

cancer

October 12, 2009

References

- [1] A. H. Bild, G. Yao, J. T. Chang, Q. Wang, A. Potti, D. Chasse, M. B. Joshi, D. Harpole, J. M. Lancaster, A. Berchuck, Jr. Olson, J. A., J. R. Marks, H. K. Dressman, M. West, and J. R. Nevins. Oncogenic pathway signatures in human cancers as a guide to targeted therapies. *Nature*, 439(7074):353–7, 2006.
- [2] P. Boyle and J. Ferlay. Cancer incidence and mortality in europe, 2004. *Ann. Oncol.*, 16(3):481–488, Mar 2005.
- [3] Tara M Breslin, Fushen Xu, Gregory M Palmer, Changfang Zhu, Kennedy W Gilchrist, and Nirmala Ramanujam. Autofluorescence and diffuse reflectance properties of malignant and benign breast tissues. *Ann Surg Oncol*, 11(1):65–70, Jan 2004.
- [4] Ruey-Feng Chang, Wen-Jie Wu, Woo Kyung Moon, and Dar-Ren Chen. Improvement in breast tumor discrimination by support vector machines and speckle-emphasis texture analysis. *Ultrasound Med Biol*, 29(5):679–86, May 2003.
- [5] Ruey-Feng Chang, Wen-Jie Wu, Woo Kyung Moon, and Dar-Ren Chen. Automatic ultrasound segmentation and morphology based diagnosis of solid breast tumors. *Breast Cancer Res Treat*, 89(2):179–85, Jan 2005.
- [6] S. F. Chin, A. E. Teschendorff, J. C. Marioni, Y. Wang, N. L. Barbosa-Morais, N. P. Thorne, J. L. Costa, S. E. Pinder, M. A. van de Wiel, A. R. Green, I. O. Ellis, P. L. Porter, S. Tavaré, J. D. Brenton, B. Ylstra, and C. Caldas. High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. *Genome Biol.*, 8(10):R215, 2007.
- [7] S.-F. Chin, Y. Wang, N. P. Thorne, A. E. Teschendorff, S. E. Pinder, M. Vias, A. Naderi, I. Roberts, N. L. Barbosa-Morais, M. J. Garcia, N. G. Iyer, T. Kranjac, J. F. R. Robertson, S. Aparicio, S. Tavaré, I. Ellis, J. D. Brenton, and C. Caldas. Using array-comparative genomic hybridization to define molecular portraits of primary breast cancers. *Oncogene*, 26(13):1959–1970, September 2006.

- [8] H.-Y. Chuang, E. Lee, Y.-T. Liu, D. Lee, and T. Ideker. Network-based classification of breast cancer metastasis. *Mol. Syst. Biol.*, 3:140, 2007.
- [9] I. El-Naqa, Y. Yang, N. P. Galatsanos, R. M. Nishikawa, and M. N. Wernick. A similarity learning approach to content-based image retrieval: application to digital mammography. *IEEE Trans Med Imaging*, 23(10):1233–44, Oct 2004.
- [10] Hong Guo, Lindsay B Jack, and Asoke K Nandi. Feature generation using genetic programming with application to fault classification. *IEEE Trans Syst Man Cybern B Cybern*, 35(1):89–99, Feb 2005.
- [11] B. Gusterson. Do 'basal-like' breast cancers really exist? *Nat. Rev. Cancer*, 9(2):128–134, Feb 2009.
- [12] B. A. Gusterson, D. T. Ross, V. J. Heath, and T. Stein. Basal cytokeratins and their relationship to the cellular origin and functional classification of breast cancer. *Breast Cancer Res.*, 7(4):143–148, 2005.
- [13] B. Haibe-Kains, C. Desmedt, F. Piette, M. Buyse, F. Cardoso, L. Van't Veer, M. Piccart, G. Bontempi, and C. Sotiriou. Comparison of prognostic gene expression signatures for breast cancer. *BMC Genomics*, 9:394, 2008.
- [14] C. Jones, E. Ford, C. Gillett, K. Ryder, S. Merrett, J. S. Reis-Filho, L. G. Fulford, A. Hanby, and S. R. Lakhani. Molecular cytogenetic identification of subgroups of grade iii invasive ductal breast carcinomas with different clinical outcomes. *Clin. Cancer Res.*, 10(18):5988–5997, 2004.
- [15] Zsofia Kote-Jarai, Richard D Williams, Nicola Cattini, Maria Copeland, Ian Giddings, Richard Wooster, Robert H tePoele, Paul Workman, Barry Gusterson, John Peacock, Gerald Gui, Colin Campbell, and Ros Eeles. Gene expression profiling after radiation-induced DNA damage is strongly predictive of BRCA1 mutation carrier status. *Clin. Cancer Res.*, 10(3):958–63, Feb 2004.
- [16] J. Listgarten, S. Damaraju, B. Poulin, L. Cook, J. Dufour, A. Driga, J. Mackey, D. Wishart, R. Greiner, and B. Zanke. Predictive Models for Breast Cancer Susceptibility from Multiple Single Nucleotide Polymorphisms. *Clin. Cancer Res.*, 10(8):2725–2737, 2004.
- [17] H. X. Liu, R. S. Zhang, F. Luan, X. J. Yao, M. C. Liu, Z. D. Hu, and B. T. Fan. Diagnosing breast cancer based on support vector machines. *J. Chem. Inf. Comput. Sci.*, 43(3):900–7, 2003.
- [18] T. Mattfeldt, H. A. Kestler, and H. P. Sinn. Prediction of the axillary lymph node status in mammary cancer on the basis of clinicopathological data and flow cytometry. *Med Biol Eng Comput*, 42(6):733–9, Nov 2004.

