Literature curriculum for CCBIO906 Cancer Genomics Course, UIB 2023

Core literature (~ 250 pages)

1. Cortés-Ciriano, I., Gulhan, D.C., Lee, J.JK. et al. Computational analysis of cancer genome sequencing data. Nat Rev Genet (2021). https://doi.org/10.1038/s41576-021-00431-y
2. Li, Y., Roberts, N.D., Wala, J.A. et al. Patterns of somatic structural variation in human cancer genomes. Nature (2020). https://doi.org/10.1038/s41586-019-1913-9
3. McDermott U, Downing J, Stratton M. Genomics and the continuum of cancer care. N Engl J Med (2011). http://dx.doi.org/10.1056/NEJMra0907178
4. Biesecker LG, (null) RCG. Diagnostic Clinical Genome and Exome Sequencing. New Engl J Med (2014). http://dx.doi.org/10.1056/NEJMra1312543
5. Byron SA, Van Keuren-Jensen KR, Engelthaler DM, Carpten JD, Craig DW. Translating RNA sequencing into clinical diagnostics: opportunities and challenges. Nat Rev Genet (2016) http://dx.doi.org/10.1038/nrg.2016.10
6. Collisson EA, Cho RJ, Gray JW. What are we learning from the cancer genome? Nat Rev Clin Oncol (2012). http://dx.doi.org/10.1038/nrclinonc.2012.159
7. Lei Y, Tang R, Xu J, Wang W, Zhang B, Liu J, Yu X, Shi S. Applications of single-cell sequencing in cancer research: progress and perspectives. J Hematol Oncol (2021). http://doi.org/10.1186/s13045-021-01105-2
8. Hofree M, Carter H, Kreisberg JF, Bandyopadhyay S, Mischel PS, Friend S, et al. Challenges in identifying cancer genes by analysis of exome sequencing data. Nat Commun. (2016). http://dx.doi.org/10.1038/ncomms12096
9. Gerstung, M., Jolly, C., Leshchiner, I. et al. The evolutionary history of 2,658 cancers. Nature (2020). https://doi.org/10.1038/s41586-019-1907-7
10. Suwinski P, Ong C, Ling MHT, Poh YM, Khan AM, Ong HS. Advancing Personalized Medicine Through the Application of Whole Exome Sequencing and Big Data Analytics. Front Genet (2019). http://doi.org/10.3389/fgene.2019.00049
11. Berger MF, Mardis ER. The emerging clinical relevance of genomics in cancer medicine. Nat Rev Clin Oncol (2018). http://doi.org/10.1038/s41571-018-0002-6
12. Lawrence, R., Watters, M., Davies, C. R., Pantel, K., & Lu, Y. J. (2023). Circulating tumour cells for early detection of clinically relevant cancer. *Nature reviews. Clinical oncology*, *20*(7), 487–500. https://doi.org/10.1038/s41571-023-00781-y
13. Seferbekova, Z., Lomakin, A., Yates, L. R., & Gerstung, M. (2023). Spatial biology of cancer evolution. *Nature reviews. Genetics*, *24*(5), 295–313. https://doi.org/10.1038/s41576-022-00553-x
14. van de Merbel, A. F., van der Horst, G., & van der Pluijm, G. (2021). Patient-derived tumour models for personalized therapeutics in urological cancers. *Nature reviews. Urology*, *18*(1), 33–45. https://doi.org/10.1038/s41585-020-00389-2
15. Aldea, M., Friboulet, L., et al. (2023). Precision medicine in the era of multi-omics: can the data tsunami guide rational treatment decision?. *ESMO open*, *8*(5), https://doi.org/10.1016/j.esmoop.2023.101642

Additional literature (~ 250 pages)

1. Alexandrov, L. B., Kim, J., Haradhvala, N. J., Huang, M. N., (…), PCAWG Consortium (2020). The repertoire of mutational signatures in human cancer. *Nature*, *578*(7793), 94–101. https://doi.org/10.1038/s41586-020-1943-3
2. Van Allen EM, Wagle N, Stojanov P, Perrin DL, Cibulskis K, Marlow S, et al. Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-,
3. embedded tumor samples to guide precision cancer medicine. Nat Med. (2014). http://dx.doi.org/10.1038/nm.3559

