

Literature curriculum for CCBio Cancer genomics Course, UiB 2017

Ola Myklebost, K2

1. Alexandrov LB, Nik-Zainal S, Wedge DC, Aparicio SAJR, Behjati S, Biankin AV, et al. Signatures of mutational processes in human cancer. *Nature*. 2013 Aug 14;500(7463):415–21. <http://dx.doi.org/10.1038/nature12477>
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-embedded tumor samples to guide precision cancer medicine. *Nat Med*. Nature Publishing Group; 2014 May 18;20(6):682–8. <http://dx.doi.org/10.1038/nm.3559>
3. 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 Mar 29;483(7391):603–7. <http://dx.doi.org/10.1038/nature11003>
4. Biesecker LG, (null) RCG. Diagnostic Clinical Genome and Exome Sequencing. *New England Journal of Medicine*. 2014 Jun 5;:1–8. <http://dx.doi.org/10.1056/NEJMr1312543>
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 Mar 21;17(5):257–71. <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 Nov;9(11):621–30. <http://dx.doi.org/10.1038/nrclinonc.2012.159>
7. Daber R, Sukhadia S, Morrisette JJD. Understanding the limitations of next generation sequencing informatics, an approach to clinical pipeline validation using artificial data sets. *Cancer Genetics*. Elsevier Inc; 2013 Dec 1;206(12):441–8. <http://dx.doi.org/10.1016/j.cancergen.2013.11.005>
8. Foley SB, Rios JJ, Mgbemena VE, Robinson LS, Hampel HL, Toland AE, et al. Use of Whole Genome Sequencing for Diagnosis and Discovery in the Cancer Genetics Clinic. *EBIOM*. Elsevier B.V; 2014 Dec 18;2(1):1–8. <http://dx.doi.org/10.1016/j.ebiom.2014.12.003>
9. Gawad C, Koh W, Quake SR. Single-cell genome sequencing: current state of the science. *Nat Rev Genet*. Nature Publishing Group; 2016 Jan 25;17(3):175–88. <http://dx.doi.org/10.1038/nrg.2015.16>
10. 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. *Nature Publishing Group*. Nature Publishing Group; 2017 Feb 1;49(2):170–4. <http://dx.doi.org/10.1038/ng.3774>
11. Harris G, O'Toole S, George P, Browett P, Print C. Massive Parallel Sequencing of Solid Tumours - Challenges and Opportunities for Pathologists. *Histopathology*. 2016 Aug 24. <http://dx.doi.org/10.1111/his.13067>
12. Harris TJ, McCormick F. The molecular pathology of cancer. *Nat Med*. Nature Publishing Group. Nature Publishing Group; 2010 Mar 30;7(5):15. <http://dx.doi.org/10.1038/nrclinonc.2010.41>
13. Harrison SM, Riggs ER, Maglott DR, Lee JM, Azzariti DR, Niehaus A, et al. Using ClinVar as a Resource to Support Variant Interpretation. Hoboken, NJ, USA: John Wiley & Sons, Inc; 2001. 73463 p. <http://dx.doi.org/10.1002/0471142905.hg0816s89>
14. 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*. Nature Publishing Group; 1AD;7:1–9. <http://dx.doi.org/10.1038/ncomms12096>
15. Jacoby MA, Duncavage EJ, Walter MJ. Implications of Tumor Clonal Heterogeneity in the Era of Next-Generation Sequencing. *TRENDS in CANCER*. Elsevier Ltd; 2015 Dec 1;1(4):231–41. <http://dx.doi.org/10.1016/j.trecan.2015.10.006>

16. Jones S, Anagnostou V, Anagnostou V, Lytle K, Lytle K, Parpart-Li S, et al. Personalized genomic analyses for cancer mutation discovery and interpretation. *Sci Transl Med*. American Association for the Advancement of Science; 2015 Apr 15;7(283):283ra53–3. <http://dx.doi.org/10.1126/scitranslmed.aaa7161>
17. 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*. American Association for Cancer Research; 2016 Jul;6(7):714–26. <http://dx.doi.org/10.1158/2159-8290.CD-16-0160>
18. Knoppers BM, Zawati MH, Sénécal K. Return of genetic testing results in the era of whole-genome sequencing. *Nat Rev Genet*. Nature Publishing Group; 2015 Aug 4;16(9):553–9. <http://dx.doi.org/10.1038/nrg3960>
19. 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 Mar 1;22(3):568–76. <http://dx.doi.org/10.1101/gr.129684.111>
20. 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 Mar 20;6(8):5477–89. <http://dx.doi.org/10.18632/oncotarget.3491>
21. McDermott U, Downing J, Stratton M. Genomics and the continuum of cancer care. *N Engl J Med*. 2011;364:340–50. <http://dx.doi.org/10.1056/NEJMra0907178>
22. Meric-Bernstam F, Johnson A, Holla V, Bailey AM, Brusco L, Chen K, et al. A decision support framework for genomically informed investigational cancer therapy. *JNCI Journal of the National Cancer Institute*. Oxford University Press; 2015 Jul;107(7):d1v098–8. <http://dx.doi.org/10.1093/jnci/d1v098>
23. Meyerson M, Gabriel S, Getz G. Advances in understanding cancer genomes through second-generation sequencing. *Nat Rev Genet*. 2010 Oct;11(10):685–96. <http://dx.doi.org/10.1038/nrg2841>
24. Nagarajan N, Pop M. Sequence assembly demystified. *Nat Rev Genet*. 2013 Jan 29. 45. <http://dx.doi.org/10.1038/nrg3367>
25. Shendure J, Aiden EL. The expanding scope of DNA sequencing. *Nat Biotechnol*. 2012 Nov;30(11):1084–94. <http://dx.doi.org/10.1038/nbt.2421>
26. Simonis M, Kooren J, de Laat W. An evaluation of 3C-based methods to capture DNA interactions. *Nat Meth*. 2007 Nov;4(11):895–901. <http://dx.doi.org/10.1038/nmeth1114>
27. 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>
28. Zhang X, Marjani SL, Hu Z, Weissman SM, Pan X, Wu S. Single-Cell Sequencing for Precise Cancer Research: Progress and Prospects. *Cancer Res*. 2016 Mar 3;76(6):1305–12. <http://dx.doi.org/10.1158/0008-5472.CAN-15-1907>
29. Pascal Borry, Heidi Beate Bentzen, Isabelle Budin-Ljøsne, Martina C. Corne, Heidi Carmen Howard, Oliver Feeney, Leigh Jackson, Deborah Mascalonzi, Álvaro Mendes, Borut Peterlin, Brigida Riso, Mahsa Shabani, Heather Skirton, Sigrid Sterckx, Danya Vears, Matthias Wjst, Heike Felzmann. The challenges of the expanded availability of genomic information: an agenda-setting paper. *J Community Genet* (2018) 9:103–116 <http://dx.doi.org/10.1007/s12687-017-0331-7>

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