

BIO383: Genomics Reading List

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1. WHAT IS A GENOME?

- 1.1. ► Noguera-Solano R, Ruiz-Gutierrez R, and Rodriguez-Caso JM (2013). Genome: twisting stories with DNA. *Endeavour*, 37(4):213–219. URL <http://dx.doi.org/10.1016/j.endeavour.2013.05.003>

2. CLASSICAL GENOMICS

- 2.1. ► Los Alamos National Lab. 1992. Mapping the Genome. *Los Alamos Science* 20:82–102. <http://library.lanl.gov/cgi-bin/getfile?20-02.pdf>
(You can read the first half too, it's an interesting look at the genome project as it stood in 1992.)
- 2.2. ► Sturtevant AH (1913). The linear arrangement of six sex-linked factors in *Drosophila*, as shown by their mode of association. *Journal of Experimental Zoology*, 14(1):43–59. URL <http://www.esp.org/foundations/genetics/classical/holdings/s/ahs-13.pdf>.
- 2.3. TH M (1917). The theory of the gene. *The American Naturalist*. URL <http://www.esp.org/foundations/genetics/classical/holdings/m/thm-17.pdf>
- 2.4. Scitable: Mapping Genes to Chromosomes
<https://www.nature.com/scitable/topicpage/mapping-genes-to-chromosomes-linkage-and-genetic-377>
- 2.5. Scitable: Thomas Hunt Morgan and Genetic Recombination
<https://www.nature.com/scitable/topicpage/thomas-hunt-morgan-genetic-recombination-and-gene-496>
- 2.6. What is a chromosome? (Bozeman Science)
<https://www.youtube.com/watch?v=tsVHWbXqum8>
- 2.7. Linked Genes (Bozeman Science)
https://www.youtube.com/watch?v=-_UcDhzjOio
- 2.8. Genetic Recombination and Gene Mapping (Bozeman Science)
<https://www.youtube.com/watch?v=TU44tR0hJ8A>
- 2.9. Linkage and Recombination, Genetic maps (MIT OpenCourseWare)
https://www.youtube.com/watch?v=o_ldTvszV4Y
- 2.10. Multiple Loci 1: Linkage Disequilibrium (Ashley Carter) <https://www.youtube.com/watch?v=XoymFI0IIM8>

3. SHORT READ SEQUENCING

- 3.1. ► Goodwin S, McPherson JD, and McCombie WR (2016). Coming of age: ten years of next-generation sequencing technologies. *Nature Reviews Genetics*, 17(6):333–351. URL <http://dx.doi.org/10.1038/nrg.2016.49> ***NOTE: Focus on Illumina, PacBio, and Nanopore
- 3.2. van Dijk EL, Auger H, Jaszczyszyn Y, and Thermes C (2014). Ten years of next-generation sequencing technology. *Trends in Genetics*, 30(9):418–426. URL <http://dx.doi.org/10.1016/j.tig.2014.07.001>
- 3.3. How does Sanger Sequencing Work? <http://www.youtube.com/watch?v=e2G5zx-OJlw>
- 3.4. Illumina Sequencing by Synthesis: <http://www.youtube.com/watch?v=fCd6B5HRaZ8>
- 3.5. 1st, 2nd, and 3rd Generation Genome Sequencing Technologies https://www.youtube.com/watch?v=_ApDinCBt8