4. Gawad C, Koh W, Quake SR. Single-cell genome sequencing: current state of the science. Nat Rev Genet (2016). http://dx.doi.org/10.1038/nrg.2015.16
5. Griffith M, Spies NC, Krysiak K, McMichael JF, Coffman AC, Danos AM, et al. CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nat Genet (2017). http://dx.doi.org/10.1038/ng.3774
6. Harris G, O'Toole S, George P, Browett P, Print C. Massive Parallel Sequencing of Solid Tumours - Challenges and Opportunities for Pathologists. Histopathology (2016). http://dx.doi.org/10.1111/his.13067
7. Kim E, Ilic N, Shrestha Y, Zou L, Kamburov A, Zhu C, et al. Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. Cancer Discovery (2016). http://dx.doi.org/10.1158/2159-8290.CD-16-0160
8. Knoppers BM, Zawati MH, Sénécal K. Return of genetic testing results in the era of whole-genome sequencing. Nat Rev Genet.(2015). http://dx.doi.org/10.1038/nrg3960
9. Koboldt DC, Zhang Q, Larson DE, Shen D, McLellan MD, Lin L, et al. VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Res (2012). http://dx.doi.org/10.1101/gr.129684.111
10. Liu B, Conroy JM, Morrison CD, Odunsi AO, Qin M, Wei L, et al. Structural variation discovery in the cancer genome using next generation sequencing: computational solutions and perspectives. Oncotarget (2015). http://dx.doi.org/10.18632/oncotarget.3491
11. Kurnit KC, Dumbrava EEI, Litzenburger B, et al. Precision Oncology Decision Support: Current Approaches and Strategies for the Future. Clin Cancer Res (2018). http://doi.org/10.1158/1078-0432.CCR-17-2494
12. Meyerson M, Gabriel S, Getz G. Advances in understanding cancer genomes through second-generation sequencing. Nat Rev Genet (2010). http://dx.doi.org/10.1038/nrg2841
13. Nagarajan N, Pop M. Sequence assembly demystified. Nat Rev Genet (2013). http://dx.doi.org/10.1038/nrg3367
14. Shendure J, Aiden EL. The expanding scope of DNA sequencing. Nat Biotechnol (2012). http://dx.doi.org/10.1038/nbt.2421
15. Simonis M, Kooren J, de Laat W. An evaluation of 3C-based methods to capture DNA interactions. Nat Meth (2007). http://dx.doi.org/10.1038/nmeth1114
16. Yang L, Luquette LJ, Gehlenborg N, Xi R, Haseley PS. Diverse Mechanisms of Somatic Structural Variations in Human Cancer Genomes. Cell (2013). http://dx.doi.org/10.1016/j.cell.2013.04.010
17. Zhang X, Marjani SL, Hu Z, Weissman SM, P an X, Wu S. Single-Cell Sequencing for Precise Cancer Research: Progress and Prospects. Cancer Res (2016). http://dx.doi.org/10.1158/0008-5472.CAN-15-1907
18. Borry P, Bentzen HB, Budin-Ljøsne I, Corne MC, Howard HC, Feeney O, et al. The challenges of the expanded availability of genomic information: an agenda-setting paper. J Community Genet (2018). http://dx.doi.org/10.1007/s12687-017-0331-7
19. Paczkowska, M., Barenboim, J., Sintupisut, N. et al. Integrative pathway enrichment analysis of multivariate omics data. Nat Commun (2020). https://doi.org/10.1038/s41467-019-13983-9
20. Lim B, Lin Y, Navin N. Advancing Cancer Research and Medicine with Single-Cell Genomics. Cancer Cell (2020). http://doi.org/10.1016/j.ccell.2020.03.008
21. Nature outlook, 25 March 2020. How cancer genomics is transforming diagnosis and treatment? https://www.nature.com/articles/d41586-020-00845-4
22. Barretina J, Caponigro G, Stransky N, Venkatesan K, Margolin AA, Kim S, et al. The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature (2012) https://doi.org/10.1038/nature11003