

Molecular Diagnosis

(Part II)

F. Markowetz

*Department of Computational Molecular Biology
Max Planck Institute for Molecular Genetics
Berlin, Germany*

The second lecture on classification will deal with feature selection (filter and shrinkage methods); classification by Nearest Shrunken centroids (Tibshirani et al., 2002); model selection and assessment (Hastie et al., 2001, ch.7); pitfalls in model selection (Simon et al., 2003; Ambroise and McLachlan, 2002); and interpretation of results (Ein-Dor et al., 2005).

References:

- [1] **Ch. Ambroise and G. J. McLachlan.** *Selection bias in gene extraction on the basis of microarray gene-expression data.* Proc. Natl. Acad. Sci. USA, **99**(2002), 6562-6566. URL <http://dx.doi.org/10.1073/pnas.102102699>.
- [2] **L. Ein-Dor, I. Kela, G. Getz, D. Givol, and E. Domany.** *Outcome signature genes in breast cancer: is there a unique set?* Bioinformatics, **21**(2005), 171-178. URL <http://dx.doi.org/10.1093/bioinformatics/bth469>.
- [3] **T. Hastie, R. Tibshirani, and J. Friedman.** *The Elements of Statistical Learning.* Springer, 2001. URL <http://www-stat.stanford.edu/tibs/ElemStatLearn/>.
- [4] **R. Simon, M. D. Radmacher, K. Dobbin, and L. M. McShane.** *Pitfalls in the use of DNA microarray data for diagnostic and prognostic classification.* J Natl Cancer Inst, **95**(2003), 14-18.
- [5] **R. Tibshirani, T. Hastie, B. Narasimhan, and G. Chu.** *Diagnosis of multiple cancer types by shrunken centroids of gene expression.* Proc Natl Acad Sci USA, **99**(2002), 6567-6572. URL <http://dx.doi.org/10.1073/pnas.082099299>.