of interest with interrupted coverage. Orange fragment is a pseudoread generated from this situation under the hypothesis that the beige fragment exists but is underrepresented: that is, the bridge is there, but needing repair





Chaisson, M. J. P., Wilson, R. K., and Eichler, E. E. (2015).
Genetic variation and the de novo assembly of human genomes.
Nature Publishing Group, 16.



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QUESTIONS?