4. ASSEMBLING GENOMES AND TRANSCRIPTOMES

- 4.1. ► Sohn Ji and Nam JW (2016). The present and future of *de novo* whole-genome assembly. *Briefings in Bioinformatics*, bbw096. URL <http://dx.doi.org/10.1093/bib/bbw096>
- 4.2. Baker M (2012). *De novo* genome assembly: what every biologist should know. *Nature Methods*, 9(4):333–337. URL <http://dx.doi.org/10.1038/nmeth.1935>
- 4.3. Birney E (2011). Assemblies: the good, the bad, the ugly. *Nature Methods*, 8(1):59–60. URL <http://dx.doi.org/10.1038/nmeth0111-59>
- 4.4. Fan W and Li R (2012). Test driving genome assemblers. *Nature Biotechnology*, 30(4):330–331. URL <http://dx.doi.org/10.1038/nbt.2172>
- 4.5. Debruijn Graphs and Eulerian Walks (Ben Langmead) <https://www.youtube.com/watch?v=TNYZZKrkjCSk>
- 4.6. Genome Assembly (MIT OpenCourseware) <https://www.youtube.com/watch?v=ZYW2AeDE6wU>
- 4.7. Introduction to genome assembly (Mihai Pop) <https://www.youtube.com/watch?v=kxEsN4seqPY>
- 4.8. Genome Assembly (Niema Moshiri) <https://www.youtube.com/watch?v=bPVIbO7UI3k>
- 4.9. How the Königsberg bridge problem changed mathematics (TedED) <https://www.youtube.com/watch?v=nZwSo4vfw6c>

5. SEQUENCE ALIGNMENT AND GENOME MAPPING

- 5.1. ► Pfeifer SP (2016). From next-generation resequencing reads to a high-quality variant data set. *Heredity*, 118(2):111–124. URL <http://dx.doi.org/10.1038/hdy.2016.102>
- 5.2. ► 1000 Human Genomes Consortium (2012). An integrated map of genetic variation from 1,092 human genomes. *Nature*, 491(7422):56–65. URL <http://dx.doi.org/10.1038/nature11632>
- 5.3. 1000 Human Genomes Consortium (2015). An integrated map of structural variation in 2,504 human genomes. *Nature*, 526(7571):75–81. URL <http://dx.doi.org/10.1038/nature15394>
- 5.4. Trapnell C and Salzberg SL (2009). How to map billions of short reads onto genomes. *Nature Biotechnology*, 27(5):455–457. URL <http://dx.doi.org/10.1038/nbt0509-455>
- 5.5. Library Complexity and Short Read Alignment (MIT) <https://www.youtube.com/watch?v=P3ORBMon8aw>
- 5.6. Suffix Tries and Trees (Ben Langmead) <https://www.youtube.com/watch?v=hLsrPsFHPcQ>
- 5.7. Burrows-Wheeler Transform (Ben Langmead) <https://www.youtube.com/watch?v=4n7NPk5lwbI>

6. RNA-SEQ AND DIFFERENTIAL EXPRESSION

- 6.1. ► Conesa A, Madrigal P, Tarazona S, Gomez-Cabrero D, Cervera A, McPherson A, Szczeńniak MW, Gaffney DJ, Elo LL, Zhang X, *et al.* (2016). A survey of best practices for RNA-seq data analysis. *Genome Biology*, 17(1). URL <http://dx.doi.org/10.1186/s13059-016-0881-8>

- 6.2. ► The GTEx Consortium (2015). The Genotype-Tissue Expression (GTEx) pilot analysis: multi-tissue gene regulation in humans. *Science*, 348(6235):648–660. URL <http://dx.doi.org/10.1126/science.1262110>
- 6.3. RNASeqLopedia <https://rnaseq.uoregon.edu/>
- 6.4. Introduction to RNA Sequencing <https://www.youtube.com/watch?v=Ji9nFCYI7Bk>

