GP References

- [1] Schwamborn K, Caprioli RM (2010) Molecular imaging by mass spectrometry: Looking beyond classical histology. Nat Rev Cancer 10(9):639–646.
- [2] McDonnell LA, Heeren RMA (2007) Imaging mass spectrometry. Mass Spectrom Rev 26(4):606–643.
- [3] Aichler M, Walch A (2015) MALDI imaging mass spectrometry: Current frontiers and perspectives in pathology research and practice. Lab Invest 95(4):422–431.
- [4] Addie RD, Balluff B, Bovée JVMG, Morreau H, McDonnell LA (2015) Current state and future challenges of mass spectrometry imaging for clinical research. Anal Chem 87(13):6426–6433.
- [5] Deininger S-O, Ebert MP, Fütterer A, Gerhard M, Röcken C (2008) MALDI imaging combined with hierarchical clustering as a new tool for the interpretation of complex human cancers. J Proteome Res 7(12):5230–5236.
- [6] Balluff B, et al. (2015) De novo discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. J Pathol 235(1):3–13.
- [7] van der Maaten LJP, Hinton GE (2008) Visualizing high-dimensional data using t-SNE. J Mach Learn Res 9:2579–2605.
- [8] Mahfouz A, et al. (2015) Visualizing the spatial gene expression organization in the brain through non-linear similarity embeddings. Methods 73:79–89.
- [9] Ji S (2013) Computational genetic neuroanatomy of the developing mouse brain: Dimensionality reduction, visualization, and clustering. BMC Bioinformatics 14:222.
- [10] Fonville JM, et al. (2013) Hyperspectral visualization of mass spectrometry imaging data. Anal Chem 85(3):1415–1423.
- [11] van der Maaten L (2014) Accelerating t-SNE using tree-based algorithms. J Mach Learn Res 15:3221–3245.
- [12] Shekhar K, Brodin P, Davis MM, Chakraborty AK (2014) Automatic Classification of Cellular Expression by Nonlinear Stochastic Embedding (ACCENSE). Proc Natl Acad Sci USA 111(1):202–207.
- [13] Steinbach M, Karypis G, Kumar V (2000) A Comparison of Document Clustering Techniques (University of Minnesota, Minneapolis), Tech Rep 00-034.
- [14] Canny J (1986) A computational approach to edge detection. IEEE Trans Pattern Anal Mach Intell 8(6):679–698.
- [15] Tusher VG, Tibshirani R, Chu G (2001) Significance analysis of microarrays applied to the ionizing radiation response. Proc Natl Acad Sci USA 98(9):5116–5121.
- [16] Duda RO, Hart PE, Stork DG (2012) Pattern Classification (Wiley, New York).
- [17] Youden WJ (1950) Index for rating diagnostic tests. Cancer 3(1):32–35.
- [18] Greaves M, Maley CC (2012) Clonal evolution in cancer. Nature 481(7381):306–313.
- [19] Murugaesu N, Chew SK, Swanton C (2013) Adapting clinical paradigms to the challenges of cancer clonal evolution. Am J Pathol 182(6):1962–1971.
- [20] Jones EA, et al. (2011) Multiple statistical analysis techniques corroborate intratumor heterogeneity in imaging mass spectrometry datasets of myxofibrosarcoma. PLoS One 6(9):e24913.
- [21] Willems SM, et al. (2010) Imaging mass spectrometry of myxoid sarcomas identifies proteins and lipids specific to tumour type and grade, and reveals biochemical intratumour heterogeneity. J Pathol 222(4):400–409.
- [22] Dzyubachyk O, et al. (2013) Automated algorithm for reconstruction of the complete spine from multistation 7T MR data. Magn Reson Med 69(6):1777–1786.
- [23] Seol H, et al. (2012) Intratumoral heterogeneity of HER2 gene amplification in breast cancer: Its clinicopathological significance. Mod Pathol 25(7):938–948.
- [24] Maley CC, et al. (2006) Genetic clonal diversity predicts progression to esophageal adenocarcinoma. Nat Genet 38(4):468–473.
- [25] Gerlinger M, et al. (2012) Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. N Engl J Med 366(10):883–892.
- [26] Dalerba P, et al. (2011) Single-cell dissection of transcriptional heterogeneity in human colon tumors. Nat Biotechnol 29(12):1120–1127.