- [19] Tim W Nattkemper, Bert Arnrich, Oliver Lichte, Wiebke Timm, Andreas Degenhard, Linda Pointon, Carmel Hayes, Martin O Leach, and The UK MARIBS Breast Screening Study. Evaluation of radiological features for breast tumour classification in clinical screening with machine learning methods. *Artif. Intell. Med.*, 34(2):129–39, Jun 2005.
- [20] C M. Perou, T. Sørli, M. B. Eisen, M. van de Rijn, S. S. Jeffrey, C. A. Rees, J. R. Pollack, D. T. Ross, H. Johnsen, L. A. Akslen, O. Fluge, A. Pergamenschikov, C. Williams, S. X. Zhu, P. E. Lønning, A. L. Børresen-Dale, P. O. Brown, and D. Botstein. Molecular portraits of human breast tumours. *Nature*, 406(6797):747–752, Aug 2000.
- [21] T. Sørli, C. M. Perou, R. Tibshirani, T. Aas, S. Geisler, H. Johnsen, T. Hastie, M. B. Eisen, M. van de Rijn, S. S. Jeffrey, T. Thorsen, H. Quist, J. C. Matese, P. O. Brown, D. Botstein, P. Eystein Lønning, and A. L. Børresen-Dale. Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications. *Proc. Natl. Acad. Sci. USA*, 98(19):10869–10874, Sep 2001.
- [22] A. I. Su, J. B. Welsh, L. M. Sapinoso, S. G. Kern, P. Dimitrov, H. Lapp, P. G. Schultz, S. M. Powell, C. A. Moskaluk, H. F. Jr. Frierson, and G. M. Hampton. Molecular Classification of Human Carcinomas by Use of Gene Expression Signatures. *Cancer Res.*, 61(20):7388–7393, 2001.
- [23] E. van Beers and P. Nederlof. Array-CGH and breast cancer. *Breast Cancer Research*, 8(3):210, 2006.
- [24] M. J. van de Vijver, Y. D. He, L. J. van't Veer, H. Dai, A. A. M. Hart, D. W. Voskuil, G. J. Schreiber, J. L. Peterse, C. Roberts, M. J. Marton, M. Parrish, D. Atsma, A. Witteveen, A. Glas, L. Delahaye, T. van der Velde, H. Bartelink, S. Rodenhuis, E. T. Rutgers, S. H. Friend, and R. Bernards. A gene-expression signature as a predictor of survival in breast cancer. *N. Engl. J. Med.*, 347(25):1999–2009, Dec 2002.
- [25] L. J. van 't Veer, H. Dai, M. J. van de Vijver, Y. D. He, A. A. M. Hart, M. Mao, H. L. Peterse, K. van der Kooy, M. J. Marton, A. T. Witteveen, G. J. Schreiber, R. M. Kerkhoven, C. Roberts, P. S. Linsley, R. Bernards, and S. H. Friend. Gene expression profiling predicts clinical outcome of breast cancers. *Nature*, 415(6871):530–536, Jan 2002.
- [26] A. Vincent-Salomon, C. Lucchesi, N. Gruel, V. Raynal, G. Pierron, R. Goudefroye, F. Reyat, F. Radvanyi, R. Salmon, J.-P. Thiery, X. Sastre-Garau, B. Sigal-Zafrani, A. Fourquet, and A. Delattre. Integrated genomic and transcriptomic analysis of ductal carcinoma in situ of the breast. *Clin. Cancer Res.*, 14(7):1956–1965, Apr 2008.
- [27] Y. Wang, J.G.M. Klijn, Y. Zhang, A.M. Sieuwerts, M.P. Look, F. Yang, D. Talantov, M. Timmermans, M.E. Meijer-van Gelder, J. Yu, T. Jatkoe, E.M.J.J. Berns, D. Atkins, and J.A. Foekens. Gene-expression profiles to

predict distant metastasis of lymph-node-negative primary breast cancer. *Lancet*, 365(9460):671–679, 2005.

- [28] S. R. Wellings and H. M. Jensen. On the origin and progression of ductal carcinoma in the human breast. *J. Natl. Cancer Inst.*, 50(5):1111–1118, May 1973.