7. STUDENT CHOICE PAPERS

- 7.1. Jarvis DE, Ho YS, Lightfoot DJ, Schmöckel SM, Li B, Borm TJA, Ohyanagi H, Mineta K, Michell CT, Saber N, *et al.* (2017). The genome of *Chenopodium quinoa*. *Nature*, 542(7641):307–312. URL <http://dx.doi.org/10.1038/nature21370>
- 7.2. Ariey F, Witkowski B, Amaratunga C, Beghain J, Langlois AC, Khim N, Kim S, Duru V, Bouchier C, Ma L, *et al.* (2014). A molecular marker of artemisinin-resistant *Plasmodium falciparum* malaria. *Nature*, 505(7481):50–55. URL <http://dx.doi.org/10.1038/nature12876>
- 7.3. Berasategui A, Salem H, Paetz C, Santoro M, Gershenzon J, Kaltenpoth M, and Schmidt A (2017). Gut microbiota of the pine weevil degrades conifer diterpenes and increases insect fitness. *Molecular Ecology*, 26(15):4099–4110. URL <http://dx.doi.org/10.1111/mec.14186>
- 7.4. Lenz PRN, Beaulieu J, Mansfield SD, Clément S, Despots M, and Bousquet J (2017). Factors affecting the accuracy of genomic selection for growth and wood quality traits in an advanced-breeding population of black spruce (*Picea mariana*). *BMC Genomics*, 18(1). URL <http://dx.doi.org/10.1186/s12864-017-3715-5>
- 7.5. Dutheil JY, Munch K, Nam K, Mailund T, and Schierup MH (2015). Strong selective sweeps on the x chromosome in the human-chimpanzee ancestor explain its low divergence. *PLoS Genetics*, 11(8):e1005451. URL <http://dx.doi.org/10.1371/journal.pgen.1005451>
- 7.6. Savage JE, Jansen PR, Stringer S, Watanabe K, Bryois J, de Leeuw CA, Nagel M, Awasthi S, Barr PB, Coleman JRI, *et al.* (2018). Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. *Nature Genetics*, 50(7):912–919. URL <http://dx.doi.org/10.1038/s41588-018-0152-6> (Read while in pre-print on *bioRxiv*)
- 7.7.
- 7.8. Hacquard S, Kracher B, Hiruma K, Münch, Garrido-Oter R, Thon MR, Weimann A, Damm U, Dallery JF, Hainaut M, *et al.* (2016). Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. *Nature Communications*, 7(1). URL <http://dx.doi.org/10.1038/ncomms11362>
- 7.9. Letourneau A, Santoni FA, Bonilla X, Sailani MR, Gonzalez D, Kind J, Chevalier C, Thurman R, Sandstrom RS, Hibaoui Y, *et al.* (2014). Domains of genome-wide gene expression dysregulation in Down’s syndrome. *Nature*, 508(7496):345–350. URL <http://dx.doi.org/10.1038/nature13200>
- 7.10. Daron J and Slotkin RK (2017). EpiTEome: Simultaneous detection of transposable element insertion sites and their DNA methylation levels. *Genome Biology*, 18(1). URL <http://dx.doi.org/10.1186/s13059-017-1232-0>
- 7.11. Chandrasekhara C, Mohannath G, Blevins T, Pontvianne F, and Pikaard CS (2016). Chromosome-specific NOR inactivation explains selective rRNA gene silencing and dosage control in *Arabidopsis*. *Genes & Development*. URL <http://dx.doi.org/10.1101/gad.273755.115>
- 7.12. Lippert C, Sabatini R, Maher MC, Kang EY, Lee S, Arikan O, Harley A, Bernal A, Garst P, Lavrenko V, *et al.* (2017). Identification of individuals by trait prediction using whole-genome sequencing data. *Proceedings of the National Academy of Sciences*, 114(38):10166–10171. URL <http://dx.doi.org/10.1073/pnas.1711125114>
- 7.13. Mendizabal I, Shi L, Keller TE, Konopka G, Preuss TM, Hsieh TF, Hu E, Zhang Z, Su B, and Yi SV (2016). Comparative methylome analyses identify epigenetic regulatory loci of human brain evolution. *Molecular Biology and Evolution*, 33(11):2947–2959. URL <http://dx.doi.org/10.1093/molbev/msw176>

- 7.14. Liu S, Lorenzen ED, Fumagalli M, Li B, Harris K, Xiong Z, Zhou L, Korneliussen TS, Somel M, Babbitt C, *et al.* (2014). Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. *Cell*, 157(4):785–794. URL <http://dx.doi.org/10.1016/j.cell.2014.03.054>
- 7.15. Zanini F, Brodin J, Thebo L, Lanz C, Bratt G, Albert J, and Neher RA (2015). Population genomics of inpatient HIV-1 evolution. *eLife*, 4. URL <http://dx.doi.org/10.7554/eLife.11282>